

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...264

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2467:

AATCGGATGG	TAAATGGCT	GTCAATGAAT	GGGTTGATGG	TGGACGTTAT	TATGTTGGCG	60
CTGACGGAGT	TTGGAAGGAA	GGTCAAGCAA	GTACAGTTTC	TTCTAGTAAT	GATAGCAATA	120
GTGAATATTT	CTGCTGCTTT	AGGAAAGGCA	AAAAGTTATA	ATTCGTTATT	CCACATGTCA	180
AAAAAACGTA	TGTATAGACA	ATTAACCTCT	GATTTTGATA	AATTTTCAAA	TGATGCAGCT	240
CAATATGCCA	TTGATCATT	AGAT				264

(2) INFORMATION FOR SEQ ID NO:2468:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1134 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2468:

AAACGGATGG	TACCGCGTGT	CAACGCTCCG	AGTGGAGTTT	TTGGCATGTG	GTTTTCTTTT	60
TATCTACGAG	AGACTGATGG	AGGAAATATG	TCAACTATTG	AAGAACAATT	AAAAGCGCTT	120
CGCGAAGAAA	CGCTGGCTAG	CTTGAAGCAG	ATTACTGCTG	GAAATGAAAA	AGAGATGCAA	180
GATTTGCGTG	TCTCTGTCC	TGGTAAAAAG	GGTTCGCTCA	CTGAAATCCT	CAAAGGGATG	240
AAAGATGTTT	CTGCTGAGAT	GCGTCCAATC	ATCGGGAAAC	ACGTCAATGA	AGCTCGTGAT	300
GTCTTGACTG	CTGCTTTTGA	AGAAACAGCT	AAGCTCTTGG	AAGAAAAGAA	AGTCGCGGCT	360
CAACTGGCTA	GCGAGAGTAT	CGATGTGACG	CTTCCAGGTC	GTCCAGTTGC	GACTGGTCAC	420
CGTCACGTTT	TGACACAAAC	CAGTGAAGAA	ATCGAAGATA	TCTTCATCGG	TATGGGTTAT	480
CAAGTCGTGG	ATGGTTTTGA	AGTGGAGCAA	GACTACTATA	ACTTTGAACG	TATGAACCTT	540
CCAAAAGACC	ACCCAGCTCG	TGATATGCAG	GATACTTTCT	ATATCACTGA	AGAAATCTTG	600
CTCCGTACCC	ACACGTCTCC	AGTTCAGGCG	CGTGCTATGG	ATGCCCATGA	TTTTTCTAAA	660
GGTCCTTTGA	AGATGATCTC	GCCAGGGCGT	GTCTTCCGTC	GCGATACGGA	CGATGCGACC	720
CACAGTCACC	AATTCACCA	AATCGAAGGC	TTGGTAGTTG	GGAAAAATAT	CTCTATGGCT	780
GATCTTCAAG	GAACGCTTCA	GTTGATTGTC	CAAAAAATGT	TTGGTGAAGA	GCGTCAAATT	840
CGTTTGCGTC	CATCTTACTT	CCCATTACACA	GAGCCATCTG	TTGAGGTGGA	TGTTTCTTGC	900
TTCAAGTGTG	GTGGAGAAGG	CTGTAATATA	TGTAAGAAAA	CAGGTTGGAT	CGAAATTATG	960
GGGGCCGGTA	TGGTTCACCC	ACGTGTCCTT	GAAATGAGTG	GTATCGATGC	GA CTGTATAC	1020
TCTGGCTTTG	CCTTTGGTCT	TGGACAAGAG	CGTGTAGCTA	TGCTCCGTTA	TGGAATCAAC	1080
GATATCCGTG	GATTCTACCA	AGGAGATGTC	CGCTTCTCAG	AACAGTTTAA	ATAA	1134

(2) INFORMATION FOR SEQ ID NO:2469:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 354 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...354
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2469:

ACCATTGTGG TGAACACGAG CCATTTATCA AATTGTCCAA AATGTAAGTC AGAATATGTC	60
TACGAAGACG GTGCCCTACT GGTTCGCCCA GAGTGTGCTC ATGAGTGGAA TCCTGCTGAA	120
GTTGCAGAAAG TAGAAGAAGG TCTTGTCGCT ATCGATGCCA ACGGAAATAA ATTGGCTGAT	180
GGTGATATAG TAACTCTCAT CAAGGACTTG AAAGTAAAAG GTGCGCCAAA AGATTTGAAA	240
CAAGGGACGC GCGTGAAAAA TATCCGCATC GTAGAAGGCG ACCACAATAT CGACTGTAAG	300
ATTGATGTTT TTGGTGCCAT GAAACTTAAA TCAGAGTTTG TGAGGAAGAT TTAA	354

(2) INFORMATION FOR SEQ ID NO:2470:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 402 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...402
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2470:

CGGTTGCGTG TTAAGAGGCT TGTTATGAN CACTCAATGG CTCGGCACCT CGGTGCAGTA	60
TATAATTTGC CACATGGTGT TTGCTGTGCC ATGTTGCTAC CAGTTATAGA GCGTGAAAAT	120
GCTAAACGTG TACCAGAAGC TTTCCGCAAT GTTGCCAAAG CCTTGGGACT TCATGTAGAA	180
GGTAAATCAG ATCAAGAAATG TGCCGATTAT GCGATTGTTG AGATTGAGAA GCTTTCTGAG	240
ACAGTAGGTA TTCCTAAGAA ACTGACTGAA CTTGGTATTG AAGAAAAAGA TTTCGACTTT	300
GAATACCTTT CTAAGAATGC CTTGATTGAT GCCTGCGCAC CAGGAAATCC ATTTATGCCA	360

(2) INFORMATION FOR SEQ ID NO:2471:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 894 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...894

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2471:

AACGTCGTGG	TGCAAGAAAA	AATAATTGTG	ATTGTTGGAC	CGACTGCTGT	TGGAAAGACG	60
GCTCTAGCTA	TTGAAGTTGC	AAAGCGTTTT	AATGGCGAAG	TGGTTAGTGG	AGATAGCCAG	120
CAAGTCTATC	GAGGACTTGA	TATTGGGACG	GCCAAGGCTA	GTCCAGAAGA	GCAGGCAGCT	180
GTTCCTCATC	ATTTAATCGA	TGTTAGAGAG	ATAACCGAGT	CTTACTCGGC	TTTTGATTTT	240
GTTTCAGAA	CTAAGATGAC	TATTGAGGGT	ATTCAACAAC	GTGGCAAGCT	AGCCATTATC	300
GCCGGTGGGA	CTGGACTTTA	TATCCAGAGC	TTGCTAAAAG	GTTACCACCT	AGGTGGGGAG	360
ACTCCTCATG	AGGAGATTTT	AGCTTATCGA	GCTAGTTTGG	AGCCATATTC	AGATGAGGAA	420
TTAGCCCATT	TGGTGGAGCA	AGCAGGCCCT	GAGATTCCCC	AGTTTAATCG	TCGTCGTGCT	480
ATGCGTGCCT	TAGAAATTGC	CCATTTTGGT	CAGGATTTGG	AAAATCAAGA	GATCTTGTAT	540
GAACCGCTGA	TTATCTGCTT	GGATGATGAA	CGTAGTCAAC	TTTATGAGCG	TATCAACCAC	600
CGAGTGGATT	TGATGTTTGA	GGCTGGGCTT	TTGGATGAGG	CCAAGTGGCT	GTTTGACCAT	660
TCCCTAATG	TACAGGCTGC	TAAAGGAATT	GGCTATAAGG	AACTCTTTCC	TTATTTCCGT	720
GGAGAGCAGA	CCTTTGAGGA	AGCTCGTGAG	AGTCTTAATC	AGGCGACCCG	TCGTTTTGCC	780
AAGCGTCAGC	TGACCTGGTT	CCGTAATCGC	ATGCTGGTCA	CCTTTTATCA	TATTGGAGAA	840
TCTGGTGTAC	AAGACCGCAT	TTTAAGCCAG	ATAGAGGAGT	CTTTAGATGA	TTGA	894

(2) INFORMATION FOR SEQ ID NO:2472:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2472:

TTTCTAGTGG TAAAGTTGTT TGATTTGTGT TATAGTGAAT ATGCATGGGA TAGCCTTTCT	60
AAATGGTTTA TTAAGCAATT CTATTTTACC AAGACTATCG TAACCATGCA AAAAAGCAAC	120
GGCAAATCCG TTGCCTTTTT TGGATATAAG AGACTATTGT CCCAGACTCT TTTCTTTGTA	180
TAA	183

(2) INFORMATION FOR SEQ ID NO:2473:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1011 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1011

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2473:

GAATCATCGG TAGTCTCGTC TTTATCCTAC TTCTCTGGAG AGGGGGACGA AAAGATGCAG	60
ACTAAAAGCA AACATACCAA GCTCTTCTGG ATTCTCATT A TTCTTGCCAT CGGAGCTTGT	120
CTTCTCTACT TTTGGCCCAT CACTCACCTG TCAGCCTTTG CTTGGAAGTT GCGTTCCTCA	180
AAGATCATCG TTTATCTCTT GGTAGCCATC GCGACTGGGA TTTCGACCAT TAGTTTTCAA	240
ACCGTGACGG AAAATCGCTT CCTGACGCCT AGTATTTTGG GAATTGAATC CTTCTACGTC	300
CTACTACAAA CCCTACTACT GGTTTTTTGAA AGCAAGTTTC TTCAACTTGG CAAATCCCCT	360
ATCTTAGAAT TCCTAGTCTT ACTTCTTGTC CAGTCCCCTC TCTTTCTCGC CTTACAAGGT	420
TACTTGAAGA CACTGATGAA GCAAGACCTG GTCTTCATCC TGCTGATCTG TCTAGCGCTC	480
AGAAGTCTCT TTCGAAATAT CAGCACCTTC CTTCAAGTCC TAATGGATCC AAACGAATAC	540
GATAAACTGC AAAATAGTCT TTTTGCCTCC TTTCAACATC TCAACACTTC CATCCTAGCC	600
ATCGGTTCTC TGATCATCCT CGCTTTGACA ATCTTTTTCT TTCGAAAAGC AGTCGTTCTA	660
GATGTCTTGC ACCTGCAAAG AGAAACGGCT CAGATATTGG GACTCGATGT TGAAAAAGAA	720
CAGAAAGAGC TCCTCTGGGG AATCGTGCTT TTGACCTCAA CGGCCACTGC CTTGGTAGGA	780
CCTATGGCCT TCTTCGGCTT TATGCTGGCC AACCTCACCT ACCTGATTGT CAAAGACTAT	840
CAGCACAAGT TACTCTTTAT AGTGGCCATT CTGATTGGAT TTATTAGCTT AACCTTGGGG	900
CAAGCCTTGA TTGAACGAGT CTTTGCACCT GAAATTCGTA TCAGTATGAT CATTGAGAGT	960
GTGGGTGGCT TCTTATTCTT TATCTTACTA TATAGGAGGG CTCGTCAGTG A	1011

(2) INFORMATION FOR SEQ ID NO:2474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2474:

TGTATCCCGG	TTAACGAAAG	TTTTGGACTT	ATACTCTCCG	AAAATGCTCT	TCAAACCGAC	60
GTCAACGTCG	CCTTGCCGTG	CGTATGGTTA	CTGAATACGT	CAGTTCTATC	CACAACCTCA	120
AAACAGTGTT	TTGAGCAATC	TGCGGCTAGT	TTCCTAGTTT	GCTCTTTGAT	TTTCATTGAG	180
TACTAA						186

(2) INFORMATION FOR SEQ ID NO:2475:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 447 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...447

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2475:

GTGGAAACGG	TCAAGCGTTT	GAGAAAGTAT	CCCAAGATTG	AGATTGTTTC	CCATTTGATC	60
AATGGTTTGC	CTGGTGAAAC	CCATGAGATG	ATGGTTGAAA	ATGTCCGCCG	TTGTGTCACG	120
AATAACGATA	TTCAAGGGAT	TAAACTGCAT	TTGCTCCATC	TTATGACAAA	TACTCGTATG	180
CAACGAGATT	ACCATGAGGG	ACGTTTACAA	TTGATGAGTC	AGGACGAATA	TGTCAGGGTC	240
ATCTGTGACC	AACTGGAAAT	TATTTCCAAA	CATATCGTCA	TCCATCGAAT	TACAGGAGAT	300
GCGCCTAGGG	ATATGCTGCT	TGGGCCCTATG	TGGAGCCTCA	ATAAATGGGA	AGCTCTCAAC	360
AGCATTGAGA	TGGAGATGCG	ACGTCGTGGA	AGTGTTC AAG	GATGCAAGGC	TGTAAAACAG	420
GAGTTTGAAA	ATGAAAAGAC	CAC TTGA				447

(2) INFORMATION FOR SEQ ID NO:2476:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 285 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...285
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2476:

GAGAAGACGG TATACGATCA AACCATTAC	CGTGTAGCCG AAATCGTTCA GAATGAAGAC	60
TTGTATAAGA AAGGTTTGAA TGTGAACTT	GCGCACCAAC AAATTAAGGG ATTTTGTGAA	120
GCAGAGTTTA AAAATCGTAT TAATGGAGTT	CTTAATACTA AAATAAAAAA TAGTACATTA	180
AAATCGTGTA ATAAAAAAC TATACACCAG	AGCAACAAAA ACTCCATGAT CAATTTGAAG	240
CAGAAGCAAC GGAAGATGCT AAAAAACAAG	GCGATATTGT GTTGA	285

(2) INFORMATION FOR SEQ ID NO:2477:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 885 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...885
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2477:

AGGTCACAGG TTCGACTGTT ACCAGCTATT	GGGCTAATAA GTCAGGAGCG CCAGCGACAA	60
GTTATCGCTT TGCTATTGGT GGAAGTGATG	CGGATTATCA GAATGCTTGG TCTAGTATTG	120
TGGGGAGTCT ACCAACTCCA TCCAGCTCCA	GCAGTTCAAG TAGTAGTTCT AGCGATAGCA	180
GTAACCTCAAG TACTACACGA CCTTCTTCAA	GGGCGAGACG ATAATTCTCT AAATGAAGTG	240
GCCAATCAAT GGATTGCCAC TTTTTCCTT	TCGTGTTACA ATAAGGGTAT GAATCAGTAT	300

CAGAAAAAGA	TTGTTAACGG	AAAAATTTAT	TCGCTCCTAT	CCGGCTTAAT	ATGGGGAATC	360
TGTGGAATTT	TAGGAAAGTA	CTTCCTTACT	CATTATCAGG	TGTCTTCGGG	CTGGATTACC	420
TCTATGCGTT	TGACACTGGC	AGGGAGTCTT	GTACTCATTT	GGTCTGCAAT	ACAAATTAAAA	480
TCGCAAGTGC	TAGATATTTG	GCGAGACAAAG	AAAAATTACC	TGCCCTTTTT	AGCCTATGCT	540
ATTTTGGGGA	TTTTTTCAGT	TCAGTATTTT	TTCTATCTCT	GTGTAGAATA	CTCAAATGCT	600
ACGACAGCAA	CTATTTTACA	GTTTATTAGC	CCTGTCTTTA	TCCTCTTTTA	TAATCGCTTG	660
GTTTATCAAA	AACGAGCGTC	AAAAAGCGCT	GTTTCTATG	TTTTGGTTGC	CATGCTGGGT	720
GTTTGCTTGA	TGGCGACAAA	GGGAGATCTC	TCTCAGTTAT	CCATGACGCC	GCTAGCTCTT	780
ATAACAGGTT	TGCTGAGTGC	CATGGGTGTT	ATGTTTAATG	TTATCTTGCC	CCAACCTTTT	840
GCTAAGCGTT	ATGGTTTTGT	TCTAACGAGT	TGGGTGGGGG	GATGA		885

(2) INFORMATION FOR SEQ ID NO:2478:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 474 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...474
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2478:

CCTGGTAAGG	TTGTATCAC	CAAGGTTAAG	ACTGGTTTTG	GTACAGGTGG	TTGGCAGTTG	60
GCTGCTCTAC	GCTGGTGTGC	CAAGGCTGCG	CGTAAACCGA	TTATCGCTGA	TGGAGGAATT	120
CGTACTCACG	GTGATATTGC	CAAGTCTATC	CGCTTCGGTG	CTAGCATGAT	CATGATTGGT	180
TCCCTCTTTG	CAGGACACAT	TGAAAGTCCA	GGGAAAACGA	TTGAAGTCGA	TGGTGAACAG	240
TTCAAAGAAT	ATTATGGTTC	AGCCTCACAA	TATCAAAAAG	GTGCTTACAA	AAATGTGGAA	300
GGCAAACGTA	TCTTGCTTCC	TGCTAAAGGT	CATCTGCAAG	ACACTTTAAC	TGAGATGGAA	360
CAAGACCTTC	AAAGTGCTAT	TTCTTATGCA	GGTGGACGTC	AGGTTGCTGA	CCTTAAACAC	420
GTTGATTATG	TGATCGTGAA	AAACTCCATC	TGGAATGGGG	ATGCTTCCCA	CTAA	474

(2) INFORMATION FOR SEQ ID NO:2479:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 219 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...219

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2479:

GAAAGCAAGG	TTTGGTATTG	TTTCACCAAG	GCATTTCTTG	GCTCTTTCAA	GATGCGAACC	60
AAGTCATCAA	CGGTCAATTG	CTCAAGAGCC	GCAAAAACAG	GCAAGCGTCC	AATCAACTCA	120
GGGATAATAC	CAAATTTTGA	ACTTCTCTCT	TACCANGGCG	NGCGTTGGGG	NAGGGGTACA	180
AATGTACAAG	GGGTGCNGTT	ACGNATGGGG	TCCGCTTGA			219

(2) INFORMATION FOR SEQ ID NO:2480:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 996 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...996

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2480:

GCAAGGAAGG	TTGGAGGCAC	TATGAAAACG	CGTATTACAG	AATTATTGAA	GATTGATTAT	60
CCTATTTTCC	AAGGAGGGAT	GGCCTGGGTT	GCTGATGGTG	ATTTGGCAGG	GGCTGTTTCC	120
AAGGCTGGAG	GATTAGGAAT	TATCGGTGGG	GGAAATGCCC	CGAAAGAAGT	TGTCAAGGCC	180
AATATTGATA	AAATCAAATC	ATTGACTGAT	AAACCCTTTG	GGGTCAACAT	CATGCTCTTA	240
TCTCCCTTTG	TGGAAGATAT	CGTGGATCTC	GTTATTGAAG	AAGGTGTTAA	AGTTGTCACA	300
ACAGGAGCAG	GAAATCCAAG	CAAGTATATG	GAACGTTTCC	ATGAAGCTGG	GATAATCGTT	360
ATTCCTGTTG	TTCCTAGTGT	CGCTTTAGCT	AAACGCATGG	AAAAAATCGG	TGCAGACGCT	420
GTTATTGCAG	AAGGAATGGA	AGCTGGGGGG	CATATCGGTA	AATTAACAAC	CATGACCTTG	480
GTGCGACAGG	TAGCCACAGC	TATATCTATT	CCTGTTATTG	CTGCAGGAGG	AATTGCGGAT	540
GGTGAAGGTG	CTGCGGCTGG	CTTTATGCTA	GGTGCAGAGG	CTGTACAGGT	GGGGACACGG	600
TTTGTAGTTG	CAAAAGAGTC	GAATGCCCAT	CCAAACTACA	AGGAGAAAAT	TTTAAAAGCA	660
AGGGATATTG	ACACTACGAT	TTCAGCTCAG	CACTTTGGTC	ATGCTGTTTC	TGCTATTAAA	720
AATCAGTTGA	CTAGAGATTT	TGAACTGGCT	GAAAAAGATG	CCTTTAAGCA	GGAAGATCCT	780
GATTTAGAAA	TCTTTGAACA	AATGGGAGCA	GGTGCCCTAG	CCAAAGCAGT	TGTTTACGGT	840
GATGTGGAGG	GTGGCTCTGT	CATGGCAGGT	CAAATCGCAG	GGCTTGTTTC	TAAAGAAGAA	900
ACAGCTGAAG	AAATCCTAAA	AGATTTGTAT	TACGGAGCCG	CTAAGAAAAT	TCAAGAAGAA	960
GCCTCTCGCT	GGACAGGAGT	TGTAAGAAAT	GACTAA			996

(2) INFORMATION FOR SEQ ID NO:2481:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 324 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...324
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2481:

CGGCTTGAGG	TTGCTGGATT	TACGTGGAGT	TTGTGCTTGA	GGATATATCT	TCATGGGCCC	60
TTGATAACCA	CTGTCAGCCA	AGATTTTACC	AGCTTGTC	ATATTTCTGC	GACTCATTTT	120
GAACAACTTC	ATATCGTGGC	AATAGTTCAC	CGCAATATTC	AAAGAAACAA	TTCTTTCTTG	180
GCTGGTGACA	ATCGCTTGAG	GTTCCATAGA	ATGACATTTT	TATTTTACCA	GAATAATTGG	240
CTAGTTGATT	TTTTTAGGAC	GATTTATTTT	TACCTCTGTT	GCATCCACAA	TCACCGTATT	300
CTCAGCACTA	AGATGAGTTT	TTGA				324

(2) INFORMATION FOR SEQ ID NO:2482:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 321 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...321
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2482:

TATCGTGAGG	TGAATTTTAT	GGCAAATCTA	AATCGATTCA	AATTTACATT	CGGGAAAAAA	60
TCGTTAACCT	TGACAAGCGA	ACATGACAAC	CTTTTTATGG	AGGAAATCGC	TAAGGTTGCG	120
ACAGAAAAAT	ACCAAGCAAT	TAAAGAACAA	ATGCCTAGCG	CAGATGATGA	AACAATCGCT	180
CTTTTGTGG	CAGTCAACTG	TTTATCAACT	CAGCTCAGCC	GTGAGATTGA	ATTTGACGAT	240
AAGGAGCAAG	AGCTAGAAGA	ACTCCGTCAC	AAGCTTGTGA	CTTGTAAGCA	AGAACAGAGC	300

(2) INFORMATION FOR SEQ ID NO:2483:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2483:

AGAAGCGAGG	TCCAAACTAT	TTACAAACCA	ATGTTTTGGA	AGACCCAAGA	TCGACACGGA	60
AAGGCTTTGG	TTGGTAATCG	CGTTGGTCAA	TGGCGCTATA	GAATTGGTAA	TTATCGAGTT	120
ATCGTACAAA	TTGTAGATGA	TGAATTAGTC	GTTGCTACTC	TAGAAGTTGG	TCATCGGAGA	180
GATATTTATT	AA					192

(2) INFORMATION FOR SEQ ID NO:2484:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 567 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO .

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...567

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2484:

ACCGTAGAGG	TGTTTATGAA	TGTTTGGACC	AAATTAGCAA	TGTTTTCTTT	TTTTGAAACG	60
GATCGCTTGT	ATTTGCGTCC	TTTCTTTTTT	AGTGATAGTC	AGGACTTCCG	CGAGATAGCT	120
TCAAAATCCAG	AAAATCTTCA	ATTTATTTTC	CCAACGCAGG	CAAGTCTGGA	AGAAAGTCAA	180
TATGCACTGG	CCAATTACTT	TATGAAGTCC	CCTTTGGGAG	TGTGGGCAAT	TTGTGACCAG	240

AAAAATCAAC	AAATGATTGG	TTCTATTAAA	TTTGAGAAGT	TAGATGAAAT	CAAAAAAGAA	300
GCTGAGCTTG	GCTATTTTTT	GAGAAAAGAT	GCTTGGTTCG	AAGGATTTAT	GACAGAGGTT	360
GTTAGAAAAA	TTTGTCAGCT	TTCTTTTGAG	GAATTTGGCT	TAAAACAATT	ATCTATCATT	420
ACCCACCTTG	AAAAATGAAGC	TAGCCAAAGA	GTTGCTCTTA	AGTCTGGATT	TAGTTTGTTC	480
CGTCAGTTTA	AGGGAAGTGA	TCGTTACACA	AGAAAAATGC	GGGATTATCT	TGAATTTCCG	540
TATGTAAAAG	GAGAGTTCAA	TGAGTAA				567

(2) INFORMATION FOR SEQ ID NO:2485:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 687 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...687

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2485:

AATAAAGAGG	TTCTTTTTTAT	GGAATTTATG	CTTGACACAT	TAAATTTAGA	TGAGATTAAA	60
AAGTGGTCTG	AAATTTTGCC	GCTAGCTGGG	GTAACCTCAA	ATCCCACTAT	TGCAAAAAGA	120
GAGGGTTCTA	TTAATTTTTT	TGAACGAATC	AAAGATGTAA	GAGAATTGAT	TGGCTCTACA	180
CCCTCTATTC	ATGTTTCAGG	GATTTCTCAA	GATTTTGAAG	GCATCTTAAA	GGATGCTCAT	240
GAAATTCGAA	GACAAGCAGG	AGATGATATA	TTTATCAAAG	TACCTGTTAC	TCCAGCTGGA	300
TTACGTGCAA	TAAAGGTGCT	AAAAAAAAGAG	GGCTACCATA	TCACTGCAAC	AGCTATTTAT	360
ACAGTTATTC	AGGGATTATT	AGCTATCGAA	GTAGGAGCGG	ATTACCTAGC	TCCATATTAT	420
AATAGAATGG	AAAACTGAA	CATTGATTCA	AATTCTGTCA	TTCGTCAATT	AGCTCTTGCT	480
ATTGATAGAC	AGAACTCTCC	TAGTAAGATT	TTAGCTGCAT	CCTTTAAAAA	TGTAGCACAA	540
GTAAATAATG	CTTTAGCTGC	AGGTGCGCAT	GCTGTTACAG	CAGGAGCAGA	TGTTTTTGAA	600
TCAGCTTTTCG	CCATGCCATC	TATCCAAAAG	GCGGTTGATG	ATTTTTCTGA	CGATTGGTTT	660
GTTATTCAAA	ATAGTCGTTT	CATTTAG				687

(2) INFORMATION FOR SEQ ID NO:2486:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 915 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...915

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2486:

TTATTGGAGG	TTAGGATGAA	AAAAC TCCCC	TTAGTATTTT	CAGGTTGTTT	GCTAGGTTTG	60
GCAGGAGCTG	GAAATCTTAT	TTTAGATACG	TTGCCGGTTC	TATCCCATCT	TTTTAGTCTG	120
ACTGGTTTGG	TTTTATGGAT	TTACTTTCTA	ATTCTGCATC	TCTTTAATTG	GAAAGAAACC	180
AAGCAAGAAT	TGACCAAGCC	CCCTCTTTTG	TCAGGAATGG	CAACCTTTCC	TATGGCTGGG	240
ATGATTTTAT	CGACCTATGT	CTTTCGCGTA	TTCTCTTATC	TTCTTTGGT	AGCACAAGGG	300
ATTTGGTGGT	TTTCATTTCT	CTTGGATTTG	ACCTTGATTG	CTGGTTTTAC	CATCAAGTTT	360
GCTTGTC CAG	GGCGGATGGT	TCATGCCACT	CCAAGTTGGA	CTGTTCTCTA	TGTGGGGATA	420
GCAGTGGCTG	CCTTGACCTA	TCCTCTGGTA	GGTATTATCG	AAATTGCCTA	TGCGACCTTG	480
AGTTTGGGTT	TTCTCTTGAC	CTTCTATCTC	TATCCCCTTA	TTTATAGCGA	TTTAAAGAAA	540
CATCCACTCC	CACTAGCCTT	GCTTGGACAA	GAAGGAATCT	ACTGTGCTCC	TTTCTCTCTA	600
CTCTTG GCTT	CTCTAGTTCT	AGTAGGAGGA	ACCAGCCTGC	CGACTTGGGG	CTTGATTGTC	660
ATGATTTTGG	CTTCTCAATC	CTTCTTTTTC	TTTGTTTTAA	CTCGTATGCC	CAACATTTTA	720
AAACAAGGCT	TTCAACCAGC	CTTCTCAGCC	CTCACCTTCC	CAACCATTAT	CACAGCGACC	780
TCGCTCAAGA	TGGCTCAGGG	AATTTTGAAA	CTTCCATTTC	TGGATTACCT	GGTATTGGCT	840
GAAACCATTA	TATGCCTAAC	TATTTTATTTC	TTTGTACTAG	GTGCTTATCT	GATTTGGTTA	900
CGAAAAAAGG	TCTAG					915

(2) INFORMATION FOR SEQ ID NO:2487:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 642 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...642

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2487:

TTAGAGGAGG	TTAAACTGAT	GTTGAATAAG	ATAAGAGACT	ATCTAGACTT	TTCTGGTTTG	60
CAGTACCGTA	GTCCTGATAA	AGCGGGAGCA	GAGCGAGAGA	AGATGCTGGC	GTTCCGCCAC	120
AAAGGACAAG	AGGCCCCGAA	GGCTTTTACA	GAAGTGCCCA	AAGCCTTTCA	AGCAAGCCAT	180
CCAGAATGGC	AACTCCAACA	GAAGTAGTCAG	TGGATGAATC	AGGCCAGCG	TTTGAGACCA	240
CATTTT TGGG	TTTATCTACA	GAGAGACGGA	CAAGTGACAG	AACCTATGAT	GGCCTTACGT	300
TTGTATGGGA	CATCTACTGA	CTTTGGAATT	TCTTTGGAAG	TCAGTTTCAT	CGAACGTAAG	360
AAGGATGAGC	AAACACTGGG	CAAGCAGGCC	AAAGTTT TAG	ACATTCCAAC	CGTTAAAGGG	420
ATTTATTATC	TAACCTACTC	TAATGGTCAA	AGTCAACGGT	GGGAGGCGAA	TGAAGAAAAG	480

CGTCGTACTT	TACGCGAGAA	GGTGAGAAGT	CAAGAAGTTC	GAAAAGTTTT	AGTGAAGGTA	540
GATGTTCCCTA	TGACAGAAAA	TTCGTCTGAA	GAAGAAATCG	TAGAAGGCTT	ATTGAAGTCT	600
TATTCTAAAA	TTCTCCCTA	TTATCTAGCT	ACGAGAAAAAT	AA		642

(2) INFORMATION FOR SEQ ID NO:2488:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 561 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...561
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2488:

AAGTTGTGGG	TGGAGGCGTC	CCNACGGGTT	CTCAAGGGGA	TTGACTTGGG	CCTTGGGGAA	60
CTGCGTCCAG	ATGTCATTGT	CATGGATATT	GTCATGCCTG	AGATGAATGG	GATTGACGCG	120
ACCTTAGCAA	TCCTTAAAGA	ATGGCCTGAA	GCCAAGATTT	TGATTGTGAC	TTCTTATTTG	180
GACAAATGAAA	AAATCATGCC	AGTCTTAGAT	GCTGGTGCCA	AAGGCTATAT	GCTCAAGACT	240
TCTAGTGCAG	ATGAATTGCT	TCATGCCGTC	AGTAAGGTAG	CTGCTGGCGA	GCTGGCCATT	300
GAGCAAGAGG	TTAGCAAGAA	GGTTGAATAC	CACCGCAATC	ATATGGAACT	TCATGAAGAA	360
TTGACTGCGC	GTGAGCGAGA	TGTTCTCCAA	CTCATCGCCA	AGGGCTACGA	AAATCAGCGC	420
ATCGCAGATG	ACCTCTTTAT	CTCACTCAAG	ACGGTCAAGA	CCCACGTGTC	CAACATTCTT	480
GCCAAACTTG	AAGTCAGCGA	TCGTACCCAG	GCGGCTGTCT	ATGCCTTTCA	GCACCATTTG	540
GTGGGGCAAG	AGGAGTTTTA	G				561

(2) INFORMATION FOR SEQ ID NO:2489:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 195 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature

(B) LOCATION 1...195

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2489:

GCATCGTGGG TCACAATAAT GACTGTTTTT CCTTCTCGAT TCATCTCTAA GAGAACTTC	60
AAGACCAAAT CTCTATTTTC AGGATCCAGC GAACCTGTAG GTTCATCGGC TAAAATCAGC	120
TGGCTGGGTT TTAAGATGGC TCTAGCAACT GCAATTCGTT GTTGTTCCGCC CCCAGACAAC	180
TCGGAGACCC TTTGA	195

(2) INFORMATION FOR SEQ ID NO:2490:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...288

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2490:

GGTCTTGGGG TAAAAAACA AAAGGCTTGC TTTTCAGCCA TAGAGGAGGT CATCATGTAT	60
AAACACTTAT TTTTCCTAGA TTCCAAAAC TTAGATCGGT TGACACCCTA TATTCTAGTC	120
TTGGCTTCTG ACACCATTGC TTTTAATGTT TTTGTGCTAA CCTTTGTATC TGCGGTGGTT	180
TTTAATTTCC TAAATTCCAT GCTAGCTTTA ATGGCTATAT TCATAGGGGC TGGCTATGTG	240
GTCGGATTTT GGTACTAAT ACTCAATGAA AATCAAAGAG CAAACTAG	288

(2) INFORMATION FOR SEQ ID NO:2491:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

(B) LOCATION 1...405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2491:

AGATTTTCTT	TAGCACATGA	ACTGTATCAT	CTTTATTATG	ATGAGGTGAA	GAAGAGTTCA	60
GTCAGTCTTA	TCTTGATTGG	TGAAGGAGAT	GAAACTGAAA	GAAAAGCGGA	TCAGTTTGCT	120
TCTTATTTTT	TAATTTTCCC	ATCTTCACTG	TATAGGATGG	TTGAGGAAAT	CAGAGAAAAT	180
GCCAATAGAA	CTCATCTTGA	AGTAGAAGAT	ATTATAAAAT	TGGGTCAGTT	TTATGGTATC	240
AGTCATAAAG	CTATGTTATA	TAGATTGAGG	AATGATGGAT	ACCTTGATGC	AGAAGAAATT	300
AAAAATATGG	ATATTAGTGT	TATAGAGACA	GCTTCAAGAT	TAGGCTATGA	TACAAGTTTA	360
TATCGTCCTT	TGTCAGAAAG	TAAAAAAGAA	ATGGCATTAG	GATAA		405

(2) INFORMATION FOR SEQ ID NO:2492:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 669 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...669

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2492:

CAGCCTTTAT	TGGTCCAAAT	GGTGCTGGAA	AATCGACTCT	TCCTCTCCAT	CATGAGCAGA	60
CTAACCAAGA	AAGATCAGGG	AGTTCTCAGT	ATCAAAGGAC	GTGAAATCGA	GAGCTGGAAT	120
TCGCAAGAAC	TGGCCCAAGA	ACTAACCATC	CTAAAAACAG	AAATCAATTA	CCAAGCCAAA	180
TTGACTGTTG	AAGAACTGGT	CAGTTTTGGA	CGTTTTCCCT	ACAGCCGAGG	TCGACTTAGA	240
TCAGAAGACT	GGGAAAAAAT	CCGAGAAACT	CTGAACTATT	TGGAACTGAC	CAACTTAAAA	300
GACCGCTACA	TCAATAGCCT	GTCAGGGGGG	CAACTCCAGC	GCGTCTTTAT	CGCTATGGTA	360
CTGGCCCAGG	ATACGGACTT	TATCTTGCTG	GACGAACCAC	TCAATAATCT	CGATATCAAG	420
CAAAGCGTCA	GCATGATGCA	AATTCTTCGA	CGACTGGTGG	AGGAACTCGG	CAAGACCATT	480
ATCATCGTCC	TCCACGATAT	CAACATGGCC	AGTCAGTATG	CAGATGAAAT	TGTCGCCCTTC	540
AAGGACGGTC	AGGTCTTTAG	CAAGGGAAGC	ACCGATCAAA	TCATGCAGGC	TGACCTGCTC	600
AGCCAACTTT	ATGAGATTCC	CATCACGCTA	GCTGATATCA	ATGACAAAAA	GATCTGTATC	660
TATAGCTAG						669

(2) INFORMATION FOR SEQ ID NO:2493:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1854 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1854

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2493:

AGCGATTTAT	TTAGAAAGTG	TGTAAATATG	GAATTTTCAA	AGAAAACACG	TGAATTGTCA	60
ATTAAAAAAA	TGCAGGAACG	CACCCTGGAC	CTCTTGATTA	TCGGTGGAGG	AATCACAGGG	120
GCTGGTGTAG	CCTTGCAGGC	GGCAGCTAGC	GGTCTTGAGA	CTGGTTTGAT	TGAAATGCAA	180
GACTTTTGCA	AAGGAACATC	TAGTCGTTCA	ACAAAAATTGG	TTCACGGAGG	ACTTCGTTAC	240
CTCAAACAAT	TTGACGTAGA	GGTGGTCTCA	GATACGGTTT	CTGAACGTGC	AGTGGTTCAA	300
CAAATCGCTC	CACACATTCC	AAAACCAGAC	CCATGCTCT	TACCAAGTTA	CGATGAAGAT	360
GGAGCAACCT	TTAGCCCCCT	CCGTCCTAAA	GTAGCCATGG	ACTTGTACGA	CCTTTTAGCA	420
GGTGTGAGCA	ACACACCAAC	TGCGAACAAG	GTTTTGAGCA	AGAAAGAAGT	CTTGGAACGC	480
CAGCCAAACT	TGAAGAAGGA	AGGCTTG GTA	GGAGGTGGAG	TGTATCTTGA	CTTCCGTAAC	540
AACGATGCGC	GTCTCGTGAT	TGAAAACATC	AAACGTGCCA	ACCAAGACGG	TGCCCTCATT	600
GCCAACCACG	TGAAGGCAGA	AGGCTTCCTC	TTTGACGAAA	GTGGCAAGAT	TACAGGTGTT	660
GTAGCTCGTG	ATCTCTTGAC	AGACCAAGTA	TTTGAAATCA	AGGCCCGTCT	GGTTATTAAT	720
ACAACAGGTC	CTTGGAGTGA	TAAAGTACGT	AATTTGTCTA	ATAAGGGAAC	GCAATTCTCA	780
CAAATGCGCC	CAACTAAGGG	AGTTCAC TTG	G TAGTGGATT	CAAGCAAAAT	CAAGGTTTCA	840
CAGCCAGTTT	ACTTTGACAC	AGGTTTGGGT	GACGGTCGTA	TGGTCTTTGT	TCTCCACGCT	900
GAAAACAAGA	CTTACTTTGG	TACAAC TGAT	ACAGACTACA	CAGGTGATTT	GGAGCATCCA	960
AAAGTAACTC	AAGAAGATGT	AGATTATCTA	CTTGGCATTG	TCAACAACCG	CTTTCCAGAA	1020
TCCAACATCA	CCATTGATGA	TATCGAAAGC	AGCTGGGCAG	GTCTTCGTCC	ATTGATTGCA	1080
GGGAACAGTG	CCTCTGACTA	TAATGGTGGA	AATAACGGTA	CCATCAGTGA	TGAAAGCTTT	1140
GACAACTTGA	TTGCGACTGT	TGAATCTTAT	CTCTCCAAAG	AAAAAACACG	TGAAGATGTT	1200
GAGTCTGCTG	TCAGCAAGCT	TGAAAGTAGC	ACATCTGAGA	AACATTTGGA	TCCATCTGCA	1260
GTTTCTCGTG	GGTCTAGCTT	GGACCGTGAT	GACAATGGTC	TTTTGACTCT	TGCTGGCGGT	1320
AAAATCACAG	ACTACCGTAA	GATGGCTGAA	GGAGCTATGG	AGCGCGTGGT	TGACATCCTC	1380
AAAGCAGAAT	TTGACCGTAG	CTTTAAATTG	ATCAATTCTA	AAACTTACCC	TGTTTCAGGT	1440
GGAGAATTGA	ACCCAGCAAA	TGTGGATTCA	GAAATCGAAG	CCTTTGCGCA	ACTTGGAGTT	1500
TCACGTGGTT	TGGATAGCAA	GGAAGCTCAT	TACCTAGCAA	ATCTTTACGG	TTCAAATGCA	1560
CCGAAGGTCT	TTGCACTTGC	TCACAGCTTG	GAACAAGCGC	CAGGACTCAG	CTTGGCAGAT	1620
ACTTTGTCCC	TTCACTATGC	AATGCGCAAC	GAGTTGGCTC	TTAGCCCAGT	TGACTTCCTT	1680
CTTCGTCGTA	CCAACCATAT	GCTCTTTATG	CGTGATAGCT	TGGATAGCAT	CGTTGAGCCA	1740
GTTTTGGATG	AAATGGGACG	ATTCTATGAC	TGGACAGAAG	AAGAAAAAGC	AACTTACCGT	1800
GCTGATGTCG	AAGCAGCTCT	CGCTAACAAC	GATTTAGCAG	AATTAAAAAA	TTAA	1854

(2) INFORMATION FOR SEQ ID NO:2494:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 882 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...882

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2494:

GAAGGTTTAT	TATCTTTAAT	GAATACACTC	GCAGAGAAAT	TCAGATTGAA	AAGAAAAGAG	60
TTGAGACTCT	CCCAACAAAC	TCTTGCAGAA	GGAATTTGTG	AACAAAGTCA	GATTAGTAAA	120
ATTGAGAGAG	GGCATTTCAT	TCCCTCCGCA	GACCTTTTGT	TCAAACCTCTC	TCAACGACTT	180
GAAGTACCAT	TAGATTATTT	TTTTAATGAA	CAAATTGAAA	TTAAATCTAA	CCTCTCTAAT	240
TTCAAGCAAT	TGTCTGCTCG	ACTATTAGAC	GATAGAAATT	ATGACGATTT	GGAATATATT	300
TATAGAATAG	AGATTGAACG	AAGTACTTTT	CTAACACTAG	AAGACCGAAC	TTACCTTGAA	360
TGGATTAAAG	CTATTATTGA	CTTCTATCAA	TATGACAGTA	AGTGTGAGGC	AATTTCTTCA	420
TTGGAAAATA	TATTATTAAA	AGTCTCTTCA	AATACTCTGA	TTTATTTAAA	GGCGTTGAAT	480
ACTCTATCTA	ATTTCTATTC	CTTAGTGGGT	CGTGAACAAG	AATATGAGGC	AACTACTCT	540
CATTTAATAG	AGTTGTATCA	GACAAAAAAT	TTGGACCATC	AAGAGTTTTT	ATTTGGCTAC	600
ATCAGAGTTC	GTTACAACCTA	CGCTCACTAC	CTAGTATCAA	AGGAAAAATA	TAATGAAGCC	660
ATCCAAGAAG	CTCTTGAAAC	GATTGAACCT	TGTAAACAAA	GACAGACAAG	CTACCAATTG	720
GCTCCTCTAC	TTATTCTTGT	AGGAAATGCT	GGAGCCAAAT	TTCTAGACAG	AGAACAAGTC	780
AAAAATTATT	ATATAGAAGC	AAGAGAGTTA	TGTAAGATTT	ATAACAATCC	TTTAATGTTG	840
ATGAAGATAG	AAAATTATTT	GAAGGAACCTA	GATACTGTTT	AG		882

(2) INFORMATION FOR SEQ ID NO:2495:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 195 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...195

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2495:

CCAATATTAT	TGGAGGGGGT	GAGTGGGGAA	ACCCGGTGGC	ATTGGCATT	CCCAAGGACC	60
AAGCGCAACC	CCGAGGGGT	TCAAACAATT	TTAGGTGTTA	GCAAAAAATT	TTTAGTGAAT	120
TTNTTCATAG	GGTTAAATAC	CCTTCTTTTT	TTNNTTCAAA	TATTTTACCA	CCAAATGAAA	180
AGTAAATAA	AATGA					195

(2) INFORMATION FOR SEQ ID NO:2496:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1512 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1512
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2496:

CCCCAATTAT	TCACCCCTAA	TCTAAAAACC	ATCCAGAATC	CTTGCCTTAG	CTTAGATCCT	60
GGATGGTTTC	TTTTTTCACC	CAATGGGTGT	TTTTTACTAG	ACAAAAAAGA	GTTTCCCCTT	120
TATGGTATAA	GTGTAGAAAA	AAACACAAAA	AGAAAGGAAA	CTCACATGAA	CAGTTTACCA	180
AATCATCACT	TCCAAAACAA	GTCTTTTTAC	CAACTATCTT	TCGATGGAGG	TCATTTAACC	240
CAGTATGGTG	GTCTTATCTT	TTTTCAGGAA	CTTTTTTCCC	AGTTGAAACT	AAAAAGACGG	300
ATTTCTAAGT	ATTTAGTAAC	GAATGACCAA	CGCCGCTACT	GTCGTTATTC	GGATTTCAGAT	360
ATCCTTGTC	AGTTCCCTCT	TCAACTGTTA	ACAGGCTATG	GAACGGACTA	TGCTTGTA	420
GAATTGTCAG	CTGATGCCTA	CTTTCCAAAA	TTGTTGGAAG	GAGGGCAGCT	TGCTTCACAG	480
CCAACCTTAT	CCCGTTTTCT	TTCCAGAACT	GACGAGGAAA	CAGTCCATAG	TTTGCGATGC	540
CTCAACCTTG	AATTGGTCGA	ATTCTTTTTA	CAGTTTCACC	AGCTAAACCA	ACTCATTGTA	600
GATATCGATT	CTACCCATTT	CACAACTTAT	GGCAAGCAAG	AAGGTGTTGC	TTATAACGCT	660
CACTATCGTG	CTCATGGCTA	TCATCCTCTT	TATGCTTTTCG	AGGGGAAGAC	AGGTATTGT	720
TTCAATGCC	AGCTTCGTCC	TGGTAATCGT	TATTGTTCTG	AAGAGGCAGA	CAGCTTTATC	780
ACACCTGTTT	TAGAACGGTT	TAATCAACTT	CTCTTTCGAA	TGGATAGTGG	CTTTGCGACC	840
CCAAAATTAT	ACGATTTAAT	TGAAAAAACA	GGGCAATACT	ACCTCATAAA	ACTCAAGAAA	900
AATACTGTTT	TGAGCCGTCT	TGGAGACCTT	TCCCTCCCTT	GCCACAGGA	TGAGGACTTA	960
ACCATCTTGC	CCCACTCCGC	CTACTCAGAA	ACTCTCTATC	AAGCAGGATC	TTGGTCGCAC	1020
AAGCGTCGTG	TCTGCCAGTT	CTCTGAACGA	AAAGAAGGAA	ACTTGTTCTA	CGATGTTATT	1080
TCTCTCGTTA	CAAAATATGAC	GAGTGAACA	AGCCAAGACC	AGTTTCAGCT	TTATCGTGGA	1140
CGTGGTCAAG	CCGAGAATTT	CATCAAGGAG	ATGAAGGAGG	GATTTTTTGG	CGATAAAACG	1200
GATAGTTCAA	CCTTAATCAA	AAACGAAGTT	CGTATGATGA	TGAGCTGTAT	CGCCTACAAT	1260
CTCTATCTTT	TTTTCAAACA	TCTAGCTGGA	GGTGACTTCC	AAACTTTAAC	AATCAAACGC	1320
TTCCGCCATC	TTTTTCTTCA	CGTGGTAGGA	AAATGTGTTC	GAACAGGACG	CAAGCAGCTC	1380
CTCAAATTGT	CTAGTCTCTA	TGCCTATTCC	GAATTGTTTT	CAGCACTTTA	TTCTAGGATT	1440
AGAAAAGTCA	ACCTGAATCT	TCCTGTTCCCT	TATGAACCAC	CTAGAAGAAA	AGCGTCGTTA	1500
ATGATGCATT	AA					1512

(2) INFORMATION FOR SEQ ID NO:2497:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 864 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...864

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2497:

AAAAAATTAT	TTTCATGTGC	TTTAGCATT	TCAACGATTG	GAACATTGTC	AACGATTGAT	60
AAATCAGGAG	TTCTTCCTTT	TTTCAGCGCAA	ACGGTGCAGG	CTGACATACA	AACGCTTACC	120
CCAATGGCAA	AATATTATAT	TATTCTTCCG	AAGGATGCAG	AAATATATAA	AACTTGGAGA	180
GGTACTGTCA	ATATTCCCAT	TATTGATGCT	ACAAAACTA	CTCCAGAATT	ATCTTATTTT	240
AAAGAAGATC	ATCGCAACTA	TATAGCTAAT	GAGAATAAGT	CTGGTGCCAA	TTACATAGAG	300
TGGAAGGGAA	CAGTAGAAGA	GTTTAAAGAG	GCCATTAAGA	AGTTGACTGA	TAAAAAATCA	360
ACTACTGCAA	CACCAAAAAA	GGATGAAAAG	CCAACACCAA	AACCGGATGA	GAAGCCAAAA	420
CCAACACCTA	CAGTTCAGTC	TGGTTGGGTA	GGTTCATCCT	ATTATCAAGA	TGGTAAAAAA	480
GTCATTAGTA	AGTGGATTTT	TGATAAAAAA	TATAATTCAT	ACTTCTATCT	AGATGCATCA	540
GGAAATTATG	TTCAAAACGC	TTGGGTAGGT	AACTATTATC	TTAAATCAGG	CGGATACATG	600
GCTAAAGGTG	AATGGGTTTA	TGATGCCACC	TATCAAGCTT	GGTATTATTT	GACATCAGAT	660
GGTTCCTTATG	CTTACAGTAC	ATGGCAAGGA	AATTACTATC	TAAAATCGGA	TGGTAAAATG	720
GCTGTCAATG	AATGGGTTGA	TGGTGACGT	TATTATGTTG	GCGCTGACGG	AGTTTGGAAG	780
GAAGGTCAAG	CAAGTACAGT	TTCTTCTAGT	AATGATAGCA	ATAGTGAATA	TTTCTGCTGC	840
TTTAGGAAAAG	GCAAAAAGTT	ATAA				864

(2) INFORMATION FOR SEQ ID NO:2498:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 303 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...303

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2498:

TTAGAATTAT	TTGGAGGAAT	CATTAACATG	GCAAACAAAC	AAGATTTGAT	CGCTAAAGTA	60
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GCAGAAGCTA	CAGAATTAAC	TAAGAAAGAC	TCAGCAGCAG	CAGTTGAAGC	TGTATTTGCA	120
GCAGTAGCTG	ACTATCTTGC	AGCTGGTGAA	AAAGTTCAGT	TGATCGGTTT	TAGTAACTTT	180
GAAGTTCTGT	AGCGCGCAGA	ACGTAAAGGT	CGCAACCCAC	AAACTGGTAA	AGAAATGACA	240
ATTGCAGCTT	CTAAAGTACC	AGCATTCAAA	GCTGGTAAAG	CTCTTAAAGA	CGCTGTTAAA	300
TAA						303

(2) INFORMATION FOR SEQ ID NO:2499:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 288 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...288
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2499:

TGCCCTTTTT	TGTTTCAATA	TACTATGGCT	CCGATGACCT	ATAAAGATAC	GATGACGAGT	60
GACTTTTTTCG	AAGCTTGCTT	CCAAAAATTC	TTACTACCTA	CTTTAGATAC	ACCATCCCTT	120
ATCATTATGG	ACAATGCAAG	GTTTCACAGA	ATGAACATGT	GTAAGGAGCA	GGGCATAGAC	180
TGTTACCACT	TCCTACCTAT	TCACCTGAGT	ATAATCCCAT	TGAGAAAATA	TGGGCTTACA	240
TCAAAAACAT	CTCAGAATAA	TATTGTCAAA	TTACGATGCT	TTTCTTGA		288

(2) INFORMATION FOR SEQ ID NO:2500:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 882 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...882
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2500:

AAAAGGTTAT	TACATATGTC	ACGCCAAACA	CCGTCACTCT	CATTTGAAGT	GTTCCCTCCA	60
AACCCAGCCG	TGGGTAATGG	TAACATTATT	TCAGCCTTGC	AGGATATGCA	GGAGTTGGCT	120
CCCCATTTTA	TCAGTGTAAC	TGCCAGCAAT	AATAAATTTA	ATATCAAGGA	AACGACGGTT	180
CGTTTGGCTG	ACTTTATCCA	AAATGATTTG	GCGATTCCGA	CCATTGCCCA	CTTGCCAGCT	240
ATTTATCTAA	CTAAGGACAA	GGTTGCTGAA	ACTATTGCTG	ACTTGGACAA	AGTTGGGGTG	300
CAGAAAATCT	TGGCTCTTCG	TGGGGATATT	ATTCCAGACG	TGGAACCACA	AAAGGATTTT	360
CGCTATGCAA	CCGACTTGAT	TGAGTTTATC	AAGGAACAAA	CCCCTCACTT	TGATATTATT	420
GGAGCTTGCT	ATCCAGAAGG	GCATCCAGAT	TCGCCAAATC	AGATTTTCAGA	TATTCAAAAT	480
CTTAAGAAGA	AAGTGGATGC	AGGCTGTTTCG	AGCCTCGTAA	CTCAGCTCTT	CTTTGACAAAT	540
GAGCGCTTCT	ATGATTTTCA	GGACAAGTGC	ATCTTGGCTG	GGATTGATGT	TCCCATTTCAT	600
GCAGGAATTA	TGCCAATTCT	GAATCGAAAT	CAGGCTCTCC	GACTCTTGAA	GACTTGTGAG	660
AATATCCATC	TTCCACGCAA	ATTTAAAGCC	ATCTTAGACA	AGTATGAGCA	TGACCCTGAA	720
TCGCTCAGAG	CAGCAGGACT	TGCCATATGCA	GTGGACCAAA	TCGTGGACTT	GGTAACTCAG	780
GATGTTGCCG	GTGTGCATCT	CTATACGATG	AATAATGCTG	ATACAGCAAA	ATACATCCAT	840
CAAGCAACCC	ATGCCTTGTT	TAATCACCAG	TCTCTAGGAT	AA		882

(2) INFORMATION FOR SEQ ID NO:2501:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 585 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...585
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2501:

CTGGAATTTT	TGAATAAAGG	AGGACAAATG	AAAAAAGTAA	TGTTTGCTGG	CTTAAGTCTC	60
TTGTCATTAG	TTGTATTGAT	GGCCTGTGGT	GAGGAAGAAA	CTAAAAAGAC	TCAAGCAGCA	120
CAACAGCCAA	AACAACAAAC	GACTGTACAA	CAAATTGCTG	TTGGAAAAGA	TGCTCCAGAC	180
TTACATATGC	AATCCATGGA	TGGCAAAGAA	GTTAAGTTAT	CTGATTTTAA	GGGTAAAAAG	240
GTTTACTTGA	AGTTTTGGGC	TTCATGGTGT	GGTCCATGCA	AGAAAAGTAT	GCCAGAGTTG	300
ATGGAACTAG	CGGCGAAACC	AGATCGTGAT	TTCGAAATTC	TTACTGTTCAT	TGCACCAGGA	360
ATTCAAGGTG	AAAAAACTGT	TGAGCAATTC	CCACAATGGT	TCCAGGAACA	AGGATATAAG	420
GATATCCCAG	TTCTTTTATGA	TACCAAAGCA	ACCACCTTCC	AAGCTTATCA	AATTCTGAAGC	480
ATTCCTACAG	AATATTTAAT	TGATAGCCAA	GGAAAGATTG	GAAAGATTCA	ATTTGGTGCT	540
ATCAGTAATG	CGGATGCAGA	AGCAGCATTT	AAAGAAATGA	ACTAG		585

(2) INFORMATION FOR SEQ ID NO:2502:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1359 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1359
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2502:

GGAGGTCTAT	TTATGGATCA	ACAAAACGGG	TTGTTTGGTT	TTCTTGAAAA	CCATGTTATG	60
GGACCAATGG	GCAAACTTGC	TCAGTTTAAA	GTAGTACGTG	CTATCACGGC	TGCAGGTATG	120
GCTGCTGTAC	CATTTACTAT	TGTAGGATCA	ATGTTTTTGG	TATTCAGTAT	TTTGCCACAA	180
GCTTTCTCAT	TTTGCCCAAT	TGTGGCAGAT	ATTTTCTCTG	CTTCATTTGA	TAAATTCAGA	240
TCACCTTACA	TGGTTGCAAA	CTATGCGACT	ATGGGTTCTC	TATCTCTTTA	TTTCGTTCTA	300
TCACTTGCA	TGGAATGAC	AAAAATTTAT	GCAGAGGAAG	AAGAACTCAA	TATGAATCCT	360
CTTAATGGTG	CCTTGCTTGC	CTTGATGGCT	TTTGTCATGA	CAGTACCGCA	AATCATTTTT	420
GATGGTGGA	TGATGAAGAC	TGTGACAAGT	CTAAAAGAAG	GTGCAGTAAT	TGCAGATGGA	480
TGGGCAATGG	GAAATGGAGT	CGCACGTTTT	GGGACAACAG	GGATTTTTTAC	CGCAATCAT	540
ATGGCAATTG	TGACTGTTCT	TATTTATCGT	ATGTGTGTTA	AACATAATTG	GGTTATTAAA	600
ATGCCCTGAAG	CTGTTCCAGA	AGGAGTTTCT	CGTGGATTTA	CCGCTTTGGT	TCCGGGATTT	660
GTTGTTGCAT	TTGTTGTTAT	CTTTATCAAC	GGTCTTCTTG	TAGCAATGGG	AACAGATATT	720
TTTAAAGTCA	TTGCAATTCC	ATTTGGTTTT	GTATCCAATC	TGACTAATTC	GTGGATTGGT	780
TTAATGATTA	TTTATCTATT	GACTCAACTA	CTTTGGATTG	TAGGTATCCA	CGGTGCGAAC	840
ATTGTTTTTT	CATTTGTTAG	TCCAATTGCT	CTTGCCAACA	TGGCTGAAAA	TGCTGCTGGC	900
GGGCACTTCG	CTGTTGCAGG	TGAATTTTCT	AATATGTTTG	TAATTGCAGG	TGGTTCCTGGT	960
GCAACTTTAG	GACTATGTTT	ATATATTGCT	TTTGCCTCTA	AATCTGAACA	GCTTAAAGCA	1020
ATAGGACGAG	CATCTGTAGT	TCCAGCCTTA	TTTAATATTA	ATGAACCATT	AATTTTTTGA	1080
TTACCTATTA	TCTATAATCC	AGCCTTGGCT	ATACCATTTA	TTTTAGCACC	AATGGTTACT	1140
GCTACTATTT	ATTACGTAGC	GAATTCTCTA	AACTTTATTA	AGCCAATTAT	CGCACAGGTT	1200
CCATGGCCAA	CTCCAGTAGG	GATTGGAGCT	TTCTTAGGGA	CAGCAGATCT	TCGAGCTGTA	1260
TTAGTTGCTC	TAGTATGTGC	ATTTGCAGCA	TTCCTAGTCT	ATCTTCCATT	CATCCGTGTA	1320
TATGATCAAA	AATTGGTGAA	AGAAGAGCAA	GGTATCTAA			1359

(2) INFORMATION FOR SEQ ID NO:2503:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 363 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...363

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2503:

ATTAGGCTAT	TTTTTGGTAT	AATAAAAGTT	ATGGAAATCG	AAAAAACCAA	TCGTATGAAT	60
GCGCTCTTTG	AATTTTATGC	GGCGCTTTTG	ACAGATAAGC	AAATGAATTA	TATAGAGCTT	120
TACTACGCTG	ATGATTACAG	TCTTGCTGAG	ATAGCTGAGG	AGTTTGGTGT	TAGTCGTCAG	180
GCTGTCTATG	ACAATATCAA	GCGAACAGAA	AAGATTCTGG	AAGATTATGA	GATGAAATTG	240
CACATGTACT	CGGACTACAT	TGTCCGTAGT	CAGATTTTGT	ACCAAATCTT	GGAGCGCTAT	300
CCCAAGGATG	ATTTTCTGCA	GGAGCAGATA	GAAATTTTAA	CAAGCATTTGA	TAATAGAGAA	360
TAA						363

(2) INFORMATION FOR SEQ ID NO:2504:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 510 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...510

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2504:

AGAAGGCTAT	TCGCTCATTG	GGACCTGTCA	ACTTGGAAGC	TATTGACCAG	TACGAAGAAG	60
TTCACAACCG	GTCTGGACTT	TCTAAATAGT	CAGCGAGATG	ATATTTTGTG	AGCGAAAAAT	120
CTGCTCCTTG	AAACCATTAC	AGAGATGAAT	GATGAGGTCA	AGGAACGCTT	TAAATCAACC	180
TTTGAAGCTA	TTCGTGAGTC	CTTTAAAGTG	ACCTTCAAGC	AGATGTTTGG	CGGAGGTCAG	240
GCAGACTTGA	TATTGACTGA	GGGCGACCTT	TTAACAGCTG	GTGTGGAGAT	TTCTGTTCAC	300
CTCCGAGATA	AGAAAATCCA	GTCGCTTAAC	CTCATGAGTG	GTGGTGAAAA	AGCTCTTCGG	360
CTCTTGCCCT	GCTTTTCTCC	ATTATTCTGT	TCAAGACCAT	TCCTTTTGTG	ATCTTGATG	420
AGGTGGAAGC	TGCGCTGGAT	GAAGCCAATG	TTAAACGTTT	TGGGGATTAC	TTCAACCGCT	480
TTGACAAGGA	CAGCCAGTTT	ATCGTCGTAA				510

(2) INFORMATION FOR SEQ ID NO:2505:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...228

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2505:

ATGGTTATAT	TTTTGCTTAA	AATGAAACAT	TTTTTTGCAG	GAATTGGTGA	AATAAACTTT	60
GTAAGTTATT	TATTGTATAT	ATGTGTAGGA	ATAGCCCCTT	TTTTTCACGT	ATATATAATA	120
GGTTCCTGAAA	TGAATTTTGT	GAAAATAGTG	TTATCTATTT	TGGGAATTAT	ATTTGTTTGT	180
ATTTTAACTA	TTGCTCGAAT	TTATAGGACT	TTTTTCTATA	AAGAATAG		228

(2) INFORMATION FOR SEQ ID NO:2506:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 708 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...708

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2506:

TACTATATAT	TGAAAGGAGG	TGATAATATG	GTAGAACAAA	GAAAATCAAT	TACCATGAAA	60
GATGTTGCTT	TAGAAGCAGG	AGTTAGTGTT	GGAACGTGTT	CACGTGTAAT	TAATAAAGAA	120
AAAGGCATTA	AAGAAGTAAC	TTTGAAAAAA	GTGGAACAAAG	CGATTAAAAC	TTTGAATTAC	180
ATTCCAGATT	ACTACGCTAG	AGGAATGAAA	AAAAATCGAA	CAGAAACGAT	TGCAATCATT	240
GTACCAAGTA	TCTGGCATCC	CTTCTTTTCA	GAATTTGCTA	TGCATGTGGA	AAATGAAGTC	300
TATAAGAGAA	ATAACAAATT	ACTCTTATGT	TCTATCAATG	GTACAAATAG	AGAGCAAGAC	360
TATCTGGAGA	TGTTGCGTCA	TAATAAAGTT	GATGGAGTGG	TTGCCATTAC	CTATAGTCCA	420
ATTGAACATT	ACTTGACGTC	AGGAATTCCC	TTTGTTAGTA	TTGACCGCAC	ATACTCAGAT	480
ATTGCCATTC	CTTGTGTTTC	ATCAGATAAT	GATGCAGGTT	GGAGAGAAGC	AGCTAAACAA	540
TTAATTAGTA	AAGGATGTCA	GCATTTAGCC	TTTGTGGGCG	GACATAATAC	AACCATTAAAT	600
GAAACCAAAC	GTCGTAGAAT	TCATTTGAAA	AGTATGTCCA	AGAGCATAAA	ATACTTCTTA	660
GTATTTTGA	TTTGGATGAG	ACAGTTACTG	ACTATTATGG	AAAGCTAG		708

(2) INFORMATION FOR SEQ ID NO:2507:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 210 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...210
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2507:

CCTGTCTCTT TAGAGCCTTT AAGCGTTATC TTAAATACCG TGGAAAAGTC AGAGAAAGTA	60
TGGCGGCAGA TTGCCCTGAA CGCTTTGACT GGGAGTTTAT CAGATGGATT CTTTGGGATG	120
GACGTAGCAA AACTCAAAAA GAAAATTACC AAAAAGTTTG CCAAGAATAT TCACATAAAG	180
TCACTATTCT TCGAAATCAG AGAGAGCTAG	210

(2) INFORMATION FOR SEQ ID NO:2508:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 456 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...456
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2508:

AAAGAAATAT TTATTACCGA AAAAAAGGGG AAATCGAGTC AAGTACCAAC AGGCTCATCT	60
ATTCCAAAAA GATATTTACT CGATGGAAAA ACTCCTAGAA TTAGTGCTAC AAATATTGAC	120
AATGGTATCT TAGGTTACTA CGAAGATATA GATGATAAAA ATTATAGAGT TTTTGAAAAAT	180
TTTATATCTG TTTCATGTTT AGGAGCAGTC TTTTATCATA AATATAAAGC AAGCCTAGAT	240
ATGAAAAATC ATTGTTTAAA ATTAAAAAAT AAAGAATTGA ATAAAGAAGT AGCATTCTAT	300
TTAACTTCAA TTATTAGGCA AGCTTTAAAA AATACTGAAT ATAAAGATCA AATATCTAGC	360
ACAGTATTGC CAGATATCAA AATTAAATTA CCGATAGACA GTAGAGGTAC TCCAGATTGG	420

(2) INFORMATION FOR SEQ ID NO:2509:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 333 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...333
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2509:

AATAGAATAT	TTGATAATAA	TTGTTTGATA	CAAGTATACA	AATTTATTTC	TTTTTATGAT	60
ATTTGTGAAA	TGGTGTTC	CTTTCATTTA	CCTCCTGATG	AGTTGATAAC	AAATGTTATC	120
TTTAAAGAAA	AAATTAACTC	TATGTTAAAA	TGTTACATTG	ACAGGCTATT	ATATGTTTTT	180
ATAAATCCTA	CACATTTTAC	TGAAAAAGTT	AATCTACAAT	TTTATGGTAG	TTTTTTCTCA	240
TATGAATTTA	TTTGTCGTGA	AGTTGGAAAC	ATTCTTAAAA	ATAAAGGTGT	GAAATGCAAT	300
TTAAACTTTT	TTGAAGGGGA	AGAATATTTG	TAA			333

(2) INFORMATION FOR SEQ ID NO:2510:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 702 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...702
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2510:

AAGCAGATAT	TAGTATTGGT	TAAGAAAGGA	AAGAGCATGT	CAGATCGTAC	GATTGGAATT	60
TTGGGCTTGG	GAATTTTTTG	GAGCAGTGTC	CTAGCTGCCC	TAGCCAAGCA	GGATATGAAT	120

ATTATCGCTA	TTGATGACCA	CGCAGAGCGC	ATCAATCAGT	TTGAGCCAGT	TTTGGCGCGT	180
GGAGTGATTG	GTGACATCAC	AGATGAAGAA	TTATTGAGAT	CAGCAGGGAT	TGATACCTGC	240
GATACCGTTG	TAGTCGCGAC	AGGTGAAAAT	CTGGAGTCGA	GTGTGCTTGC	GGTTATGCAC	300
TGTAAGAGTT	TGGGGGTACC	GACTGTTATT	GCTAAGGTCA	AAAGTCAGAC	CGCTAAGAAA	360
GTGCTAGAAA	AGATTGGAGC	TGACTCGGTT	ATCTCGCCAG	AGTACGAAAT	GGGGCAGTCT	420
CTAGCACAGA	CCATTCTTTT	CCATAATAGT	GTTGATGTCT	TTCAGTTGGA	TAAAAATGTG	480
TCTATCGTGG	AGATGAAAAT	TCCTCAGTCT	TGGGCAGGTC	AAAGTCTGAG	TAAATTAGAC	540
CTCCGTGGCA	AGTACAATCT	GAATATTTTG	GGTTTCCGAG	AGCAGGAAAA	TTCCCCATTG	600
GATGTTGAAT	TTGGACCAGA	TGACCTCTTG	AAAGCAGATA	CCTATATTTT	GGCAGTCATC	660
AACAACCAGT	ATTTGGATAC	CCTAGTAGCA	TTGAATTCGT	AA		702

(2) INFORMATION FOR SEQ ID NO:2511:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 246 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...246
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2511:

ATAAAGATAT	TAGACAAGAG	GAAACGAATG	ACCCCAAACA	AAGAAGACTA	TCTAAAAATGT	60
ATTTATGAAA	TTGGCATAGA	CCTGCATAAA	ATTACCAACA	AGGAAATTGC	GGCTCGCATG	120
CAAGTCTCTC	CCCTGCCGT	AACTGAAATG	ATCAAACGAA	TGAAAAGTGA	AAATCTCATC	180
CTAAAGGACA	AGGAATGTGG	CTTCTACGG	ACTGACCTCG	GTCTCAAAC	GGTCTCTGAG	240
CTCTAA						246

(2) INFORMATION FOR SEQ ID NO:2512:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 453 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...453

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2512:

CCATTTGTAT	TTGCGACAGA	GAATGATTCA	CTAAATGGTG	TGTCATGCT	CTTTAATCAT	60
CTATTAACAA	ATACTCCACA	AATCTTTGCT	GATGTGCGTA	CTTATTGGAG	TCCAGAGGCT	120
GTTGAACGTG	TAACAGGATA	TAC'TTTAGAG	GGTCGTGCTG	CAGCTGGATT	CTTACATCTA	180
ATCAACTCTG	GATCTTGTAC	ATTGGATGGT	ACAGGTCAAG	CTACTCGAGA	TGGCAAACCT	240
GTTATGAAAC	CATTCTGGGA	GTTGGATGAA	AGTGAAGTAC	AGGCTATGCT	TGAAAATACA	300
GACGTTCCCA	CCAGCAAACC	GCGAATACTT	CCGTGGAGGA	GGATTCTCAA	CTCGTTTCTT	360
GACGAAGGGG	GATATGCCAG	TAACAATGGT	ACGTCTCAAT	CTTTTAAAAG	GGGTTGGTCC	420
AGTGCTACAA	ATTGCAGAAG	GTTACACACT	TGA			453

(2) INFORMATION FOR SEQ ID NO:2513:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 888 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...888

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2513:

ACCCACGTAT	TCGTTATTAG	GAAGGAGGTC	AATGTTATGA	AACCTATGCC	TTTATGGAAA	60
AGAAATTTGA	AAAAATTCCTA	TAATAACAAA	TTGGCCTTTA	TCGGCTTTAT	ATGCTTCATG	120
CTAATTCCTAT	TAGCATGTAT	TCTAGCACCT	TTATTGACAA	CCTATTCCTCC	AGATGTTGTT	180
GATTTAGGAT	CTATGAACCG	TCCTCCTTCA	GCAAAACACA	TTCTGGGAAC	AGATAAACTA	240
GGTCGTGACG	TATTTGCTCG	AATCCTATAT	GGTGGTCGAG	TTTCAATTCA	AGTAGGGATG	300
TATGGAGCGA	TTTGTGGAGC	GGTTATTGGT	ACTGTACTTG	GTGGTATTGC	TGGATATTTT	360
GGTGGGAAAA	TTGATGCTCT	TCTAGTTCGT	CTAGCAGAAT	TATTCTTAAC	ATCCCGAAT	420
ATGATTGTCA	TTCTCTTGCT	TTCAAGTATT	TTTGGACAAG	GTGTATTCAA	TCTTATCTTC	480
GTATTCTCAG	TAATGGGTTG	GATGACAACG	TTCCGAATGG	TTCGTAATGA	GTTCATGTCT	540
TTGAAACAAG	AAACATATGT	GGATGTATGT	AGAGCTTTTG	GTTTTTCTGA	CAGTCGAATT	600
ATCTTTAATA	ATATTTTAAG	AAATGCTATC	TCACCAGTAA	TTGTATCGTT	GTCTTTAAAC	660
GTTGCTGGTT	TCATTCTCAG	TGAGGCAGGT	CTTAGTTTCT	TAGGAGTAGG	TGTTCCCTCT	720
GATATTCCTA	CTTGGGGAAA	TATCATAAAT	GCTGCCAAAA	CAGCCGATGT	TATTAAAAAT	780
AGTTGGTGGT	TGTGGTTAGT	TCCAGGGTCA	ATCATTACTC	TTTTTCGTTCT	TTCTATCAAC	840
TTTATTGGTG	ATGGATTACG	AGATATAATG	GATCCGAAAC	AACAGTAG		888

(2) INFORMATION FOR SEQ ID NO:2514:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 228 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...228

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2514:

GTGACAGTAT	TTGCATATTC	AGAACCTAAC	GGGCTACCGA	TGGCAATAGC	AGTTTCTCCT	60
ACAGTTAACT	TACTAGAAATC	ACCAAACCTCA	GCTACTGTTG	TCACCTTTTTC	TGAAGAGATT	120
TTGACGACAG	CAATATCAGA	GAAAGTGTC	GCTCCGACAA	TTTCTCCAGG	TACTTTAGTC	180
CCATCTGACA	ATCGAATATC	TACTTTGCTG	GCGCCATTTA	TAACGTGA		228

(2) INFORMATION FOR SEQ ID NO:2515:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 567 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...567

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2515:

AATAAAGTAT	TAAGTAATCG	TGAAAAAAGG	ATATCTATGC	GAAAAGAAAT	TGCACCTGAA	60
TTATACAAC	ATAACAAGTT	TCCTGGTCCG	GAGTTCCATT	TACACGGGGA	CAAGGTCGAA	120
ACGGAAGGGA	TAGCTTTTTT	CTTGGTTGAA	AATATCAAGG	ATGCCTTTGA	TGTGACAAC	180
TTTAATCAGC	GTTTTTTCAG	AGTATTAACC	AAGTTTGATT	ATATCGTGGG	GGACTGGAGC	240
AACGAACAGC	TTCGCCTACG	AGGTTTTTAC	AAGGATGACC	GAACAGAAGA	AAAACCTGAA	300
AAAATCAGTC	GTTTACAAGA	CTACCTTTTA	GAGTATTGTA	GTTATGGTTG	TGCCTATTTT	360
GTCTTAGAAA	ATGAAGCCCC	TAAGCGAGCA	TCATTTGACA	AGAAAATGCG	TAAGACGGAA	420
GAAGAAACAC	CTTCTAGAAA	AGGAAAGAAA	CCGACTCAAA	CTAAACGAAA	GTCGAATGCA	480
GATAAGAAAA	ATAGACGTCG	TCAGAAAGAC	CAGCATTTCT	AGAAAGAGGA	CAAGGGACAA	540

(2) INFORMATION FOR SEQ ID NO:2516:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 270 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...270
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2516:

AAAAGAGTAT TTGTCATGGA TACAAAAATT ATGGAACAAT TTCATGAAAT GGATATAACT	60
ATGTTATCTA GTATTGAAGG AGGCAAGAAT AATTGGCAAA CTAATGTCTT AGAAGGTGGT	120
GGTGCTGCTT TTGGTGGCTG GGGGTTAGGG ACAGCTATTT GTGCTGCGAG TGGTGTGGA	180
GCGCCATTTA TGGGAGCATG TGGATACATA GGAGCTAAAT TTGGTGTGGC TCTTTGGGCA	240
GGAGTAACAG GGGCAACGAG TGGATTTTAA	270

(2) INFORMATION FOR SEQ ID NO:2517:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1035 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1035
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2517:

GTTATGGTAT TTACAGCAAA AAGCTCTAAA ATAAATATAG AAGAAGTTCG TGCCTTGTC	60
AAATTAGAAAG GTCAGGCTTT GGAGAGGAAA TCACAGCGAG ATCAAGAGCT AGAAGCCATT	120
ATACGTGGAG AAGACCAGCG AATTCTCTTG GTAATCGGGC CATGCTCATC TGACAATGAA	180

GAAGCTGTCC	TTGAATACGC	TAAGCGTTTG	GCAGTCCTAC	AAGAAGAAGT	GGCAGATCGT	240
ATCTTTATGG	TTATGCGTGT	TTATACTGCC	AAACCCCGTA	CCAACGGAGA	TGGCTATAAG	300
GGCTTGATTG	ACCAGCCTAA	CGCGACAGAA	GCGCCTAGTC	TTATCAATGG	AATCAAAGCC	360
GTTCCGCCATC	TTCACATATCG	TGTCATCACA	GAAACAGGGA	TGACAACTGC	TGATGAAATG	420
CTTTATCCTG	AAAACCTTCC	GCTTGTAGAT	GATTTTGATTT	CTTACATGGC	AGTTGGTGCC	480
CGTTCAGTTG	AAGACCAGCA	ACACCGCTTT	GTGGCAAGTG	GGGCAGGATT	TTCTACTGGT	540
TTTAAAAATC	CAACCTCTGG	AAATCTCAAT	GTCATGTTTA	ATGGGATTTA	TGCTGCTCAA	600
AACAAACAAA	GTTTCCCTTTT	CTTAGGAAAA	GAAGTAGAAA	CAACTGGGAA	CCCGCTTTCA	660
CACGCTATTG	TTCGTGGTGC	TCCTTAATGAG	TATGGAAAAA	ATATTCCCAA	CTACTATTAT	720
GACAAATTTAA	TTGATACCAT	TGCCCAGTAT	GAGAAAAATGG	GCTTGAAAAA	TCCTTTTATC	780
ATCATTTGATA	CCAATCATGA	CAATTCTGGT	AAGCAGTATA	TTGAACAGAT	CCGAATTGTC	840
CGCCAGACCT	TGATTAACCG	TGCTTGGAAT	GAAAAAATTA	AGCAGTTCGT	TCGTGGTTTT	900
ATGATTGAGT	CTTATCTGGA	AGATGGTCGA	CAAAATGAGC	CAGAAGTATT	TGGTAAGTCT	960
ATCACAGACC	CTTGCCCTGGG	TTGGGATAAC	ACAGAAGCTC	TTGTCAGAGA	AATTTACAAA	1020
ACGTTAGGAG	AATAA					1035

(2) INFORMATION FOR SEQ ID NO:2518:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 897 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...897

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2518:

AAGGAGGTAT	TTATGACATA	CTACGTTGCA	ATTGATATCG	GTGGAACCAA	CATCAAGTAT	60
GGTTTGTTTG	ATCAAGAGGG	GCAACTTCTT	GAATCGCATG	AAATGCCAAC	TGAGGCGCAT	120
AAGGGTGGAC	CTCATATCTT	ACAAAAGACC	AAAGATATCG	TAGCTAGTTA	TTTAGAAAAA	180
GGCCCAGTAG	CAGGTGTTGC	CATATCTTCT	GCTGGGATGG	TGGATCCGGA	TAAGGGTGAG	240
ATTTTCTATG	CTGGGCCCTCA	AATCCCTAAC	TACGCAGGCA	CCCAGTTCAA	AAAGGAAATC	300
GAAGAAAGCT	TTACTATTCC	TTGTGAGATT	GAAAATGATG	TCAACTGTGC	AGGTCTTGCT	360
GAGGCAGTAT	CTGGTTCAGG	CAAGGGAGCA	AGTGTGACAC	TTTGCTTGAC	CATTGGAACC	420
GGTATCGGTG	GTTGCTTGAT	TATGGATAGG	AAAGTCTTCC	ATGGTTTTAG	TAATTCAGCC	480
TGTGAAGTCG	GGTATATGCA	TATGCAGGAT	GGAGCTTTTC	AGGATCTCGC	TTCTACAACA	540
GCTTTAGTGA	AATATGTAGC	TGAAGCCCAT	GGAGAAGATG	TTGATCAGTG	GAATGGCCGA	600
CGTATCTTTA	AGGAAGCTAC	TGAAGGAAAC	AAAATCTGCA	TGGAAGGTAT	TGACCGTATG	660
GTTGACTATC	TAGGAAAAGG	TCTGGCAAAT	ATTTGTTATG	TGGCCAATCC	AGAAGTGTTT	720
ATTCTTGGTG	GTGGTATCAT	GGGGCAAGAG	GCTATCCTCA	AACCTAAGAT	CCGCACAGCC	780
TTGAAAGAGG	CATTGGTACC	AAGTTTAGCA	GAAAAAACAC	GATTAGAATT	TGCCCATCAC	840
CAAAATACAG	CAGGGATGTT	GGGTGCATAT	TATCATTTTA	AGACAAAACA	ATCCTAG	897

(2) INFORMATION FOR SEQ ID NO:2519:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1539 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1539
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2519:

AGGAGATTTT	TGATGAAATC	AAAAATAGTT	TTGGGAGCTT	CGCTAGCGAT	CGCAACACTT	60
AGCTTAGTAT	CTCTTGTCGA	GATTGAAGGA	CTCTCACCGT	TTTTAATAGA	GAATGTTAGC	120
GCAAACTACTC	ATTCTGCAAA	TAAAGTTATT	AATCATAAAG	TAAGTATTTA	CTTAGAAAAAT	180
GCTGATGAAG	GTAAAGGTCT	AACTGTAAAC	TTTTCAACAG	ACAGTGTTAG	TCCAAATTTA	240
TTTGATGAGT	TCGAAAAAAA	GAGTGGAAAT	ACAATAACTA	CTATGTTAGT	GAATGCTAAG	300
ACAGGTGAAG	TTGTAGAAAA	AAGATTAACA	CCAAGCGTTT	TTTTACGTTT	CAATGATTTA	360
ACCAGTGGGA	CCATATCTTC	GTTTATTTTT	AGTGAATATC	CTGATGGAGA	ATATAAATAT	420
GTTGTGTCTA	AAGGAGACTT	TATCGATCCT	AAGACTCAGT	TAAACATCA	GTATAGAGGA	480
GAATCTCCAG	TTTTTAGAAT	ACGTAATCGA	AAATATGTGG	AGTTGGGAAC	AACTGATAAA	540
AAATTAGATG	AAAGACGTGA	TAATAGCGTT	TATAAAGATG	GGGTTGTTGA	ACACAAGGTA	600
AATTTAAGTT	TAACAAGTTA	TCAAGGAGGT	AATGGAGTTA	CTGCAATTTT	TTCAACTGAT	660
AGTGTTAACT	CTAACTTACT	TAATCTTTTT	GGTGAAAAGG	CTAAAAAAGT	TTTGATTAGG	720
TCTAAGTTAA	TTAATGTTAA	GACTGGCGAG	GTTATTGATG	AAACGTTTTT	TCCAAAAGTA	780
AGTTTAACCT	CTAAAAATTT	GAAAAGTGGT	TCTACAGCAG	TATTTTATTT	TATAGATTTA	840
ACTGATGGCG	AATATAAATA	TGTTGCGTAT	GAAAGCCAGC	AATATACTGA	TCCTCAAACA	900
ACATTGACTC	ATCAGTATAG	AGGAGAACTC	CCTATTTTTT	GTATCAAAGA	TGGAAAAATTT	960
TCTGGTTTAG	TATCTGCCCT	AAAACCAGAC	GAAAACCCGA	AGCCAACGCC	AAAACCGGAT	1020
GAGAAACCAA	AACCTTCAGC	ACCACAACAG	GAGAAACCAA	AACCTACAGT	TCAGTCTGGT	1080
TGGGTAGGTT	CATCTTATTA	TCAAAATGGT	AAAAAAGTCA	CTAGTAAGTG	GATTTTTGAT	1140
AAAAAATATA	ATTCTACTT	CTATCTAGAT	GCATCAGGAA	ATTATGTTCA	AAACGCTTGG	1200
GTAGGTAAC	ATTATCTCAA	ATCAGGCGGA	TACATGGCTA	AAAGTGAGTG	GATTTATGAT	1260
AAGAACTATG	GTTCACTACT	CTATCTAACA	TCAGAAGGCA	GCTACGCTCG	TAACACTTGG	1320
TCAGGCAATT	ATTATTTGAA	GTCAAATGGT	AAGATGGCTA	AAAGTGAGTG	GGTATACGAT	1380
AGTAACTACA	AATCATATTA	CTACTTGACA	TCAGAAGGAA	GTTATGCTCG	TAACACTTGG	1440
GTAGGCAATT	ACTATCTTAA	ATCAAACGGT	AAAATGGCTG	TTAATGAACG	TACACCAGAT	1500
GGTTATCGTG	TAGATGGTTC	AGGTAAATGG	GTAAATAA			1539

(2) INFORMATION FOR SEQ ID NO:2520:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 777 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...777

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2520:

ATACAATCTT	TGAAGAGACG	CAGAAGGGAG	ATAACTAAGA	TGAAACGATG	GATAGCACTT	60
AGTAAGATAG	ATTTTTTTATT	GACCAAACGA	CAATTAATTT	ATTATCTATT	GTCGGTAGGG	120
ATGCCGACGG	CTTTCTATTT	ATTTTTTTTCT	GGTATCTATC	AGGACACACC	AGGTGAACTC	180
GCGAATTTTA	TGCGTGATTA	TCTTATCTCC	ATGACTGCAT	TTTCCATGAT	GTCAACAGCT	240
ATCTTCTCAT	TCCCAGTTGT	TTTACATACC	GACAAGATCA	ACAACTGGCA	GAAAACATTG	300
CGTCATAGCC	CTGTAAATAT	GGTAGAATAT	TATCTATCAA	AGATAACAAG	TATGCTGGTT	360
GATTATTTGG	TTTCAATCTT	GGTGGTTTTT	TCAGTTGGGC	ATTTTGTAAG	AGGTGTGGAC	420
ATGTCCTTG	GAAATTGGAT	TGGGGCTGCA	CTTTTGCTGA	TAGTAGGAAG	TATTGCCTTC	480
GTAGCGCTTG	GTTTGACCTT	GACTCTCTTA	CCAAC TAGTC	AGTTGATGTC	TGTCGTGGGC	540
AATCTTCTTT	ATCTAGGGTT	GGCTGTTTTA	GGTGGACTCT	GGATGCCTAT	CTCTTTATTT	600
CCAGACTGGA	TGCAAGTAGT	AGGTAAGTGT	CTCCCGACCT	ATCAGTTGAT	GGAGTTGCTC	660
AAGACCTTCT	TAAATGAGGG	TGGCATCAAT	CTATCAGCCA	CAGTTTATTT	ACTTGTTTTT	720
TCAGTAGTTT	TGTTTGTTTT	GACCATTTAC	CTTCAAGGTC	ATAAGGAGAA	TGCTTAA	777

(2) INFORMATION FOR SEQ ID NO:2521:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 240 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2521:

GTACATTTCAT	TCAGGGGGAT	AAGAGAGATT	TTGTTCCAAT	TATGGTCAGA	GAAAGANGGT	60
AGAGCCGAGA	AATTGGGGAC	GGGTCTCATT	TTCTCAGACA	TTTTGTTGCG	TCACAACGCC	120
AAGCAAAGTT	TGATTGNTTC	GGACAAAATG	GTACCAATTC	AAAGTTTTTT	GCGATCATCC	180
GTTGACTCAC	ATTGGCAATA	TTTGTGCATA	ATCCAACCAA	ANATAGANTA	CGAGACATAA	240

(2) INFORMATION FOR SEQ ID NO:2522:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 480 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...480
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2522:

ACAACTCAT	TGAGGATGCC	TTTAAAGCGT	CCATTGAAAA	ATAGAAAGAA	GGAAAAGAAC	60
ATGAGTAAAG	AAAAAGTAAT	TTTGGCCTAT	TCTGGCGGTT	TAGACACATC	AGTTGCTATT	120
ACCTGGCTGA	AGAAAGACTA	TGATGTTGTT	GCAGTTTGTA	TGGATGTGGG	TGAAGGGAAA	180
GACTTAGATT	TCATCCATGA	TAAGGCTCTT	AAGGTTGGGG	CAGTCGAATC	TTATGTCATT	240
GATGTTAAGG	ACGAATTTGC	TACAGATTAT	GTGCTAGTGG	CTCATCAGTC	ACATGCCTAT	300
TATGAACAAA	AGTATCCCTT	GGTATCTGCC	TTGAGCCGCC	CTCTGATTTC	TAAAAAATTG	360
GTTGAAATAG	CGCATCAGAT	AGGAGCGACT	ACAATTGCTC	ATGGTTGTAC	CGGTAAGGGG	420
AATGACCAAG	TCGAATACCA	GATTGCAGTC	GCTAAGAAAG	CGAATGAAGC	TAAAAAGTGA	480

(2) INFORMATION FOR SEQ ID NO:2523:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 606 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...606
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2523:

AAAACGTCAT	TCTCATGTGA	GCTGGCGTTT	TTTCTATGCC	CACATTTCCG	GTCAAATCAT	60
TGGAAAATTC	TGACTGTTTC	AGATACAATG	GAAGAAAAAA	GATTGGAGTA	TCCTATGGTA	120

ACTTTTCTCG	GAAATCCTGT	GAGCTTTACA	GGTAAACAAC	TACAAGTCGG	CGACAAGGCG	180
CTTGATTTTT	CTCTTACTAC	AACAGATCTT	TCTAAAAAAT	CTCTGGCTGA	TTTTGATGGC	240
AAGAAAAAAG	TCTTGAGTGT	CGTTCCTTCT	ATCGATACAG	GCATCTGCTC	AACTCAAACA	300
CGTCGTTTTA	ATGAAGAAAT	GGCTGGACTG	GACAACACGG	TCGTATTGAC	TGTTTCAATG	360
GACCTACCTT	TTGCTCAAAA	ACGTTGGTGC	GGTGCTGAAG	GCCTTGACAA	TGCCATTATG	420
CTTTCAGACT	ACTTTGACCA	TTCTTTCGGG	CGCGATTATG	CCCTCTTGAT	CAACGAATGG	480
CACCTATTAG	CACGCGCAGT	CTTTGTCCCTC	GATACTGACA	ATACGATTCA	CTACGTTGAA	540
TACGTGGATA	ATATCAATTTC	TGAGCCAAAC	TTCGAAGCCG	CAATTGCAGC	TGCTAAAGCC	600
CTATAG						606

(2) INFORMATION FOR SEQ ID NO:2524:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 702 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...702

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2524:

GGACTGTCTT	TATTTTCATAG	TATAGGAGAA	AATAGAATGA	AAAAGATAAT	CTCACACCGC	60
TACTTTTATTA	TAGTTTTTCT	ACTAGTTATT	GCTGACCAGA	AGTTCAGTGT	TTTAGTTTTTA	120
CGCAGTGACC	TTGTTGCTGG	GCTATCTGAC	TTTGCCTATT	ATCTGTCGGA	TATGATGTTG	180
AATTTTCTTG	TGTTTTTATT	TGCTCTTATT	GCTATGATTT	GGTCGGGGAA	ATGGCAGAAA	240
ATCAATAGTA	GAAAGTTTAA	AGGATCCTAT	CTTTTCTATT	CCTTCCTAGC	TCTGCTTGCT	300
TTTGTTGCTT	GGAATTTTGT	CACCTTTTTT	CTTTTCCCAC	CTACTCGAAA	TGAAATTTCT	360
TATCAACATG	CTGCTCCTAC	TTTTACAGGA	GCTACGGCAT	TTTTGATGTA	TTTTTTTTTAT	420
CCTGTGATTG	CAGGTCCCAT	TTTTGAAGAC	ATGATTTATC	GTGGATTAGT	GATGACTGCT	480
CTGGAAAAAG	GAAAGAAATG	GGGGCTAGAT	GTACTTGGTT	CCGCTGTTTT	ATTTGGGGTC	540
TCGCACATTA	GTAATCACGG	TTGGGTCTTG	ACAGACTTTG	TCTTCTATAT	GGGTGGAGGT	600
CTTATATTTG	CAGTCTTATT	TAGAATGACA	AAGTCAATTT	ATTGGCCTAT	TGGACTGCAT	660
ATAGTCTACA	ATGGCATTGG	TCAGCTTTTG	ATGTTACTGT	AA		702

(2) INFORMATION FOR SEQ ID NO:2525:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 492 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...492

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2525:

CTCACACCAT	TGTTATCAGC	ATACCATTTA	ATCAAGAGAC	CTGTGATAGA	CAAGTGCCAG	60
ATATCAAAGA	TATCGACATC	AAGTGTATCG	GTTTTCTTCA	TAGCAAGCAT	CACTACGTTG	120
ACAATCAACA	TGATGAGCAA	GAAGTATAGT	GTCCAAGCAG	AACCCCAAGT	GATTGTTGCG	180
AGTGGTGCCC	AACCAACGTC	GGTAATACTC	AATTGTATAC	CAGTGTTTTT	AACGAATTTT	240
GCAAGTGATG	CTGAGAAAGC	ACCATTTAGC	ATACCGATGA	TAGCACCGAT	ACCTGTAAGA	300
GCGATGGCAA	GTTTGATACC	ACCTTCAAGC	GCTTTGGAGA	ATTTCACTCC	AAAAAGTAAA	360
GCCAATACTG	TCAAAATGAT	TAACATGATG	ACAGGTCCAC	CCATTTCTAA	GATGGGATTG	420
AAAACCTTTC	CGATTAGGTC	AAAGATTGCA	TCCATAACAG	TTCTCCCTT	TTTTATGTTA	480
TATGAATGTT	AA					492

(2) INFORMATION FOR SEQ ID NO:2526:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 363 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...363

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2526:

TTTGAGCCAT	TTTATCCCCT	TTCTTATGCC	AAATCAGAAA	CTGAAATACC	ACGAAGGGCA	60
GCAATTTCTT	CAGCGCGTTT	CAATTGTTTC	AAACCTTCAA	CAGTTGCACG	AACAATGTTG	120
ATTGGAGTGT	TAGAACCAAG	TGATTTAGAT	GTAATATCTG	CCACACCTGC	CAATTCCACA	180
ACGGCACGAA	CTGCACCACC	AGCGGCAACT	CCAGAACCTT	CTACAGCAGG	TTTCAACAAT	240
ACTTTAGCTC	CACCGAATTC	TGAAAGAACT	TCGTGTGGGA	TTGTTGTTCC	AACCATAGGA	300
ACTTCGATCA	AGTTTTTCTT	AGCATCATCT	ACTGCTTTAC	GGATTGCTTC	TGGAATTCT	360
TGA						363

(2) INFORMATION FOR SEQ ID NO:2527:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 468 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...468

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2527:

TTCGAAACAT	TTGCTTGTA	TTTGCGGAGG	AACATCAATA	TGGATGGAAT	AACAAAAGAT	60
TTTATAAAAA	CGGCTAAACT	AATGAAACAA	TTATGGCCCC	AATTGACCGA	TAAAGAAGCT	120
ATTGTAGAAG	TAAAAAATA	TACGAATGGC	AAAAATACTG	CAATCTTTAC	TGAAGTTGAA	180
GGTGACACAA	TTGTAGGTCT	AGCACTATGT	TCACTCAGAT	TTGATTATGT	TGAAGGTTGT	240
AAATATAGTC	CTGTTGGATT	CTTAGAAGGG	ATTATTGTTG	ACGAGGAATA	TCGTTTAAAG	300
GATATTGCTA	AAAATCTCTG	TACAAAATGT	GAGGAATGGG	CGAAAAATAA	AGGATGTAAG	360
GAATTTGCAA	GTGACTGTAC	TTTAACGAAT	ACGGATTCTA	TAAGATTTC	TCTCAATATT	420
GGATTTTCAGG	AGGCAAATAG	AATTATTTCAT	TTTAAGAAAA	AATTATAA		468

(2) INFORMATION FOR SEQ ID NO:2528:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 261 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...261

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2528:

CTCTTGACAT	TGCCCTTGGC	TCAGGTGGTT	ATCCTAAGGG	ACGTATCATC	GAAATCTATG	60
GCCCAGAGTC	ATCTGGTAAG	ACAACGGTTG	CCCTTCATGC	AGTTGCACAA	GCGCAAAAAG	120
AAGGTGGGAT	TGCTGCCTTT	ATCGATGCGG	AACATGCCCT	TGATCCAGCT	TATGCTGCGG	180
CCCTTGGTGT	CAATATTGAC	GAATTGCTCT	TGTCTCAACC	AGACTCAGGA	GAGCAAGGTC	240
TTGAGATTGC	GGGAAAATTG	A				261

(2) INFORMATION FOR SEQ ID NO:2529:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1263 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2529:

ATTATGACAT	TTTCATTTGA	TACAGCTGCT	GCTCAAGGGG	CAGTGATTAA	AGTAATTGGT	60
GTCGGTGGAG	GTGGTGGCAA	TGCCATCAAC	CGTATGGTCG	ACGAAGGTGT	TACAGGCGTA	120
GAATTTATCG	CAGCAAACAC	AGATGTACAA	GCATTGAGTA	GTACAAAAGC	TGAGACTGTT	180
ATTCAGTTGG	GACCTAAATT	GACTCGTGGT	TTGGGTGCAG	GAGGTCAACC	TGAGGTTGGT	240
CGTAAAGCCG	CTGAAGAAAG	CGAAGAAACA	CTGACGGAAG	CTATTAGTGG	TGCCGATATG	300
GTCTTCATCA	CTGCTGGTAT	GGGAGGAGGC	TCTGGAAGTG	GAGCTGCTCC	TGTTATTGCT	360
CGTATCGCCA	AAGATTTAGG	TGCGCTTACA	GTTGGTGTGG	TAACACGTCC	CTTTGGTTTT	420
GAAGGAAGTA	AGCGTGGACA	ATTTGCTGTA	GAAGGAATCA	ATCAACTTCG	TGAGCATGTA	480
GACACTCTAT	TGATTATCTC	AAACAACAAT	TTGCTTGAAA	TTGTTGATAA	GAAAACACCG	540
CTTTTGGAGG	CTCTTAGCGA	AGCGGATAAC	GTTCTTCGTC	AAGGTGTTCA	AGGGATTACC	600
GATTTGATTA	CCAATCCAGG	ATTGATTAAC	CTTGACTTTG	CCGATGTGAA	AACGGTAATG	660
GCAAAACAAAG	GGAATGCTCT	TATGGGTATT	GGTATCGGTA	GTGGAGAAGA	ACGTGTGGTA	720
GAAGCGGCAC	GTAAGGCAAT	CTATTCACCA	CTTCTTGAAA	CAACTATTGA	CGGTGCTGAG	780
GATGTTATCG	TCAACGTTAC	TGGTGGTCTT	GACTTAACCT	TGATTGAGGC	AGAAGAGGCT	840
TCACAAATTG	TGAACCAGGC	AGCAGGTCAA	GGAGTGAACA	TCTGGCTCGG	TACTTCAATT	900
GATGAAAAGTA	TGCGTGATGA	AATTCGTGTA	ACAGTTGTCG	CAACGGGTGT	TCGTCAAGAC	960
CGCGTAGAAA	AGGTTGTGGC	TCCACAAGCT	AGATCTGCTA	CTAACTACCG	TGAGACAGTG	1020
AAACCAGCTC	ATTACATGG	CTTTGATCGT	CATTTTGATA	TGGCAGAAAC	AGCTGAATTG	1080
CCAAAACAAA	ATCCACGTCG	TTTGGAACCA	ACTCAGGCAT	CTGCTTTTGG	TGATTGGGAT	1140
CTTCGCCGTG	AATCGATTGT	TCGTACAACA	GATTCAGTCG	TTTCTCCAGT	CGAGCGCTTT	1200
GAAGCCCCAA	TTTCACAAGA	TGAAGATGAA	TTGGATACAC	CTCCATTTTT	CAAAAATCGT	1260
TAA						1263

(2) INFORMATION FOR SEQ ID NO:2530:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 498 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...498

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2530:

AAAATGGCAT	TTAAAGACAA	TGCAGTTGAA	TTAGAAGAAC	GCGTAGTTGC	TGTCAACCGT	60
GTTACAAAAG	TTGTTAAAGG	TGGACGTCGT	CTTCGTTTCG	CAGCTCTTGT	TGTTGTTGGT	120
GACCACAATG	GTCGCGTAGG	ATTTGGTACT	GGTAAAGCTC	AAGAAGTTCC	AGAAGCAATC	180
CGTAAAGCAG	TAGATGATGC	TAAGAAAAAC	TTGATCGAAG	TTCTTATGGT	TGGAACAACA	240
ATCCCACACG	AAGTTCTTTC	AGAAATTCGGT	GGAGCTAAAG	TATTGTTGAA	ACCTGCTGTA	300
GAAGGTTCTG	GAGTTGCCGC	TGGTGGTGCA	GTTCGTGCCG	TTGTGGAATT	GGCAGGTGTG	360
GCAGATATTA	CATCTAAATC	ACTTGGTTCT	AACACTCCAA	TCAACATTGT	TCGTGCAACT	420
GTTGAAGGTT	TGAAACAATT	GAAACGCGCT	GAAGAAATTG	CTGCCCTTCG	TGGTATTTCA	480
GTTTCTGATT	TGGCATAA					498

(2) INFORMATION FOR SEQ ID NO:2531:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 201 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2531:

AGAAAGGCAT	TTAACATCAC	TTTGCAAAAG	GCAAATACTA	AACTAGAGAA	ACCGATAAAC	60
CAGCCCCCTTA	GTTCCCATAT	TTTCAGGCAC	ACACTCCTTA	GTACACTAGC	TGAGAAGAAT	120
GCTATAATGG	TTAGAGTGGA	ACACAAAAAC	GCTAAAACAG	TAAATAACAT	CTACACTCAC	180
GTAAGTAAAA	GAATGGAGTA	A				201

(2) INFORMATION FOR SEQ ID NO:2532:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1233 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1233

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2532:

AAAGCTCCTT	TCGGTTTTGA	TACAATAGTT	TCAAAATTG	AGAGGAGCTT	TAATATGAAT	60
CGCTATGCAG	TGCAGTTGAT	TAGCCGTGGG	GCTATCAATA	AAATGGGAAA	TATGCTCTAT	120
GATTATGGAA	ATAGTGCTG	GTTGGCTTCT	ATGGGGACTA	TAGGACAGAC	AGTTTTAGGA	180
ATGTATCAGA	TTTCTGAGCT	CGTCACATCT	ATTCTCGTCA	ATCCCTTTGG	CGGAGTTATT	240
TCAGACCGTT	TTTCTCGTCG	TAAGATTTTA	ATGACGGCAG	ATCTTGTTTG	TGGGATTCTT	300
TGTCTGGCTA	TTTCTTTCAT	AAGGAATGAT	AGCTGGATGA	TTGGCGCTTT	GATTGTTGCT	360
AACATTGTGC	AGGCTATTGC	TTTTGCCCTT	TCTCGCACAG	CCAATAAAGC	TATCATAACT	420
GAAGTGGTGG	AGAAAGATGA	GATTGTGATC	TATAATTCTC	GCCTAGAGCT	GGTTTTGCAG	480
GTTGTAGGTG	TTAGCTCTCC	TGTTCTTTCC	TTCTTGTTT	TACAGTTTGC	AAGTCTCCAT	540
ATGACGCTAC	TGCTAGACTC	GCTGACTTTT	TTCATTGCTT	TTGTTCTAGT	GGCTTTCCTT	600
CCAAAAGAGG	AAGCAGAAGT	TCAAGAGAAA	AAGGCTTTTA	CTGGGAGAGA	TATTTTTGTA	660
GATATCAAGG	ATGGGTTACA	CTATATCTGG	CATCAGCAAG	AAATTTTCTT	CCTTTTGCTG	720
GTAGCTTCCA	GCGTTAATTT	CTTTTTTGCA	GCTTTTGAAT	TTCTACTTCC	CTTTTCGAAT	780
CAGCTTTACG	GGTCAGAAAG	AGCCTATGCA	AGTATTTTAA	CTATGGGGGC	TATTGGTTCC	840
ATCATTGGGG	CTCTTCTAGC	TAGTAAAATT	AAAGCTAATA	TTTATAATCT	TTTGATTTTA	900
CTGGCTTTGA	CAGGTGTCGG	AGTTTTTATG	ATGGGATTAC	CACTTCCAAC	TTTTCTTTCC	960
TTTTCTGGAA	ATTTAGTTTG	TGAATTGTTT	ATGACGATTT	TTAATATTCA	CTTTTTTACT	1020
CAAGTACAAA	CCAAGTTTGA	GAGCGAATTT	CTTGAAGAG	TACTGAGTAC	AATTTTTTACC	1080
TTAGCTATTC	TATTTATGCC	TATTGCAAAA	GGATTTATGA	CAGTCTTGCC	AAGTGACAT	1140
CTCTCTTCTT	TCCTGATAAT	TGGAAGTGGT	GTTATCATCT	TGTCTTGTAT	ATCGTTTATT	1200
TATGTTTCGAA	CTCATTTTGA	AAAATTGATA	TAA			1233

(2) INFORMATION FOR SEQ ID NO:2533:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 228 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature

(B) LOCATION 1...228

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2533:

ATATATCCTT	TAGGATTTAG	CGTTCCAATA	ATAAGGGTCA	AGACGGCGAT	ACCAACGCCT	60
GAAAAGACAA	AACCTGCGAT	GGCAGGAAGA	AAATGTTCTC	CAGATAGAGC	ACCTAGAGAA	120
GGCGGAAAAA	TCAAGTTCCC	CGCACCAAAA	AATATTCCAA	ACAGGAGCAA	ACCTGTTAGG	180
GTACCTTTTT	TAGCCATAAA	AATTTCTTC	ATATTTATAA	AATACTGA		228

(2) INFORMATION FOR SEQ ID NO:2534:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...246

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2534:

TGTCTTCAAT	TGATCAAAAT	TTGTTTTTTC	AGAGTAGTCA	TAAGTGAATG	TAATATATTT	60
CCAATCTGCC	GAACCTTTAT	ACATACCAAG	CGTAGCATAA	TCTGGACCAC	TCTGTACTCC	120
GGTCTCACTA	TTTTTTCTAA	AAAGATAATG	TTTGAAGCAA	TTAAATACAT	TCCAAAAAAT	180
TCGACCTTGG	ACTACATTTT	CGTACTTGAT	CCAAGCGCTA	AAAGTAACTT	TTTGGTACAA	240
CCTTGA						246

(2) INFORMATION FOR SEQ ID NO:2535:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 230 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

(B) LOCATION 1...230

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2535:

TGGTTCAATT	ATTATTCAC	CTAAGTAGTC	ATATGCTCTT	TATTTATGTG	AGTTTTTACC	60
TTTTAAAGGA	TCTTGTTAGA	TGGGAGAAGG	TTTTAAAAGT	GACAGATGAG	AATACAAGAA	120
AAGTTCGTTT	ATTAGTAGCC	TTTTTTAGCA	TTGTCATAGG	CTACATCCTG	AGTTCTTTCT	180
TTATTAGCCT	GTATCATTTG	TGGCAAGAAG	CGCTTAGAGG	ATTATTATGA		230

(2) INFORMATION FOR SEQ ID NO:2536:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2536:

ATGGCACAAT	TGACAATCAA	TGGGGTGGCT	GTGAAGCCTC	CCAAATCTTT	TCAAGTCGGT	60
ATTCAAGATA	TCGATGGAGA	GACAGGGCGT	AATGCCAATG	GCGACATGGT	GCGTGACCGT	120
ATCACGACCA	AACGCAAAC	TAGACTGTGAA	TGGGGTATGA	TGACTCAGGG	AGAAATAAGT	180
CAGCTTTTAC	ATGCTGTATC	ATCTAAATTT	TTTGAGGTAT	CTTATCCAGA	CCCCATGGAT	240
GGCCAAGTCA	CAAAGACTTT	CTATGTCGGT	GATAGGACAG	CTCCTAGCTA	TACCTTTACT	300
GAGAAGCTTA	AACCTTGGTC	TGGCGCTAAA	TTTAATCTGG	TAGAGAGGTA	A	351

(2) INFORMATION FOR SEQ ID NO:2537:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2537:

AAAAACAAT	TAATGAGAAG	CGGTCGTGAT	AAAAAGATTG	CGGGTGTTTG	TGCTGGGGTG	60
GCCCATATC	TGGATATGGA	TCCGACTATC	GTTCAAGTCA	TTTGGGGTGT	TCTTACTTGC	120
TGTTACGGAT	CTGGAATTGT	AGCTTACATT	ATTTTATGGA	TTATCGCACC	AGTAGCAACT	180
GTCTTCACCA	CGGGATTTC	A				201

(2) INFORMATION FOR SEQ ID NO:2538:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1749 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...1749

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2538:

CTTTTGCAAT	TCGTGGTGAA	GACGACAGCT	CGGATAAGAA	ATAACTTGAG	CCGATGGGTT	60
GGACGTCGTC	GTGACCTTGG	TGGTTTGATC	TTTATCGATC	TTCGTGACCG	TGAAGGAATC	120
ATGCAGTTGG	TTATCAACCC	TGAAAAAGTA	TCTGCAGAGG	TTATGGCAAC	AGCTGAAAGC	180
CTTCGTAGCG	AATTTGTTAT	TGAGGTGACT	GGTCAGGTCG	CTGCGCGTGA	GCAAGCCAAT	240
GATAAGTTGC	CAACTGGTGC	GGTTGAGTTA	AACGTGACAG	CTCTTATTGT	GCTTAATACA	300
GCTAAGACAA	CACCATTTGA	GATTAAGGAT	GGCATTGAGG	CAAATGACGA	TACACGTTTG	360
CGTTACCGTT	ACCTTGACCT	TCGTCTGTTA	GAAATGTTGG	AAAATCTTAA	ACTTCGTGCC	420
AAGGTGACCC	ACTCTATCCG	CAACTACTTG	GATGAGTTGG	AGTTTATCGA	CGTGGAGACA	480
CCATTCCCTTT	CTAAGTCAAC	GCCTGAAGGG	GCGCGTGATT	ATTTAGTGCC	GTCTCGTGTT	540
AATAAGGGGC	ATTTTACGTC	TCTTCCTCAA	AGTCCACAAA	TCACGAAACA	GCTCTTGATG	600
AATGCTGGTT	TTGACCGTTA	CTACCAAATC	GTTAAATGTT	TCCGTGACGA	GGACTTGCGT	660
GGAGACCGCC	AGCCTGAATT	TACTCAGGTC	GACTTGGAAG	CGTCCTTCCT	TACTGAGCAA	720
GAAATCCAAG	ATATTACAGA	AGGCTTGATC	GCGCGCGTGA	TGAAGGAAAC	AAAAGGCATC	780
GAAGTAACGC	TACCATTTCC	TCGTATGAAA	TACGATGATG	CTATGGCTCT	TTACGGTTCT	840
GACAAGCCAG	ATACTCGTTT	TGACATGTTG	CTTCAGGACT	TGACAGAAGT	GGTCAAAGGT	900
GTAGACTTTA	AAGTCTTTTC	AGAAGCACCT	GCTGTAAAAG	CGATTGTGGT	CAAAGAAGCT	960
GCGGACAACT	ATTACAGTAA	AGACATCGAC	AAGATGACGG	AAGTAGCCAA	ACAGTATGGT	1020
GCCAAAGGTC	TTGCTTGGGT	CAAGGTGGTT	GATGGAGAAT	TAAACGGACC	AGTTGCCAAG	1080
TTCTTGACTG	GTATCCAAGA	AGAATTGACA	ACAGCGCTTG	CTCTTGAAGA	TAAGGACTTG	1140
GTTCTCTTTG	TGGCGGATAC	GCTTGAAGTG	GCTAATGCAA	CAC TGGGTGC	CCTTCGTGGA	1200
CGTATTGCTA	AAGAGCTTGG	CTTGATTGAT	AATGATAAGT	TCAACTTCCT	TTGGGTGGTT	1260
GACTGGCCGA	TGTTTGAATG	GTCTGAAGAA	GAAGGCCGCT	ACATGAGCGC	CCACCATCCT	1320
TTCACCCCTC	CACAGGAAGA	GACTGTTTCA	GAATTAGAAG	GTGATTTGGC	TAAGGTTTCGT	1380

GCCATTGCTT	ACGATATCGT	CTTGAACGGT	TATGAGCTTG	GTGGTGGTAG	CCTTCGTATC	1440
AACCAAAAAAG	ACCTTCAAGA	ACGCATGTTC	AAGGCTCTTG	GTTTCTCAAC	TGAAGAAGCC	1500
AATGACCAGT	TTGGTTTCCT	TCTTGAAGCC	ATGGACTATG	GTTTCCCACC	ACACGGTGGT	1560
TTGGCTATCG	GGCTTGACCG	TTTTGTTCATG	TTGCTTGCTG	GAGAAGAAAA	TATCCGTGAA	1620
GTCATTGCCT	TTCTTAAGAA	CAACAAGGCA	ACTGACCCAA	TGACACAAGC	TCCATCAACA	1680
GTCGCTCTCA	AACAACCTAGA	GGAACCTCAGC	TTACAAGTAG	AAGAAGATGA	AACAAACAAA	1740
ACGAATTAA						1749

(2) INFORMATION FOR SEQ ID NO:2539:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1314 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1314
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2539:

CCTATGTTTT	TTAAATTATT	AAGAGAAGCT	CTTAAAGTCA	AGCAGGTTCTG	ATCAAAAATT	60
TTATTTACAA	TTTTTATCGT	TTTGGTCTTT	CGTATCGGAA	CTAGCATTAC	AGTTCCTGGT	120
GTGAATGCCA	ATAGCTTGAA	TGCTTTAAGT	GGATTATCCT	TCTTAAACAT	GTTGAGCTTG	180
GTGTCGGGGA	ATGCCCTAAA	AAACTTTTCG	ATTTTTGCCC	TAGGAGTTAG	TCCCTATATC	240
ACCGCTTCTA	TTGTGTGCCA	ACTCTTGCAA	ATGGATATTT	TACCCAAGTT	TGTAGAGTGG	300
GGTAAACAAG	GGGAAGTAGG	TCGAAGAAAA	TTGAATCAAG	CTACTCGTTA	TATTGCTCTA	360
GTTCTCGCTT	TTGTGCAATC	TATCGGGATT	ACAGCTGGTT	TTAATACCTT	GGCTGGAGCT	420
CAATTGATTA	AAACTGCTTT	AACTCCACAA	GTTTTTCTGA	CGATTGGTAT	CATCTTAACA	480
GCTGGTAGTA	TGATTGTAC	TTGGTTGGGT	GAGCAAATTA	CAGATAAGGG	ATACGGAAAC	540
GGTGTTCCTA	TGATTATCTT	TGCCGGGATT	GTTTCCTCAA	TTCCAGAGAT	GATTCAGGGC	600
ATCTATGTGG	ACTACTTTGT	GAACGTCCCA	AGTAGCCGTA	TCACTTCATC	TATCATTTTC	660
GTAATCATTT	TGATTATTAC	TGTATTGTTG	ATTATTTACT	TTACAACCTA	TGTTCAACAA	720
GCAGAATACA	AAATTCCAAT	CCAATATACT	AAGGTTGCAC	AAGGTGCTCC	ATCTAGCTCT	780
TACCTTCCGT	TAAAGGTAAA	CCCTGCTGGA	GTTATCCCCTG	TTATCTTTGC	CAGTTCGATT	840
ACTGCAGCGC	CTGCGGCTAT	TCTTCAGTTT	TTGAGTGCCA	CAGGTCATGA	TTGGGCTTGG	900
GTAAGGGTAG	CACAAGAGAT	GTTGGCAACT	ACTTCTCCAA	CTGGTATTGC	CATGTATGCT	960
TTGTTGATTA	TTCTCTTTAC	ATTCTTCTAT	ACGTTTGTAC	AGATTAATCC	TGAAAAAGCA	1020
GCAGAGAGCC	TACAAAAGAG	TGGTGCCTAT	ATCCATGGAG	TTCGTCCTGG	TAAAGGTACA	1080
GAAGAATATA	TGTCTAAACT	TCTTCGTCGT	CTTGCAACTG	TTGGTTCCCT	CTTCCTTGGT	1140
GTGATTTCCTA	TTTTACCGAT	TGCAGCTAAA	GATGTATTTG	GTCTTTCTGA	TGTTGTTGCC	1200
TTTGGTGGA	CAAGTCTCTT	GATCATTTATC	TCTACAGGTA	TCGAAGGAAT	CAAGCAATTG	1260
GAAGGTTACC	TATTGAAACG	TAAGTATGTT	GGTTTCATGG	ACAGAACAGA	ATAA	1314

(2) INFORMATION FOR SEQ ID NO:2540:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2337 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2540:

CAATTCCCTT	TCTGCTTTTT	TTTTGATATA	ATAACCTTAA	CTGTCATTCT	ATATGGAGGT	60
TCTATGCGTT	TTAATCAATA	TAGTTATATC	AATTTTCCAA	AAGAAAATGT	CTTATCTGAA	120
CTAAAAAAT	GTGGCTTTGA	TTTACAAAAT	ACAGCCAATC	ACAAAGACTC	ACTTGAAACC	180
TTTTTTACGTC	GTTTCTTTTT	CACTTATCAA	GACACCAACT	ACCCACTTTC	TATCCTAGCA	240
GCTGATAAAA	AAACAGACCT	GCTGACATTT	TTTCAATCAG	AAGATGAAC	GACAGCAGAT	300
ATTTTTTTATA	CTGTTGCTTT	TCAACTTTTA	GGCTTTTCTT	ATTTGGTTGA	CTTCGAAGAT	360
AGTGACGTTT	TTCTGTAAAGA	AACTGGATTT	CCCATTATAT	ATGGTGACTT	GATTGAAAAT	420
CTCTATCAGT	TACTCAATAC	TCGCACCAAA	AAAGGAAAATA	CTCTTATCGA	CCAACCTGTT	480
AGTGATGGTC	TTATTCGGGA	GGATAATGAC	TACCACTACT	TTAACGGCAA	GAGTTTGGCT	540
ACTTTTTCTA	ACCAGGATGT	CATTTCGTGAA	GTCGTTTACG	TTGAGTCTCG	TGTCGATACT	600
GACCAAAAAG	GGCTATCAGA	CCTAGTAAAG	GTTAGCATT	TTCGCCCTCG	TTTTGATGGA	660
AAAATCCCTG	CCATCATGAC	AGCCAGCCCT	TATCATCAGG	GAACCAATGA	CAAGGCTAGT	720
GACAAGGCTC	TCTACAAGAT	GGAGGGCGAG	CTTGAGGTTA	AACTTCCCTCA	CAAGATTGAG	780
CTAGAGAAAC	CTCAACTAAA	TCTCGTCCAA	CCCCAAGGTA	AAGCTGAGCT	TATAGCAGAG	840
GCTGAGGAAA	AGCTAACTCA	CATCAACTCT	AGCTATACAC	TAAACGACTA	CTTCCTTCCG	900
AGAGGCTTTG	CCAACTCTCTA	TGTCTCAGGT	GTTGGTACCA	AAGACTCGAC	AGGTTTCATG	960
ACTAATGGAG	ACTACCAGCA	AATCGAGGCT	TATAAAAATG	TCATCGATTG	GC'TTAACGGC	1020
CGTTGCCGTG	CCTTTACTGA	TCACACGCGC	CAGCGTCAAG	TCAAGGCTGA	TTGGTCAAAC	1080
GGAAAAGTTG	CTACAACAGG	ACTTTCCTAT	CTAGGTACCA	TGTCCAATGG	TC'TTGC GACT	1140
ACAGGAGTCG	ATGGTTTAGA	AGTTATCAT	GCCGAGGCAG	GAATTTTCATC	ATGGTACAAC	1200
TACTACCGTG	AAAACGGTCT	GGTGACTAGC	CCAGGTGGTT	ATCCAGGTGA	GGACTTTGAC	1260
TCCCTTGCTG	AGTTAACCTA	TTCTCGTAAT	CTCTTAGCTG	GCGACTATAT	CCGTGGCAAT	1320
GAAGCTCACC	AAGCTGACTT	AGAAAAAGTG	AAAGCTCAGC	TAGACCGAAA	AACTGGGGAC	1380
TACAATCAAT	TTTGGCATGA	CCGCAATTAT	CTGCTCAAATG	CCCATAAAGT	AAAGGCAGAG	1440
GTTGTCTTTA	CTCATGGTTC	TCAGGATTGG	AATGTCAAAC	CAC'TTCATGT	TTACCAGATG	1500
TTCCATGCTC	TTCCCTACTCA	TATACACAAG	CATCTCTTTT	TCCATAATGG	TGCCCATGTT	1560
TACATGAACA	ATTGGCAATC	AATTGACTTC	CGTGAGTCCA	TAAATGCCTT	ATTGACCAAG	1620
AAATTACTAG	GACAGGAAAC	AGACTTTCAA	CTTCCTACTG	TTATCTGGCA	GGACAATACA	1680
GCTCCACAGA	CTTGGTTATC	ACTTGATAAC	TTCCGGTGGGC	AAGAAAAC	TGAAACCTTC	1740
TCACTTGGTC	AAGAAGAGCA	AGCTATTCAA	AACCAGTACC	CAGATAAGGA	TTTTGAGCGC	1800
TATGGTAAGA	CATACCAAAC	CTTCAATACA	GAGCTCTATC	AAGGGAAAGC	CAATCAGATT	1860
ACTATTAACC	TTCTGTGAC	TAAAGATCTC	CACCTAAACG	GTCGCGCTCA	GCTCAATCTT	1920
CGTATCAAAT	CCAGTACAAA	CAAGGGGCTC	TTATCTGCCC	AACTGGCTAGA	ATTTGGGCCA	1980
AAGAAATACC	TACAACCTTA	TCCAGCTATT	TTAAGTGCTA	GAACCATTGA	CAACGGTCGC	2040
TATCACATGT	TGGAAAATCT	CTGTGAATTG	CCATTTAGAC	CAGAGGCACA	ACGAGTCGTG	2100
ACAAAAGGTT	ACCTTAATTT	ACAAAATAGA	AATGATTTAC	TGTTAGTAGA	GGATATTACT	2160
GCAGATGAAT	GGATGGACGT	TCAATTTGAA	CTGCAGCCAA	CTATTTACAA	GCTAAAAGAA	2220

GGAGACACTC	TCCGTTTAGT	CCTCTATACT	ACTGACTTTG	AAATCACCAT	CCGTGACAAT	2280
ACAGACTACC	ACTTGACTGT	CGACCTCGCT	CAGTCCATGC	TTACCTTACC	TTGCTAA	2337

(2) INFORMATION FOR SEQ ID NO:2541:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 741 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...741

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2541:

GACCCTAAAT	TCCAGATTTT	AGACATCATC	AATAAGGATA	CACAACAAGG	AATCTTTGGC	60
AAACTGGACT	ATGAAGCTCC	ATCTTGTCCT	GAGTGCGGAA	GTCAAATGAA	GAAATATTAC	120
TTTCAAAAAC	CTTCTAAAAT	TCCTTATCTT	GAAACAAC TG	GTATGCC TAC	TAGAATTCTC	180
CTTAGAAAGC	GTGCTTTCAA	GTGCTATCAT	TGTTCTAAAA	TTATGGTTGC	TGAAACTTCT	240
ATCGTCAAGA	AGAATCATCA	AATCCCTCGT	ATCATCAACC	AAAAGATTGC	TCAAAAGTTA	300
ATTGAAAAGA	TTTCTATGAC	TGATATTGCC	CATCAGCTTT	CCATCTCAAC	TTCAACTGTC	360
ATTCGTAAGC	TCAATGATTT	TCACTTTAAA	CATGATTTTT	CTTGTCTTTC	TGAGATTATG	420
TCTTGGGATG	AGTATGCTTT	TACAAAGGGA	AAGATGAGCT	TCATTGCGCA	AGATTTTAAAC	480
AAGCTCAATA	TCATCACTGT	TCTTGAGGGT	AGAACACAAG	CTATCATTCG	AAATCACTTT	540
CTTCGCTACG	ATAGAGTTGT	CCGATGTCGC	GTCAAAAATTA	TTACTATGGA	TATGTTT TAGT	600
CCTTACTATG	ACTTGGCTAA	ACAGCTTCGC	TTTCAAATTT	CTAGGCTCAG	GCTGAAACAG	660
TCTCCCAGAC	TGTTTCACTC	CCGAATGCTA	AAATCGTGTT	GGATCGCTTT	CACATTGTAC	720
AACATCTTAG	CCGTGCTATG	A				741

(2) INFORMATION FOR SEQ ID NO:2542:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 612 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...612

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2542:

TATACTAAAT	TACTAGAGGC	AAATCCCCAG	TATGTGGTCC	TCAATCCCCTT	GGAAGCCAAG	60
GCAAAATGGC	GGGACTTGT	TGGCAATGAT	AATCCCATTC	ATGTGGAAGT	TGGAAGTGGA	120
AAGGGTGCCT	TTGTTTCAGG	TATGGCCAAG	CAAAACCCCTG	ACATCAACTA	TATCGGGATT	180
GATATTCAAA	AGTCTGTTTT	GAGCTACGCT	TTGGACAAGG	TGCTTGAAGT	TGGAGTGCCT	240
AACATCAAGC	TCTTGTGGGT	AGATGGTTCT	GACTTGACTG	ACTACTTTGA	AGACGGTGAG	300
ATTGATCGCT	TGTATCTGAA	CTTTTCAGAT	CCATGGCCGA	AAAAACGCCA	TGAAAAGCGT	360
CGTTTGACCT	ACAAGACCTT	TTTGGACACC	TTCAAACGTA	TCTTGCCTGA	AAATGGAGAA	420
ATTCATTTCA	AAACGGATAA	CCGTGGCTTG	TTTGAGTACA	GTTTAGTGAG	CTTTTCTCAA	480
TATGGCATGA	AACTCAATGG	TGTCTGGCTA	GATTTGCATG	CCAGTGATTT	TGAAGGCAAT	540
GTCATGACAG	AATACGAGCA	AAAATTCTCA	AACAAGGGGC	AAGTTATCTA	CCGAGTTGAG	600
GCAGAAATTTT	AA					612

(2) INFORMATION FOR SEQ ID NO:2543:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2543:

TATAATAAAT	TTGAAGTAAT	ATTCAAGGAG	AATCAAATGA	TTTACGAATT	TTGTGCTGAA	60
AATGTGACTT	TACTTGAAAA	AGCGATGCAG	GCTGGAGCTC	GTCGGATTGA	ACTCTGTGAT	120
AATCTAGCAG	TTGGTGGGAC	AACACCTAGC	TATGGAGTGA	CTAAGGCAGC	GGTTGAAGTG	180
GCAGCTAACT	ACGATACAAC	CATCATGACC	ATGATTTCGC	CACGTGGTGG	TGACTTTGTC	240
TATAATGACC	TAGAAATTGC	TATCATGCTA	GAAGACATTT	GTTTGACTGC	TCAGGCCTGG	300
AAGTCAAGGG	GTTGTATTTG	GAGCTTTAAC	TGCTGA			336

(2) INFORMATION FOR SEQ ID NO:2544:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 570 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...570

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2544:

ATGACCAAAT	TACTTGTAGG	CTTGGGAAAT	CCAGGGGATA	AATATTTTGA	AACAAAACAC	60
AATGTTGGTT	TTATGTTGAT	TGATCAACTA	GCGAAGAAAC	AGAATGTCAC	TTTTACACAC	120
GATAAGATAT	TTCAAGCTGA	CCTAGCATCC	TTTTTCCTAA	ATGGAGAAAA	AATTTATCTG	180
GTTAAACCAA	CGACCTTTAT	GAATGAAAGT	GGAAAAGCAG	TTCATGCTTT	ATTAACCTAC	240
TATGGTTTGG	ATATTGACGA	TTTACTTATC	ATTTACGATG	ATCTTGACAT	GGAAGTTGGG	300
AAAATTCGTT	TAAGAGCAAA	AGGCTCAGCA	GGTGGTCATA	ATGGTATCAA	GTCTATTATT	360
CAACATATAG	GAAGTCAGGT	CTTTAACCGT	GTTAAGATTG	GAATTGGAAG	ACCTAAAAAT	420
GGTATGTCAG	TTGTTTCATCA	TGTTTTGAGT	AAGTTTGACA	GGGATGAGTA	TATCGGTATT	480
TTACAGTCTG	TTGACAAAAGT	TGACGATTCT	GTAAACTACT	ATTTACAAGA	GAAAAATTTT	540
GAGAAAACAA	TGCAGAGGTA	TAACGGATAA				570

(2) INFORMATION FOR SEQ ID NO:2545:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 399 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...399

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2545:

ATTTTTTTTT	CACTTTCCCC	CACACCCACC	CCCATTCCCN	TTTCTTCCTT	TCTTTCCCCC	60
TCCCAACCTC	CCCCCNCCCC	CNCCTTTTCC	TTCCCCCTTT	TTCCCCANAC	CTCCCNCAAC	120
ACCCTTTTTT	TCCTTCTTTT	CCCCCCCCCN	NCCNTCACCC	CNCCTTCTTC	CTCCTTTCCC	180
TCCCTCCCN	TTTTCTCCCC	CCCCTTCNNN	TTTCCCTCTT	TTTTTTNNTT	TCCCTTTTNN	240
NNNNNNNTNN	TTTTTTTTTT	TTNNNNNNNN	NNTTNNNNNT	ATTNNNTTNC	CCCCANNNNN	300
NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNTATTCAA	TGAAAATCAA	AGAGCAAACCT	360
AGAAAGCTAG	CCGCAGGTTG	TTCAAAACAC	TGTTTTTAG			399

(2) INFORMATION FOR SEQ ID NO:2546:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1974 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1974
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2546:

ATGAAAAAAT	TTTATGTAAG	TCCAATTTTT	CCTATTCTAG	TAGGATTGAT	TGCGTTTGGA	60
GTCTTATCCA	CTTTCATTAT	TTTTGTAAAT	AATAATCTGT	TGACGGTTTT	AATTTTGTTT	120
CTTTTTGTAG	GAGGCTATGT	TTTTTTATTT	AAGAACTGA	GAGTGCAATTA	TACAAGGAGT	180
GATGTAGAAC	AGATACAGTA	TGTAAACCAC	CAAGCGGAAG	AAAGTTTGAC	ATCTCTATTG	240
GAACAGATGC	CTGTAGGTGT	TATGAAATTG	AATTTATCTT	CTGGAGAGGT	TGAGTGGTTT	300
AATCCCTATG	CTGAATTGAT	TTTGACCAAG	GAAGATGGTG	ATTTTGATTT	GGAAGCTGTT	360
CAAACGATTA	TCAAGGCTTC	AGTAGGAAAT	CCGTCTACTT	ATGCCAAGCT	TGGTGAGAAG	420
CGTTATGCTG	TTCATATGGA	TGCTTCTTCA	GGTGTTTTGT	ATTTTGTAGA	TGTATCCAGG	480
GAACAAGCCA	TAACAGATGA	ATTGGTAACA	AGTCGACCAG	TGATTGGGAT	TGTCTCTGTG	540
GATAATTATG	ATGATTTGGA	GGATGCAACT	TCTGAGTCAG	ATATTAGTCA	AATCAATAGT	600
TTTGTAGCTA	ATTTTATATC	AGAGTTTTCA	GAAAAATACA	TGATGTTTTT	TCGTCGGGTA	660
AGTATGGATC	GATTTTATCT	ATTTACTGAC	TACACGGTGC	TTGAGGGCTT	GATGAATGAT	720
AAATTTTCTG	TTATTTGATG	TTTCAGAGAA	GAGTCGAAAC	AGAGACAGTT	GCCCTTGACC	780
TTAAGTATGG	GATTTTCTTA	TGGCGATGGA	AATCATGATG	AGATAGGGAA	AGTTGCTTTG	840
CTCAATTTGA	ACTTGGCTGA	AGTACGTGGT	GGCGACCAGG	TGGTTGTTAA	GGAAAACGAC	900
GAAACGAAAA	ATCCAGTTTA	TTTTGGTGGT	GGGTCTGCTG	CTTCAATCAA	GCGTACACGG	960
ACTCGTACGC	GCGCTATGAT	GACAGCTATT	TCAGATAAGA	TTCCGAGTGT	AGATCAGGTT	1020
TTTGTAGTCG	GTCACAAAAA	TTTAGACATG	GATGCTTTTG	GCTCTGCTGT	AGGTATGCAG	1080
TTGTTGCGCA	GCAATGTGAT	TGAAAAATAG	TATGCTCTTT	ATGATGAAGA	ACAAATGTCT	1140
CCAGATATTG	AACGAGCTGT	TTCAATTCATA	GAAAAAGAAG	GAGTTACGAA	GTTGTTGTCT	1200
GTTAAGGATG	CAATGGGGAT	GGTGACCAAT	CGTTCTTTGT	TGATTCTTGT	AGACCATTCA	1260
AAGACAGCCT	TAACATTATC	AAAAGAATTT	TATGATTTAT	TTACCCAAAC	CATTGTTATT	1320
GACCACCATA	GAAGGGATCA	GGATTTTCCA	GATAATGCGG	TCATTACTTA	TATCGAAAGT	1380
GGTGCAAGTA	GTGCCAGTGA	GTTGGTAACG	GAATTGATTC	AGTTCCAGAA	TTCTAAGAAA	1440
AATCGTTTGA	GTCGTATGCA	AGCAAGTGTT	TTGATGGCTG	GTATGATGTT	GGATACTAAA	1500
AATTTACCT	CGCGAGTAAC	TAGTCGGACA	TTTGATGTTG	CTAGCTATCT	CAGAACGCGC	1560
GGAAGTGATA	GTATTGCTAT	CCAGGAAATC	GCTGCGACAG	ATTTTGAAGA	ATATCGTGAG	1620
GTCAATGAAC	TTATTTTACA	GGGGCGTAAA	TTAGGTTTCA	ATGTACTAAT	AGCAGAGGCT	1680
AAGGACACGA	AATGCTATGA	TACAGTTGTT	ATTAGTAAGG	CAGCAGATGC	CATGTTAGCC	1740
ATGTCAGGTA	TTGAAGCGAG	TTTTGTTCTT	GCGAAGAATA	TACAAGGATT	TATCTCTATC	1800
TCAGCTCGAA	GTCGTAGTAA	ACTGAATGTA	CAACGGATTA	TGGAAGAGTT	AGGCGGTGGA	1860
GGCCACTTTA	ATTTGGCAGC	AGCTCAAATT	AAAGATGTAA	CCTTGTCAGA	AGCAGGTGAA	1920
AAACTGACAG	AAATTGTATT	AAATGAAATA	AAGGAAAAGG	AGAAAAGAAGA	ATGA	1974

(2) INFORMATION FOR SEQ ID NO:2547:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1332

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2547:

GCGTGTTTTT	CTTGCTTGAT	TATAAACCCA	AAAGATTTGT	TTCCTATACT	GTGGTTGTCT	60
CATTTTTTGC	TGTTGCAGCT	TTATCTCTTT	ATCAGTTGGT	TGACTTACCT	CTTAATCCAA	120
AAAAATGACAA	TCAGCTCTCT	GCTGAAAGGT	TTTTCATCTT	TCAAATTTGG	TCTTATCTTC	180
AATTATGTGA	TGAAAAATAGG	GACAACTATT	TTACTGACGG	CCTTACTGAT	TGGGGTGGGC	240
AGAAGTTTAG	AACAAGAAAA	CAAAGAACTT	GCTTATCAGC	AACAGTGGGT	AAGTCAAGGT	300
AATTACCTGA	CCTTAGAAAC	CTTCAAACTC	AATGATAATC	TGTGGCAAGA	AGAGCTAGCA	360
GGGTCAGGGA	AATCTACAGA	TTATTTCTAT	CGATTTTATC	AGGATTTGGT	AGAAAAAACG	420
CAGGCGGGCT	ATGTGCAGAG	TAGCAGTCTT	CCTGTAAAAA	ATTTTGTCCA	ATCAGAACAG	480
ATTCAGCAAT	ATCAGTTAAC	AGATACGGTG	GATGTTTACT	ATGCCAATCG	CAATTTTCTA	540
AAGAGCAAGG	GATTCAAGCT	ACCAGATACC	GGTATTAAAA	AAGTTATTTT	GATGCCAGCA	600
AGTACGAAAG	GTGAAGAAGA	TAAAAATCAG	CTCTTGGGGA	AGTTAATTGC	CTTTCATTTCG	660
ATGAAGTATG	AAGAGCAGCA	AAAACGAACG	ATAGAGGAGA	TGGATGTCGA	GATTGCCTAT	720
TATGAAGGAG	ATTGGTCATT	TTTCCCATAT	AGTGATAAGC	GAAAGGAAAA	TCTCTCCAAT	780
CCAATTATTA	GCTTGGTCAA	TGATTCTGAT	ATGATGTGGG	ATGAGAAAGC	CTCCCTGTCA	840
ACAACCTGGCT	TAAATAATCC	GATTAAAAAT	GAAAATACGG	TTCAACATCA	AAAAGAGATT	900
ACAGAGTTAG	TTGAGAAATT	GTCAGATGGA	AATTATTTAA	AATTTTCATC	TATTCAAGCC	960
ATTCAACAAG	AGAAAGTGGA	TTCTTATCGA	GATGCTGTTT	GGAATTTTAA	CCTACTCTTT	1020
GCTTTGTTTG	GTCTCCTTAG	CATGATGATT	TCCTACTTCT	TACTAGTAAC	AACTTTCTTA	1080
TTGAAGCGCA	GGGATATCAT	TACCAAGAAG	TTTATGGGGT	GGAAACTGGT	CGATCGCTAC	1140
CGTCCTCTCC	TCGTTCTGCT	CTTGCTGGGC	TATAGTTTCC	CTCTTCTAGT	CTTGATTTTC	1200
TTTGCCCATG	CGTTCTTACC	ACTTCTACTG	TTTGCAGGTT	TTACATGTCT	GGATATACTA	1260
TTTGTGCTAG	GCTTAGCTTC	TAGGATGGAG	AAAAGAAGTC	TAGTAGAGTT	ATTGAAAGGG	1320
GGCATCTTAT	GA					1332

(2) INFORMATION FOR SEQ ID NO:2548:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...387

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2548:

TTAAGTTTTT	CTATCACAGA	CATAAAAGAT	ATATATTGGT	TTATCAGGAA	AGTTTCTGAT	60
AAACTAGCAA	GTACTTTACA	TTTGAATGGA	GACAGTATGA	AAAAATTTAG	CCTATTACTA	120
GCTATCCTAC	CATTTTTGGT	TGCCTGTGAG	AATCAAGCTA	CACCCAAAGA	GACTAGCGCT	180
CAAAAGACAA	TCGTCCTTGC	TACAGCTGGC	GACAGTGCAC	CATTTGACTA	CGAAGACAAG	240
GGCAATCTGA	CAGGCTTTGA	TATCGAAGTT	TTAAAGGCAG	TAGATGAAAA	ACTCAGCGAC	300
TACGAGATTC	AATTCCAAAG	AACCGCCTGG	GAGAGCATCT	TCCCAGGACT	TGATTCTGGT	360
CACTATCAGG	CTGCGGCAAT	AACTTGA				387

(2) INFORMATION FOR SEQ ID NO:2549:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 549 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2549:

GGAGACTTTT	CTTTTTGGAG	GTTTGTCATG	AAAACAAAAG	AAGTTGTAGA	CGAATTGACC	60
GTCAAACGAG	CGATTACGCG	TATTACTTAT	GAGATTATCG	AACGCAACAA	AGATTTGAAT	120
AAGATTGTCT	TGGCTGGTAT	TAAAACTCGT	GGTGTCTTTA	TTGCCCACCG	AATCCAAGAA	180
CGTTTGAAGC	AGTTAGAAAA	TCTTTCAGTT	CCTGTTGTGG	AATTGGATAC	TAAACCTTTC	240
CGTGATGATG	TTAAAAGTGG	AGAAGATACT	TCTTTGGTTT	CTGTGATGT	GACAGACCGC	300
GAAGTTATCT	TGGTGGATGA	TGTGCTCTAT	ACAGGTCGTA	CCATCCGTGC	TGCTATTGAT	360
AATATTGTCG	GCATGGTCG	TCCTGCGCGT	GTGAGTTTAG	CAGTTCTAGT	CGATCGTGGA	420
CATAGAGAAT	TGCCAATCCG	TCCAGATTAC	GTTGGAAAAA	ATATCCCAAC	CAGTCGTTCT	480
GAAGAAATCA	TCGTAGAGAT	GACAGAACTT	GATGACCAAG	ACAGAGTTCT	GATTACTGAA	540
GAAGCTTAG						549

(2) INFORMATION FOR SEQ ID NO:2550:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1215 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1215
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2550:

AGGCTGTTTT	CCACAGATTT	CACAGACTCT	ATTATTACTA	TTATCTTTCT	AATACTAAAA	60
ATAAATAAAG	GAGAATCCAT	GATTCATTTT	TCAATTAATA	AAAATTTATT	TCTACAAGCA	120
TTAAATACTA	CTAAGAGAGC	TATTAGTTCT	AAAAATGCCA	TTCTATTTT	ATCAACAGTA	180
AAAAATTGACG	TGACCAATGA	AGGTATTACT	TTAATTGGTT	CAAATGGTCA	AATTTCAATT	240
GAAAAATTTTA	TTTCTCAAAA	AAATGAAGAT	GCTGGTTTGT	TAATTACTTC	TTTAGGTTTCG	300
ATCCTTCTTG	AAGCTTCTTT	CTTTATCAAT	GTAGTATCTA	GTTTACCTGA	TGTAACTCTT	360
GATTTTAAAG	AAATTGAACA	AAATCAAATT	GTTTTAACCA	GTGGCAAATC	AGAAATTACC	420
CTAAAAGGAA	AAGATAGCGA	ACAATATCCA	CGAATCCAAG	AAATTTTCAGC	AAGCACTCCT	480
TTAATACTTG	AAACAAAATT	ACTCAAGAAA	ATTATTAATG	AAACAGCCTT	TGCTGCAAGT	540
ACACAAGAGA	GTCGTCCGAT	TTTAACAGGT	GTCCACTTCG	TATTGAGTCA	ACACAAAGAG	600
TTAAAAACAG	TTGCAACAGA	CTCTCATCGC	CTAAGCCAGA	AAAAATTGAC	TCTTGAAAAA	660
AATAGTGATG	ATTTTGATGT	CGTAATTCCT	AGCCGTTCCT	TACGCGAATT	TTCAGCGGTA	720
TTTACAGATG	ATATCGAAAC	TGTAGAGATT	TTCTTTGCCA	ATAACCAAAT	CCTCTTTAGA	780
AGCGAAAAATA	TTAGCTTCTA	TACTCGTCTC	CTAGAAGGAA	ACTATCCTGA	TACAGATCGC	840
TTGATTCCAA	CAGACTTTAA	CACACTATT	ACTTTTAATG	TGGTAAACTT	ACGCCAGTCA	900
ATGGAGCGTG	CCCGTCTTTT	ATCAAGTGCG	ACTCAAAATG	GTAAGTGAA	ACTTGAAATT	960
AAGGATGGGG	TTGTTAGCGC	CCATGTTTAC	TCTCCAGAAG	TTGGTAAAGT	AAACGAAGAA	1020
ATCGATACTG	ATCAGGTTAC	TGGTGAAGAT	TTGACCATTA	GTTTCAACCC	AACTTACTTG	1080
ATTGATTCTC	TTAAAGCTTT	AAATAGCGAA	AAGGTGACCA	TTAGCTTTAT	CTCAGCTGTT	1140
CGTCCATTTA	CTCTTGTGCC	AGCAGATACT	GACGAAGACT	TCATGCAGCT	CATTACACCA	1200
GTTCTGTACAA	ATTAA					1215

(2) INFORMATION FOR SEQ ID NO:2551:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 186 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2551:

TGCTGGTTTT CAAGTACGGT CTATGAATTT GTCAAGTCGG GTCGCTATCC GAGAAATGGC	60
TGGTTCCGTC GTTTGAATGC TCATGATGAG GAGCATATCA CGGCTAGTCT GGACTCAGTT	120
GGCATGTGGG ACATCGAGAC AAACGCTTGG GTTCTCTATC TGGGGGACAA AAGCAGCGAG	180
CGGTGA	186

(2) INFORMATION FOR SEQ ID NO:2552:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2552:

AAAGTGAAAT TTAAAATCAA ACAAGATTTC TATGATTGGG AATCAAATGT GAAACGACTG	60
GCAGGAGAGG AACTTGAGAT TACTGAGGAG CGCTATGCTG AGCTGGCTGA CAATATTGCC	120
AGCAACGGTG TCACTATCTC AGACGTTCTT GAGAAAATCC TCCCTGAACC TGAGTTCTTA	180
GAAGAGGATT GA	192

(2) INFORMATION FOR SEQ ID NO:2553:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 408 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...408

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2553:

TGTCAGCTTT	CAAAATGCCA	TGGAATATCT	GGTCTTGAAA	GAAATATAAA	CTCAAAAATG	60
AATGATAAAG	ACAGGAAAGG	GGCTTGTTTT	ATGGACACAA	AAGAATTATT	TGACGCGCTG	120
GATGATTTTT	CCCAACAATT	ATTGGTAACC	TTAGCCGATG	TGGAAGCCAT	CAAGAAAAAT	180
CTCAAGAGCT	TGGTAGAAGA	AAATACAGCT	CTTCGCTTGG	AAAATAGTAA	GTTGCGAGAA	240
CGCTTGGGTG	AGGTGGAAGC	AGACGCTCCC	GTCAAGGCCA	AGCATGTTTC	CGAAAGTGTC	300
CGTCGTATTT	ACCGTGATGG	ATTTACGTA	TGTAATGATT	TTTATGGACA	ACGTCGAGAG	360
CAGGACGAAG	AATGTATGTT	CTGTGATGAG	TTGTTATACA	GGGAGTAA		408

(2) INFORMATION FOR SEQ ID NO:2554:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 885 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...885

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2554:

AAGGAGCTTT	CAAAAGGAGA	AGGGCTAGGG	AATAAAATCT	TGGCCAATAT	TCGTGAAGTA	60
GATGCGATTG	TTACAGTAGT	TCGTGCTTTT	GATGATGAAA	ATGTGATGCG	CGAGCAAGGA	120
CGTGAAGACG	CCTTTGTAGA	TCCACTTGCA	GATATTGATA	CAATTAATCT	GGAATTAATT	180
CTTGCTGACT	TAGAAATCAGT	GAACAAACGA	TATGCGCGTG	TAGAAAAAGAT	GGCACGTACG	240
CAAAAAGATA	AAGAATCAGT	AGCAGAATTC	AATGTTCTTC	AAAAGATTAA	ACCAGTCCTA	300
GAAGACGGGA	AATCAGCTCG	TACCATTGAA	TTTACAGATG	AGGAACAAAA	GGTTGTCAAA	360
GGTCTTTTCC	TTTTGACGAC	TAAACCAGTT	CTTTATGTAG	CTAATGTGGA	CGAGGATGTG	420
GTTTCAGAAC	CTGACTCTAT	CGACTATGTC	AAACAAATTC	GTGAATTTGC	AGCGACAGAA	480
AATGCTGAAG	TAGTCGTTAT	TTCTGCGCGT	GCTGAGGAAG	AAATTTCTGA	ATTGGATGAT	540
GAAGATAAAA	AAGAGTTTCT	TGAAGCCATT	GGTTTGACAG	AATCAGGTGT	AGATAAGTTG	600
ACGCGTGCAG	CTTACCACTT	GCTTGGAATTG	GGAACCTACT	TCACAGCTGG	TGAAAAAGAA	660
GTTTCGCGCTT	GGACTTTCAA	ACGTGGTATG	AAGGCTCCTC	AAGCAGCTGG	TATTATCCAC	720
TCAGACTTTG	AAAAAGGCTT	TATTCGTGCA	GTAACCATGT	CATATGAAGA	TCTAGTGAAA	780
TACGGATCTG	AAAAGGCCGT	AAAAGAAGCT	GGACGCTTGC	GTGAAGAAGG	AAAAGAATAT	840
ATCGTTCAAG	ATGGCGATAT	CATGGAATTC	CGCTTTAATG	TCTAA		885

(2) INFORMATION FOR SEQ ID NO:2555:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1101 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1101
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2555:

CAGGCTATTT	CGGAGATTCC	TGGGGTCTTG	CGTTTGACCT	TGGGGGAACC	TGATTTTACA	60
ACGCCAGACC	ATGTCAAGGA	GGCGGCCAAG	CGAGCGATTG	ATCAGAACCA	ATCCTACTAT	120
ACAGGGATGA	GTGGTCTGCT	GACTCTACGT	CAGGCAGCCA	GTGACTTTGT	TAAGGAAAAG	180
TACCAACTGG	ACTATGCTCC	TGAAAAATGAA	ATCTTGTTTA	CAATTGGGGC	GACAGAGGCT	240
TTATCTGCGA	CTTTGACGGC	TATTTTGGAA	GAGGGCGACA	AGGTACTTTT	GCCAGCTCCT	300
GCTTATCCAG	GCTATGAACC	GATTGTTAAC	TTAGTTGGGG	CAGAAATTGT	TGAGATTGAT	360
ACGACTGAAA	ATGGTTTTGT	CTTGACTCCT	GAGATGTTGG	AGAAGGCCAT	TTTGGAGCAG	420
GGTGATAAGC	TCAAGGCGGT	TATTCTCAAC	TATCCAGCCA	ATCCGACAGG	AATTACCTAC	480
AGTCGAGAGC	AGTTAGAGGC	CTTGGCAGCT	GTTTTACGCA	AGTACGAAAT	TTTTGTTGTC	540
TGTGATGAGG	TTTACTCAGA	ATTGACCTAC	ACAGGCGAAG	CCCATGTGTC	TCTAGGAACG	600
ATGTTGAGAG	ACCAGGCTAT	TATTATCAAT	GGTTTGTCTA	AATCGCATGC	CATGACAGGT	660
TGGCGTTTGG	GGCTGATTTT	CGCTCCTGCG	GCCTTCACAG	CCCAGTTAAT	CAAGAGTCAC	720
CAATACTTGG	TCACTGCCGC	AAATACCATG	GCGCAACATG	CTGCGGTAGA	AGCCTTGACG	780
GCTGGTAAAA	ATGATGCGGA	GCCCATGAAG	AAGGAATATA	TCCAGCGTCG	GGACTATATC	840
ATCGAAAAAA	TGACTGCTCT	TGGTTTTGAG	ATTATCAAAC	CAGACGGTGC	CTTCTATATT	900
TTTGCTAAAA	TTCCAGCGGG	CTACAATCAA	GACTCCTTTG	CTTTTCTGAA	GGATTTTGCT	960
CAGAAGAAGG	CCGTTGCCCT	TATCCCTGGT	GCAGCCTTTG	GACGTTACGG	GGAAGGCTAC	1020
GTCCGCCAT	CTTATGCAGC	CAGCATGGAG	ACTATCAAAG	AAGCCATGAA	ACGACTTGAG	1080
GAGTACATGA	GAGAAGCATG	A				1101

(2) INFORMATION FOR SEQ ID NO:2556:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 816 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2556:

AAGGATATTT	CTATGCAACC	AACTTACAAC	ATTGACAATC	CAAACCTGTC	TTATGAAGCG	60
AAGCGTGATT	TATGGCGGAT	AGGTTTTGGT	CTGCAGAAAG	TTGACAATCT	AGTGCCATCA	120
GCGTATATGG	AATCTTTGGC	TGAGAAACAG	TCCCGGGGAG	AACTGACTTA	TGAGCAGGTT	180
TATGAGGATG	CAACGGCTTA	TCACCATACT	ATTGATGCAA	GTACGGAAGA	GGCAGACTTG	240
GTTTCTCTAC	GTATTGTAGA	ACTATTGTCT	CGAAGAGGCT	TTAGCTTTAG	TCCTGCGACC	300
TTACTTGCTA	TTCATAAGGA	GTTGTTTCAA	GATATATTTG	AACCCTCTAT	TCCGGTG GGG	360
CAATTTTCGTC	AGACCAATAT	CACAAAGAAT	GAACCTGTTT	TGAATGGTGA	AAGTGTGTGT	420
TACTCTGATT	ACTCCATGAT	TCAAATGACC	TTAGATTATG	ATTTTAATCA	GGAAAAACAA	480
GTTGCATATG	CGACACTAAC	TCAGGCGGAT	GTGGTTAAAC	AAATCCAGCA	TTTTATTTCA	540
GGAATCTGGC	AGATTCATCC	ATTTTCGCGAA	GGAAACACTC	GGACAGTAAC	GGTCTTTTTG	600
ATTCAGTATC	TTCGTGAGTT	TGGTTTTGAT	ATTGATAATA	CACCATTTCA	GCAACATTCC	660
AAATATTTTC	GTGATGCCTT	GGTATTAGAT	AATGCAAAGA	TTTTACAGCG	ACGTTCTGAG	720
TTTTTAACAG	CTTTTTTTGA	AAATCTCTTG	CTCGGTGGTC	AAAATGATTT	GTCTTCAGAA	780
AAAATGTATC	TAGATTTAGA	CCTCGATTTT	TCATAA			816

(2) INFORMATION FOR SEQ ID NO:2557:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 378 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2557:

ATCAGGAAAT	TCGCCGCATT	CAAAACTTAC	GTGAGGACGA	GCTTTATGTT	GCTGCCAAGG	60
ATTTTGCAAG	TCCCTGTAGA	ATTGGTCCAA	TATGTTTCATG	AACATGGAAA	ATTGCCAGTT	120
GTAAATTTTCG	CTGCTGGAGG	TGTTGCAACG	CCAGCAGATG	CTGCGTTAAT	GATGCAATTA	180
GGGGCAGAGG	GGGTCTTTGT	CGGTTCAAGT	ATTTTCAAGT	CAGGAGATCC	TGTTAAACGA	240
GCGAGTGCCA	TTGTTAAGGC	TGTGACTAAC	TTCCGTAATC	CTCAAATCCT	AGCTCAAATC	300
TCTGAAGATT	TAGGAGAAGC	CATGGTTGGT	ATTAATGAAA	ATGAAATCCA	AATTCTCATG	360
GCTGAACGAG	GAAAATAG					378

(2) INFORMATION FOR SEQ ID NO:2558:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 672 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...672
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2558:

AGGAGGAAAT	TCCCTATGAG	AAAGAAACTC	TTTCTGACTA	GTGCTGCGGT	CTTGTGGGCA	60
GTAACAGCTA	TGAATAGCGT	CCATGCAGCA	ACAGATGTTT	AAAAAGTTAT	CGATGAAACC	120
TATGTCCAAC	CTGAATATGT	CCTAGGTTCC	TCCCTATCTG	AAGACCAAAA	AAATCAAACCT	180
CTTAAAAAAC	TGGGCTACAA	TGCCTCAACA	GATACCAAAG	AACTCAAGAC	CATGACACCT	240
GATGTTTATT	CTAAAATCAT	GAATGTGGCC	AATGACTCTA	GCTTACAGTT	GTATTCATCA	300
GCCAAGATTG	AAAAGCTAGG	TGACAAATCG	CCACTTGAGG	TCAAGATTGA	AACACCAGAA	360
AATATCACTA	AGGTGACTCA	GGATATGTAC	CGAAACGCAG	CAGTAACGCT	GGGTATGGAA	420
CATGCCAAAA	TCAGTGTAGC	AGCCCCATT	CCAGTTACAG	GAGAAAGTGC	TTTAGCAGGG	480
ATTTACTATT	CGCTAGAGGC	TAATGGAGCC	AAGGTGCCAC	AAGCTAATAA	AGATTTGGCT	540
CAAGAAGAGC	TAAAAGCTTT	GTCAGATATC	AATGCTGAAA	ACAAGGACAA	ATCAGGCTAT	600
GATGCTAATA	AATTAAACGT	TGCCCTAGCT	GATATCAAGT	CAGGACTCGC	CAAAGCTAAA	660
GAAAGCAAGG	GA					672

(2) INFORMATION FOR SEQ ID NO:2559:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 255 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...255
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2559:

CGTGAAATTT	CTTTTTACCA	AAATCATTCG	CTAATTGTTT	TTTTAGGGCG	ATTGATTTTT	60
ACTTCCGTCG	CATCAATCAT	TATCGTGTCC	TCAGAGCTGA	GAGGAGTTCT	TGAAATCGTA	120
ACACCACCTT	TGAACAAGAG	TTACTTCAAC	CCATTGGCTC	CGACGGATAA	AGAAGACTTG	180
ATAAGAACTC	TAGAGTTAGC	TCCCCATGTT	GAAGGTGGCT	ATTTTAGACA	AACAAAAAAA	240
CTTCAGACAC	TATAA					255

(2) INFORMATION FOR SEQ ID NO:2560:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1224 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1224
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2560:

AAGGAGATTT	CTGGTACTAT	ATTTGCAGTT	GTGACTCTTA	ATCACTATCA	TTGGTCATTG	60
ACTGTAACCA	CCTTGTTTTT	ATTAATGATT	ATGCTACTTG	TACCAAAAAT	CTTTGCATTG	120
AAAATGCGAG	AAGTTAGTCT	AAATTTAACT	AACCAAAATG	AAGCTTTTTT	AAAATTTAGT	180
GAGACTATAT	TGAATGGATT	TGATGTGTTA	GCGTCCCTGA	ATTTTTTATA	TGTATTGCCT	240
AAGAAAATTA	CAGAAGCAGG	AATTTTATTA	AAGTTGGTTA	TACAAAGCAA	GACCACTGTA	300
GTAACGTTAG	CAGGCGATAT	TAGCTTCTTT	CTCAATATTT	TTTTTCAGAT	ATCTTTCGTT	360
TTTTTTAACAG	GCTATCTTGC	AATAAAAGGA	ATAGTGAAAA	TTGGTACTAT	TGAAGCAATA	420
GGAGCACTAA	CAGGTGTTAT	TTTTACAGCG	CTAGGTGAAT	TAGGAGGTCA	ATTATCCTTT	480
ATTATTGGTA	CGAAGCCTAT	TTTTTTAAAA	TTGTATTCAA	TTAATCCAAT	TGAGTCAAAT	540
AAAATGAATG	ATATCGAACC	AAATGAGGTG	AATAGAGATT	TTCCGTTATA	TGAAGCAAAA	600
AATATTTGCT	ATAAGTATGG	AGATAAAGAA	ATATTAAAAA	ACTTAAATTT	TTGTTTTCAA	660
CGTAATGAAA	AGTATTTAAT	TTTAGGTGAA	AGTGGAAGCG	GGAAATCTAC	ATTATTAAAA	720
TTATTGAATG	GCTTTTTGAG	AGATTATAGT	GGAGAATTGC	GATTCTGCGG	GGATGATATA	780
AAAAAAACCT	CCTATTTAAA	TATGGTTTCG	AATGTTCTAT	ATGTAGATCA	AAAAGCTTAT	840
TTGTTTGAAAG	GTACGATTAG	AGATAATATT	TTATTGGAAG	AAAATTATAC	TGATGAAGAA	900
ATACTACAGT	CTTTAGAGCA	AGTTGGTTTG	AGTGTAAGAA	ATTTTCCTAA	TAACATTTTA	960
GATTATTATG	TTGGTGATGA	TGGGAGATTA	CTGTCAGGAG	GGCAGAAACA	AAAAATTACT	1020
TTAGCTAGAG	GGCTAATTAG	AAATAAGAAA	ATAGTATTAA	TTGACGAGGG	AACTTCTGCT	1080
ATCGATAGGA	GAACCTCGTT	AGCGATTGAA	CGTAAGATAT	TAGATAGAGA	GGATTTGACT	1140
GTCATTATTG	TTACCCATGC	TCCGCATCCG	GAACTTAAAC	AATATTTTAC	TAAGATATAT	1200
CAATTTCCAA	AGGATTTTAT	TTAA				1224

(2) INFORMATION FOR SEQ ID NO:2561:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 201 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2561:

TTGTGGATTT CTGTGCTGGG AATGGAGCAG TGGGGCTTTT TGCTAGCACT CGTACTCAAG	60
CACAGATATT GTCTGTTGAG ATTTTCAGGAG CGTTTGGCGG ATATGGCTGA ACGCTCTGTC	120
CGTTTGAATG GATTAGAGGA GCAAATGCAG GTCATCTGCG ATGATTTGAA AAATATGCCT	180
GCTCACATTC AGGGGAAGTA A	201

(2) INFORMATION FOR SEQ ID NO:2562:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 702 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...702

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2562:

GGGAGGATTT CTATGAAAAA GTATCAACTT CTATTCAAAA TAAGTGCAGT CTTCTCTTAC	60
TTATTTTTCG TATTTGGTCT TTCTCAGCTG ACGCTTATCG TCCAAAATTA TTGGCAATTT	120
TCTTCCAGAG TTGGCAATTT CGTCTGGATT CAAAATATCT TGAGTTTACT ATTTAGCGGA	180
GTCATGATTT GGATTCGGT TAAGACAGGC CATGGCTATC TCTTTCGCAT TCCAAGAAAA	240
AAATGGCTTT GGTATTCTAT TTTGACAGTA TTAGTGGTAG TGCTCCATAT CTCTTTTAAC	300
G TTCAGACAG CTAAACATGT TCAGTCAACT GCTGAGGGTT GGAACGTATT GATTGGTTAT	360
AGTGGGACCA ACTTTGCTGA GCTAGGTATC TATGTAACCC TGTTTTTCCT GACTCCACTA	420
ATGGAAGAGT TGATTTATAG GGGATTACTT CAACACGCCT TCTTTAAGCA TTCGCGATTT	480
GGGCTTGATT TGCTTCTTCC TTCCATTTTG TTTGCTCTTC CTCATTTTTT GAGTCTGCCT	540
AGTCTGTTAG ATATCTTCGT CTTTGCAACA TTTGGAATCA TCTTTGCCGG TTTGACCCGC	600
TATACCAAGA GTATTTATCC ATCCTATGCG GTGCATGTGA TCAATAATAT TGTAGCGACC	660
TTCCCGTTTT TGCTCACTTT TCTACATAGG GTCTTGGGGT AA	702

(2) INFORMATION FOR SEQ ID NO:2563:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 279 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...279
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2563:

TCTTCCGTTT	CCTTGTGTTG	GGGATCAAGG	AACATCTGCT	TGGTATCATT	AAATTCAATC	60
AAATCTCCAT	CTAGGAAAAA	TCCTGTCTTA	TCAGAGATAC	GTGAAGCTTG	CTGCATGGAA	120
CGGGTTACCA	GAAGCATGGT	GTA CTTGTCT	TTTAGACCAT	ACAAGGTTTC	CTCAATTTTA	180
CCAGCTGAAA	TCCGATCCAA	AGCCGAAGTT	GGCTCATCCA	AGAGGATGAT	TTTAGGACTA	240
GTTGCCAAGA	CACGGGCCAC	GCAGACACGC	TGCTGTTGA			279

(2) INFORMATION FOR SEQ ID NO:2564:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 591 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...591
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2564:

AGGGCAGTTT	CATCAAAAAA	GCGAGGAAGA	AGGATGGCAA	GAACTGAGCT	GTCAGATAAA	60
ATCGAAACAG	AACGTCTCGT	TTTACGAGTC	CGTACTGTGG	CGGATGCTGA	GGATATCCAT	120
GCCTACGCTA	GTTTGCCAGA	GGTCGCCTAT	CCAGCAGGTT	TTCTCCAGT	CAAGACCTTG	180
GAAGATGAGA	TTTATTATCT	GGAGCACATT	CTTCCGGAGC	GTAATCAAAA	GGAAAAATCTC	240

CCAGCAGGCT	ACGGGATTGT	CATCAAAGGA	ACGGATAAGA	TCGCTGGCTC	TGTCGATTTT	300
AACCATCGCT	ATGGGGACGA	TGTGCTAGAG	CTTGGCTATA	CCTTACACTC	AGACTACTGG	360
GGTCGAGGTT	ATGTTCCAGA	AGCTGCGCGT	GCCTTGATTG	ACTTAGCCTT	TAAAGATTTG	420
GGTCTTCACA	AGATTGAAC	AACTTGCTTT	GGATATAACC	TTCAAAGTAA	ACGAGTCGCG	480
GAAAAGCTTG	GCTTTACCCT	CGAAGCTCGC	ATAAGAGACC	GCAAAGATGC	TCAAGGCAAC	540
TGCTGTGATG	ATTTAAGATA	TGCCTTGCTG	AAGAGTGAAT	GGGAGGAATA	A	591

(2) INFORMATION FOR SEQ ID NO:2565:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1035 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1035

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2565:

GATATGGTTT	CTACTATTGG	TATTGTTAGT	TTATCTAGTG	GCATTATCGG	AGAAGATTTT	60
GTCAAACACG	AAGTGGACTT	GGGTATCCAA	CGTCTCAAGG	TTCTGGGACT	CAATCCCATC	120
TTTTTGGCCC	ATTCGTTAAA	AGGATTAGAC	TTTATCAAGG	ACCATCCTGA	AGCTCGTGCA	180
GAGGATTTGA	TTCATGCCTT	TTCTGATGAT	AGCATCGACA	TGATCCTATG	TGCCATAGGT	240
GGAGACGATA	CCTATCGCTT	GCTACCTTAT	CTTTTTGAAA	ATGACCAACT	CCAAAAGGCT	300
ATCAAACAAA	AAATTTTTCT	TGGCTTCTCG	GATACAACCA	TGAACCACCT	CATGTTGCAT	360
AAATTAGGAA	TCAAGACTTT	TTATGGTCAA	TCCTTTTTAG	CAGACATTTG	TGAATTAGAC	420
AAAGAAATGC	TAGCCTATAG	CCTTCACTAC	TTTAAAGAAT	TGATTGAGAC	GGGAAGAATT	480
TCAGAAATCC	GCCCTAGTGA	CGTTTGGTAT	GAGGAACGAA	CTGATTTTAG	TCCCACGGCC	540
CTGGGAACAC	CTCGTGTCAG	TCATACAAAT	ACAGGTTTTG	ACTTGTTGCA	AGGAAGTGCT	600
CAGTTCGAGG	GGAAAATCCT	CGGTGGTTGC	CTCGAATCCC	TCTACGATAT	CTTTGACAAC	660
TCTCGATACG	CAGATAGCAC	GGAACCTCTG	CAAAAATACA	AACTTTTCCC	TGACTTGTCA	720
GACTGGGAAG	GGAAAATCCT	CTTGCTCGAA	ACAAGCGAAG	AAGAGCCTAA	GCCAGAAGAC	780
TTCAAAAAGA	TGTTGCTAAC	TTTAAAGGAC	ACTGGCATAT	TCGCGGTTCAT	CAATGGACTC	840
TTGGTCGGAA	AACCTATGGA	TGAAACTTTC	CATGACGACT	ATAAAGAGGC	ACTATTGGAT	900
ATCATTGACA	ACAATATCCC	GATTGTCTAT	AATCTGAATG	TCGGCCACGC	AACTCCAAGA	960
GCAATTGTAC	CCTTTGGGGT	CCATGCTCAT	GTAGATGCAC	AGGAACAAGT	CATTCGCTTT	1020
GACTATAACA	AATAA					1035

(2) INFORMATION FOR SEQ ID NO:2566:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1593 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1593
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2566:

TCCTCGGTTT	CCGTAATGTC	TTGGAAGGTG	TCCATTGGTC	GATGTTGGAT	GGCAAGACCA	60
TCACAGAATC	CTCTCAGTTT	TGGGCAGGGG	TTAATCACTT	CCTCTGGTTG	CCTGGTGAAG	120
CTATCTTCCA	GTTCTTACCA	GTTAGGGATT	ACTTGGTCTG	TTTCTCGTAA	GATGGGAACC	180
AACCAAAATTT	TGGGAATTGT	TCTCGGAATC	TGTTTTGGTAT	CGCCTCAGTT	GCTCAATGCC	240
TATGCGGTTG	CTTCAACGCC	AGCAGCTGAT	ATCGCAGCAA	ACTGGGTTTG	GAATTTTGGT	300
TATTTTACTG	TTAATCGTAT	TGGTTACCAA	GCCCAAGTTA	TCCCAGCCTT	GCTTGCAGGT	360
TTGAGTCTGT	CTTATCTTGA	AATTTTTTGG	CGCAAACATA	TCCCAGAAGT	CATTTCCATG	420
ATTTTTGTAC	CTTTTTTGTC	ATTGATTCCA	GCCTTGATTT	TGGCTCATAC	TGCTTTGGGG	480
CCAATCGGTT	GGACAAATTG	ACAAGGACTT	TCATCAGTTG	TATTGGCAGG	TTTAACGGGT	540
CCTGTAAAAAT	GGCTCTTCGG	TGCAATTTTT	GGTGCCCTCT	ACGCTCCATT	TGTCATCACA	600
GGTCTGCACC	ACATGACCAA	TGCCATTGAT	ACACAAATTGA	TTGCGGATGC	TGGTGGCACT	660
GCCCTCTGGC	CTATGATTGC	TCTTTCCTAAT	ATTGCTCAAG	GCTCAGCCGT	GTTTGCCTAT	720
TATTTTCATGC	ATCGCCATGA	TGAGTGTGAG	GCTCAGGTTT	CAC TTCCTGC	AACCATTTCA	780
GCCTATCTCG	GTGTTACAGA	ACCAGCTCTT	TTTGGGGTTA	ACGTAAAATA	TATTTATCCA	840
TTTGTGCTG	GGATGACTGG	TTCAGCCCTT	GCAGGCATGT	TATCCGTTAC	TTTTAATGTA	900
ACTGCGGCTT	CTATTGGTAT	CGGTGGTTTG	CCAGGTATTC	TCTCTATTCA	ACCTCAATAC	960
ATGCTGCCAT	TTGCAGGAAC	TATGCTAGTT	GCGATTGTTG	TTCCAATGCT	CTTGACTTTC	1020
TTCTTTCGCA	AGGCTGGTCT	CTTCACAAAA	ATAGAGGGCG	ATACGAACTT	GCAGGCAGAA	1080
TTCGTTGCTC	AAGAAGAAGC	AGAAATTTGTG	AGCCATGAAC	CAGTAGAACT	TACTTCGGTA	1140
GAAATTATCA	GCCCACTAAC	TGGCCAAGTG	AAAGAATTGA	GTCAAGCGAC	GGATCCTGTT	1200
TTTGCAATCAG	GTGTCATGGG	GCAAGGTCTG	GTCATTGAAC	CAAGCCAAGG	TGAGTTGACC	1260
TCTCCAGTTA	ATGGAACAGT	GACGGTTCTT	TTCCCTACCA	AGCATGCCAT	CGGCATTGTC	1320
TCTGACGAGG	GAGTTGAATT	GCTCATCCAC	ATCGGTATGG	ATACAGTAGG	TCTTGATGGC	1380
AAAGGTTTTG	AAAGTCTTGT	AGTCCAAGGA	GATCACGTTA	TAGTTGGCCA	GCAACTGATT	1440
CGTTTTGATA	TGGATGTCAT	TAAGGCTGCA	GGTCTGGTGA	CAGAACTCC	TGTTATCATC	1500
ACCAACCAAG	ATGCTTATAC	AGCGACTATT	ACTGGAAC TT	ATCCGACAAC	GATCCAAGCT	1560
GGAGCATCTC	TCATGGTCGC	TACACGAATC	TAA			1593

(2) INFORMATION FOR SEQ ID NO:2567:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 363 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...363

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2567:

ACTAGGGTTT	CCACCTTCTT	TGTAGGCTTC	GATAATTTTC	TGTGGATACT	TGCTTGTAGG	60
GAGTTTAGAA	GAGGTATCTG	TAGAGTTTTG	GTTGATGAAG	AACTGGCTGC	CATTGGTGTT	120
TGGTTGACCA	GTATTAGCCA	TAGCAAGAGC	ACCGCGGATG	TTATACAAAT	AAGGAGTAAT	180
CTCGTTCTTG	AAACCAGTTC	CTTTGTCTTT	AGTCTTATCC	TTGTCATGCC	AGATGGACTG	240
ACCACCTGTA	CCGTCCCCCT	TTGGATCTCC	AGTTTGGACC	ATAAAGCCAT	CGATGACACG	300
GTGGAAGGTA	ATACCGTTAT	AGTAGCCTTC	TTTGGCGTGA	GTGAGGAAAT	TTTCAACCGC	360
TAG						363

(2) INFORMATION FOR SEQ ID NO:2568:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1041 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1041

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2568:

CTCGTTCTT	CGGTCTACTC	ATTGTTCTGC	TGGTACAATT	TGTTCTTAAA	AAAGGAAAGA	60
GAGGTAATCA	GCATGCGTAA	ATGGACAAAA	GGATTTCTCA	TCTTTGGTGT	GGTGACTACC	120
GTTATCGGCT	TTATCCTGCT	TTTTGTAGGT	ATCCAATCTG	ACGGGATTAA	GAGCCTACTT	180
TCCATGTCCA	AAGAACCTGT	CTATGATAGC	CGTACGGAAA	AGCTAACCTT	TGGCAAGGAA	240
GTCGAAAACC	TAGAAAATTAC	TCTCCACCAA	CACGCGCTCA	CCATCACAGA	CTCTTTCGAT	300
GATCAAAATCC	ACATTTCTTA	CCATCCATCT	CTTTCTGCTC	ACCATGATCT	TATCACCAAT	360
CAAAACGATA	GAACTCTGAG	TCTCACTGAT	AAGAAACTGT	CTGAAACTCC	GTTTCTCTCT	420
TCTGGAATTG	GTGGGATTCT	TCATATCGCA	AGTAGCTACT	CTAGTCGTTT	TGAAGAAGTT	480
ATTCTCCAGC	TACCAAAAGG	GAGAACTCTA	AAAGGGATCA	ACATCTCAGC	CAATCGCGGA	540
CAAACCACCA	TCATAAATGC	TAGCCTTGAA	AATGCGACCC	TCAATACAAA	CAGCTATATC	600
CTCCGAATTG	AAGGAAGTCG	TATCAAAAAC	AGTAAACTCA	CAACACCCAA	TATCGTTAAT	660
ATCTTTGATA	CAGTTCTTAC	AGATAGTCAG	CTAGAGTCAA	CAGAGAATCA	CTTCCACGCT	720
GAAAAATATCC	AAGTCCATGG	TAAGGTTGAA	CTGACTGCCA	AAGATTATCT	CAGAATCATC	780
CTAGACCAGA	AAGAAAGCCA	ACGAATTAAC	TGGGACATCT	CAAGCAACTA	TGGTTCTATC	840
TTCCAATTCA	CAAGAGAAAA	GCCTGAATCA	AGAGGTACGG	AATTAAGCAA	CCCTTACAAA	900
ACTGAAAAAA	CCGATGTCAA	GGATCAACTC	ATTGCGAGAT	CTGATGATAA	TATTGATCTA	960
ATATCCACAC	TCAGAGACGN	GNCCNTNNNN	NNTTNTACAA	AGGGCNTTAC	TTCGAAGGCC	1020

(2) INFORMATION FOR SEQ ID NO:2569:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2569:

AAACATTCTT	CAAAAACTCA	ACCTTCCATA	CCGTGTCGTT	GCTCTCTCTA	CTGGAGATAT	60
GGGCTTCTCA	GCTGCGAAGA	CTTACGACTT	GGAAGTGTGG	ATTCCAGCAC	AAAACAATTA	120
CGTGAAATCT	CAAGCTGTTC	AAACACAGAA	GATTTCCAAG	CCGTTTCGTGC	CCAAATCCGT	180
TACCGTGATG	AAGCAGATGG	CAAGGTGAAA	CTCCCTTCAT	ACCTTGAACG	GTTCTGGACT	240
TGCAGTTGGA	CGTACAGTGG	CTGCAATTCT	TGA			273

(2) INFORMATION FOR SEQ ID NO:2570:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2570:

CGGCTTGAAT	TTGCTGGATT	TACGTGGAGT	TTGTGCTTGA	GGATATATCT	TCATGAGCCC	60
TTGATAACCA	CTGTCAGCCA	AGATTTTACC	AGCTTGTC	ATATTTCTGC	GACTCATTTT	120
GAACAACCTC	ATATCATGAC	AATAGTTCAC	AGTGATATCC	AAAGAAACAA	TTCTCCCTTG	180

ACTTGTGACA ATCGCTTGAG CCTTCATAGC GTAGCATTTTC TTTTACCAG AATAATTCGC	240
TAA	243

(2) INFORMATION FOR SEQ ID NO:2571:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 282 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...282
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2571:

AAAAGCTCTT CGGCTCTTGC CTTGCTTTTC TCCATTATTC GTGTCAAGAC CATTCTTTT	60
GTCATCTTGG ATGAGGTGGA AGCTGCGCTG GATGAAGCCA ATGTTAAACG TTTTGGGGAT	120
TACTTCAACC GCTTTGACAA GGACAGCCAG TTTATCGTCG TAACCCACCG TAAGGGAACC	180
ATGGCAGCGG CTGATTCCAT CTATGGAGTG ACCATGCAAG AATCAGGTGT CTCAAAAATT	240
GTTTCGGTTA AGTTAAAAGA TTTAGAAAGT ATTGAAGGAT GA	282

(2) INFORMATION FOR SEQ ID NO:2572:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 255 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...255
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2572:

GCTGTTCCCTT CTTCAGCGAT TTTCCCTTGG TCGAGGAAGA TAATCCGGTC AGTAATGGCT	60
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TGGGCAAAC	TGCATTTCTG	TGGTACTAAA	ATCATGGTAC	TGGCTTCTTG	TGTCAAATCA	120
TTGATAAGTT	CCAGCACCTC	ACGCACCATT	TCTGGATCCA	GCGAAGCAGT	CACCTCGTCA	180
AAAAGGATGA	TTTCTGGATG	CATTAGGAGG	GCACGGACAA	TTGCAACACG	TTGCTTCTGT	240
CCACCAGATA	ATTGA					255

(2) INFORMATION FOR SEQ ID NO:2573:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1011 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1011
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2573:

CAGATGCCTT	CCCATTATAC	GAGGAATAAA	ACTTTTATGG	ACATTTATAT	TAAGAAAGCC	60
ATTATTCACC	AGTTCAGTCC	GGATGATACC	GAGCTGTTCT	TAGCAGATAA	GTTTCTCAAT	120
ATTACTCCAA	AAATCGAAGA	ATACCTACGT	AAAAAAATTG	AACATGTGTA	TTCAGATGAA	180
GCCAAGACTG	GGATTTTCGA	AGAAGAAAAT	CCCTTCTTCA	ATCATATTAC	AGACGATTTG	240
TTGGAGACAT	CAGTAACGCT	GGCTAATCTC	TGGAAAGAGG	AGTTTAGCAT	TTCTGAAAAT	300
CTCAAGACCA	ATGACTTGAT	TTTTGTTCAA	TTTTCTAAAG	AAGGTGTAGA	ACATTTCTGCT	360
TTCTTGCGAA	TTGCCCTGCG	GGAGACCTTG	ACCCACCTCG	GAGGAGAAGT	TGATAATCCA	420
ATCAAGCTGA	CTCAGAATAA	CCTGCCTGGA	TTTGGAACGG	GTGCTGACGA	GGCCTTGGTG	480
GTCAATCTTC	AGAGTCGCAA	GTATCACCTG	ATTGAAAAAC	GAATCAAGTA	CAACGGGACT	540
TTTTTTGAACT	ATTTTTTCAGA	TAATCTTCTT	GCTGTGCTC	CTAAGATTTT	TCCTAAAAAA	600
TCTATCAAGG	AACTGGAAAA	AACAGCCCAG	AGAATTGCTG	AATCTTTTAA	CACAGATGAT	660
TTTCAATTTT	AATCCAAGGT	CAAATCAGCG	ATTTTCAACA	ACCTAGAAGA	AAGCAATGAA	720
TTGTCACCTG	AGAAATTGGC	TAATGACCTT	TTTGACAACA	ATCTGACGGC	TCGTTTGAGC	780
TTTATTGACC	AAGTCAAAGA	AGCCGTACCA	GAACCTGTTT	AATTTGATGA	AATTGATGCA	840
AGTCGCCAAT	TAAAGAAATT	TGAAAACCAA	AACTCTCCTT	TATCAAATGG	AATTGAGCTC	900
ATCGTTCCCA	ATAACGTCTA	TCAAGACGCC	GAGTCTGTTG	AGTTTATCCA	AAACGAAAAT	960
GGAACCTACT	CTATCTTAAT	CAAAAATATC	GAGGATATCC	AAAGTAAATA	A	1011

(2) INFORMATION FOR SEQ ID NO:2574:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 528 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...528

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2574:

CAAACGCCTT	CCAAGGTATT	TCAAACAAAT	TGTTGCCAGG	TTCATTCCCA	GCGGTTGACG	60
TTGCAGCTTC	TTATGGATTT	GGTTCTCCAA	ATGCTGTCTT	GTCAGGATTT	ACCTTTGGTT	120
TTGATTGGTC	AATTGATTAC	AATTGTTTTG	CTCATCGTCT	TTAAAAATCC	GATTCTTATT	180
ATTACAGGAT	TTGTACCAGT	GTTCTTTGAC	AATGCAGCCA	TTGCGGTCTA	CGCTGATAAA	240
CGCGGCGGAT	GGAAAGCGGC	TGTTATCCTT	TCCTTTATAT	CAGGTGTCCT	TCAAGTTGCT	300
CTAGGAGCTC	TTTGTGTGGC	CCTTCTCGAT	TTGGCATCTT	ATGGTGGCTA	CCATGGAAAT	360
ATCGACTTTG	AATTCCCATG	GCTTGGATTT	GGATATATCT	TCAAATACCT	TGGTATTGTT	420
GGTTATGTAC	TTGTGTGTCT	CTTCTTGCTT	GTTATTCCCT	AACTTCAATT	TGCCAAAGCA	480
AAAGATAAAG	AGAAATATTA	CAACGGTGAA	GTTCAAGAAG	AAGCTTAG		528

(2) INFORMATION FOR SEQ ID NO:2575:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1083 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1083

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2575:

GGTGGTACTT	CTTCTCGAAC	AAATGAGGAT	GGAAGTTTAT	CACGTAGTAA	GGTAAAGGAT	60
ATTACCCAGC	AGTTGGCTAT	GCTGCACGAG	GCTGGTCATG	AGTTGATTTT	GGGTTCTTCA	120
GGTGCCATTG	CGGCTGGTTT	TGGAGCCTTA	GGATTTAAAA	AGCGTCCGAC	TAAAATTGCT	180
GATAAACAGG	CTTCAGCAGC	GGTAGGGCAG	GGGCTTTTGT	TGGAAGAATA	TACAACCAAT	240
CTTCTCTTGC	GTCAAATCGT	TTCTGCACAA	ATCTTGCTGA	CCCAAGATGA	CTTTGTGGAT	300
AAGCGTCGTT	ATAAAAATGC	CCATCAGGCT	TTGTGCGTTT	TGCTCAACCG	TGGGGCAATT	360
CCTATCATCA	ATGAGAATGA	TAGTGTCGTT	ATTGATGAGG	TCAAGGTTGG	GGACAATGAC	420
ACTCTAAGTG	CCCAAGTAGC	GGCGATGGTC	CAAGCAGACC	TTTTGGTTCT	CTTGACAGAT	480
GTGGACGGTC	TCTATACTGG	AAATCCTAAT	TCAGATCCAA	GAGCCAAACG	CTTGGAGAGA	540
ATCGAGACCA	TCAATCGTGA	GATTATTGAT	ATGGCTGGTG	GAGCTGGTTC	GTCAAACGGA	600
ACTGGGGGTA	TGTTAACCAA	AATCAAGGCT	GCAACTATCG	CGACGGAATC	AGGAGTTCTT	660

GTTTATATCT	GCTCATCCTT	GAAATCAGAT	TCCATGATTG	AGGCGGCAGA	GGAGACCGAG	720
GATGGTTCTT	ACTTTGTTGC	TCAAGAGAAA	GGGCTTCGTA	CCCAGAAACA	ATGGCTTGCC	780
TTCTATGCTC	AGAGTCAAGG	TTCTATTTGG	GTTGATAAAG	GGGCTGCGGA	AGCTCTCTCT	840
CAACATGGAA	AGAGTCTTCT	CTTATCTGGT	ATCGTTGAAG	CAGAAGGAGC	CTTTTCTTAC	900
GGTGATATCG	TGACAGTATT	TGATAAGGAA	AGTGGAAAAAT	CAC TTGGAAA	AGGACGCGTG	960
CAATTTGGAG	CATCTGCTTT	GGAGGATATG	TTGCGTTCTC	AAAAAGCCAA	GGGTGTCTTG	1020
ATTTACCGTG	ACGACTGGAT	TTCCATTACT	CCTGAAATCC	AACTACTTTT	TACAGAATTT	1080
TAG						1083

(2) INFORMATION FOR SEQ ID NO:2576:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 588 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...588
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2576:

ATCTTAACTT	CACACTCCCA	AAGAGGTATT	AGTGTCTGT	CTCAATCTTA	TATCAATGTT	60
ATCGGTGCTG	GTTTGGCAGG	TTCTGAAGCA	GCTTACCAA	TCGCAGAGCG	TGGTATTCCA	120
GTTAAACTTT	ATGAAATGCG	TGGTGTCAAG	TCTACACCCC	AGCATAAAAC	AGACAATTTT	180
GCTGAGTTGG	TTTGTTCCAA	TTCTTTGCGT	GGGGATGCTT	TGACAAATGC	AGTTGGTCTT	240
CTCAAGGAAG	AAATGCGTCG	CTTGGGTTCT	GTTATCTTGG	AATCTGCTGA	GGCTACACGT	300
GTTCTGCCG	GTGGAGCCCT	TGCGGTGGAT	CGTGATGGTT	TCTCTCAAAT	GGTGACCGAA	360
AAAGTGGTCA	ACCACCCCTT	GATTGAAGTG	GTGCGTGATG	AAATTACAGA	ATTGCCAACA	420
GATGTTATTA	CAGTTGTGGC	GACTGGTCCC	TTGACTAGCG	ATGCCCTGGC	TGAAAAGATT	480
CATGCCCTTA	ATAATGGCGA	TGGCTTCTAT	TTCTACGATG	CAGCAGCGCC	TATTATCGAT	540
GTCAACACTA	TCGATATGAG	TAAGGTCTAT	CTCAATAATC	TCCGTTAG		588

(2) INFORMATION FOR SEQ ID NO:2577:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 234 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...234

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2577:

TACTTAACTT CCTTCTCAGT TCCGAAGATA GCTTCTTCAA AGGTCAAATT GACACGATAC	60
TGGAGATCAT CTCCTTGCGC AGGAGCGTTT GGATTGCGCG AAGAACCGCC TCCGCCGAAG	120
AAACTTGAGA AAATATCCTC AAAACCACCG AAGCCACCTG CCCCATTGAA ACCGCCGAAA	180
CCACCAGCTC CACCAAAAACC ACCATTGGCG CCTGCAGCAC CATACTGGTC ATAG	234

(2) INFORMATION FOR SEQ ID NO:2578:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 261 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...261

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2578:

CTACCAACTT CAATGATTTT CCCCTGGTCA AGAACAATGA CACGGTTAGT TCGTTCGGCT	60
ATACTGAGAC GATGGGCTAC AAAGAGAATG GTTTTATCAG TTAGGGATAT AAGATTATCT	120
ATAACCTTTT TCTCAGTCAA GACATCAAGA CCGCTAGTAG CTTCATCTAG TATTAAAACA	180
GGAGCTTTAG TTAAAAGAGC ACGAGCGAGA GCGATTCGTT GCTTTTGTCC TCCTGATAGA	240
CCAGCTCCAT CAGAGAGCTG A	261

(2) INFORMATION FOR SEQ ID NO:2579:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 762 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...762

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2579:

ATTCGAACTT	CATTTT	TAGA	AAGGAG	TGAG	TTTATG	TCTC	AAGATG	AAAA	ATTAAT	TCGT	60	
GAACAGATT	TT	GTGATG	TTTG	TCATAA	GATG	TGGCAA	CTTG	GTTGGG	TTGC	TGCTAA	CGAT	120
GGGAATGT	TAT	CTGTTC	GATT	AGATGA	GGAT	ACCATT	TCTTG	CAACAC	CCTAC	TGGTAT	CAGC	180
AAAAGTTT	TA	TTACAC	CAGA	AAAGCT	GGTG	AAGTTAA	ATC	TTAAAG	GAGA	GATTTT	TAGAA	240
GCAGAAGG	TG	ATTACT	GTCC	TTCTAG	TGAA	ATTAAAA	TGC	ACATT	CGGTG	CTACGA	AGAA	300
CGTGAGG	ATG	TTCGTT	CAGT	TGTTCA	CGCG	CATCCAC	CGA	TTGCAA	CAGG	ATTTG	CTCTT	360
GCACACAT	TC	CTTTAG	ATAC	TTATTCA	CTA	ATTGAG	AGCG	CGATTG	TGGT	TGGGGC	AAAT	420
CCTATTAC	CC	CATTTG	GAGT	ACCGTC	TACA	ATGGAAG	TGC	CAGAAG	CAAT	TACAC	TTAT	480
CTGCCCG	ATC	ATGATG	TCAT	GCTATT	AGAA	AATCAT	GAG	CTCTGA	CTGT	CGGAAG	CGAT	540
GTCATTAC	AG	CATACT	ACCG	TATGGA	AACT	TTAGAAT	TAG	TCGCAA	AGAC	AACCTT	CCAC	600
GGAAGAA	TGT	TACTTT	CTAC	AAAGGG	CATT	GAGGAG	CAAG	AAATTG	CTCG	TCCGAC	TTTA	660
GAACGTCT	AT	TCTCAAT	GCG	AGAAAAT	TAT	AAGGTT	ACAG	GTCGTC	ACCC	AGGCTA	CCGT	720
AAATATA	ATG	GCGATG	GGTAG	TATAAAA	AGAA	ACAAAAA	AAT	AA				762

(2) INFORMATION FOR SEQ ID NO:2580:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 432 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2580:

TTACTGACTT	CGTCAG	TTTC	ATCTACA	ACC	TCAAAA	ACCAT	GTTTTG	AGCT	GACTTC	GTCA	60
GTCTTATCTA	CAACCT	CAAA	ACTGTG	TTTT	GAGCAA	CCCTG	CGGCTA	GCTT	CCTAGT	TTTG	120
TCTTTGATTT	TCATTG	AGTT	TATATTT	TAT	AGGAGC	GCAT	TATTTT	GCCTT	TTGCTG	CGTA	180
CTCTTCGTTA	CGTTTG	ATCA	TTTGTT	TTTCT	GTACCA	AAGCA	AAGATA	CCGA	TATAGA	AATAC	240
AAGGAAGGCT	ACTGCA	CCAA	GGATTG	CTTT	GATATC	ACCA	GTTGTA	GTGT	TACCAAT	TGT	300
CCAACCAAGA	AGTTTT	TCGA	TTGGTC	CTTC	AAGAGT	AGAG	TGAGTA	ATCA	ATTGAG	TTTG	360
GCTCACACCT	TCTGGG	AAG	CACCTA	CACC	TTTAGC	AAGT	TCTGTT	GCAA	ATGGT	GCAAT	420
AAGTGTACCT	GA										432

(2) INFORMATION FOR SEQ ID NO:2581:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1308 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1308
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2581:

CAGGTGACTT	CTCCATCCAA	ATTTTGTTC	AATGGTGCAA	TCAGGAATCC	TCTTAGTTTA	60
TTTGGTGAC	CTGTGACACC	AGCTAGTTAT	GGTTCGTCAG	TCGTTCCAAT	TCTTATTATG	120
GTTTGGTTGA	TGAAATATAT	TGAAAAAATG	ATTGCTAAAT	TAACACCAGC	TGTTACTAAG	180
AGTTTTTTTGC	AACCTACGCT	AGTATTATTA	GTATCAAGCT	GTATTGCCTT	AGTTGTAGTC	240
GGACCTATTG	GAGTAATTGT	TGGTGAAGGA	TTATCAAATC	TAGTTGGGCA	AATGTATGGT	300
GTAGCTGGAT	GGCTTACATT	AGCTATTCTT	GGTGCTATTA	TGCCATTTAT	TGTTATGACT	360
GGAATGCATT	GGGCTTTTGC	ACCTATTTTT	TTGGCGGCAT	CTATTGCTAC	TCCAGACGTA	420
TTAATTCCTC	CAGCAATGTT	AGGGTCAAAC	TTAGCTCAAG	GGGCTGCTTC	GATGGCTGTT	480
GCATTAAAGA	GTAATAATAA	TAATACAAAA	CAAATTGCTT	TTGCAGCAGG	TTTCTCAGCC	540
TTACTTGACG	GGATTACCGA	ACCTGCATTA	TATGGTGTGA	CTTTAAAATA	TAAAAAACCG	600
CTTTATGCAG	CTATGATTGG	TGGTGGATTA	GCGGGATTAT	TTGCAGGTCT	TACTAGTGTT	660
AAAGCATATC	TATTTGCTGT	CCCATCTTTG	ATAGCGTTGC	CTCAATTTAT	TTATTCTGAT	720
GTGCCATCAA	ATATTGTAAA	TGCTTTAATT	GTGGCGGTCA	TTTCGGTTGT	TATTACCTTT	780
GTATTAGCTT	ATATATTTGG	AATCGATGAA	GAAGAGAGTT	CTAGCAATTT	AGAAGTTAAA	840
GCTGGAGTTT	CAATAAAAAA	AATGATATTT	TCTCCTATAT	CAGGAGAAAT	CATTCCGTTA	900
AGCGATGTCC	AGGATAAAAC	ATTTTCAGAT	AAACTAATTG	GAGACGGAGT	AGCGATTATC	960
CCAAGTGAAG	GTAAGGTTTA	TGCACCATTT	GATGGGAAAA	TTACAAATAT	TTTTCCGACT	1020
AAGCACGCAA	TTGGATTGAA	GAGTGATGAG	GGTGTTGAGT	TACTAATTCA	TATTGGATTA	1080
GATACTGTTG	AGCTAAAAGG	TCAAGGTTTT	ATTAGTCATG	TAGAAGAAGG	AGACAGAGTT	1140
TTCAAAAATC	AGTTGATTTT	TGAAATGGAC	TTGAATTTAA	TCAAGACTAA	AGGCTACGAA	1200
ACAGTTACAC	CAGTAATTGT	AACGAATACC	AATGATTTTC	TAGATGTATT	AGTATTACCT	1260
AATAATCAGA	CAATCGAGCA	TTCTAAGGAA	TTACTGGTAA	TATTATAA		1308

(2) INFORMATION FOR SEQ ID NO:2582:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1184 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1184

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2582:

```
TTGGTGCTTC GATTTTCAAT CTGGTCTTTA TCGTCTATGC ATCGACCTTG TCACAAGCAT      60
CTTTTGCTGT TGCTATGGCG AATATTGTCA TGCTTCTCTC CGATCTCTTT ACAGTTTTTG      120
CAGGGATTCTG GGCAGATTAC ACGAGGGCCA AGGTCAAATG GATGGTCTAT AGCGGTTTGT      180
TTCAGGCGGT TTTATTTTTT CTGGCAGCCC TAGTTGTTCA GCAAGCTAGT TTATTTGCCT      240
TTTCTAGCCT GTGTTTTATC AATGTCATTA GTGATATCAT CAGTGATTTT GCAGGTGGCC      300
TGCGTATCGC TCTTATTAAG GAAAAAGTAG CTGAAGATGA TTTGATGGAG GCTTATTCTT      360
TTTCACAGTT CATCACCTAT ATTTTCAGCTA TTGGTGGTCA AGCTTTCGGA GTCTGGCTCT      420
TAGCTCTATC GGTCACAAT TTTTCTCTCG TTGCGGGAAT CAATGCCTGC TTTTCCCTAG      480
TATCAGCCAC TATCCTCTTT TTAGGAAAAA GCAAATTGAG CCTGTCAATG TCATCTGCTG      540
ATGGTAAAAA ACTAAAAAAT GAGAAGCTTT CTATCAAAGA CCAGTTCCTA ACAATTTATC      600
GAAATTTACG TCTCGTTTTT CTTAAAAGTG GACAGAAAAA CTTTGGTTTT ATGCTCTGTG      660
CTGTCTTGCT TGTCATGCC TTGGGTGGCG CTTTGGGTGG AATTTATAAT ATCTTCTTTT      720
TGAGCCATTC TCTCTGAAT TTTTCTTACA CAGAGGCACT ATTTATCAAT CAAGTCTGTG      780
TTTTGTTAGC AATCATCATT AGTAGCCTTA CGGGCAATGA TTATTTTGGG AAGCAGTCCT      840
TGCCTAGATT GATGATGTGG GAGACCGTAG GACTTAGTCT AGTTGGTTTG GCTAATTTAT      900
TCAATCAAGT CGTGCTTGGT TTGCTATTTT TCTTCTTTAC TCTGTATGTG TCTGGTAAAG      960
TTCAACCAAA GATTAGTGCC ATGCTCATGA AAAATCTAGC TCCAGAGGTT CTAGCTCGTA     1020
CTAGTAATTT TTTAGGTCTA TTGTTTACCT TATCCATACC TGTGGGAACA GCTTGTTTTT     1080
CACTAGTAGC CGTATGGAAT ATACAGTTGA CTTGGATGCT ATTTGTTGGT CTTTCCCTTG      1140
TAGCTATTTT TTTGACAATT CTTAATCTCA AAAATGATAT CTAA                               1184
```

(2) INFORMATION FOR SEQ ID NO:2583:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 624 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...624

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2583:

```
GCGATAGCTT CTTTATTGGC AACAGGGATG GCGTTGTTTT TCAAAGCTTC AACTGCTGCG      60
GCAACTGCTG TTTCAATCCC ACGACGAATA CCGATTGGAT TTGCACCTGC TGTGACGTTT      120
TTGATTCCCTT CACGGACGAT AGCTTGGGTC AAGACTGTTG CAGTCGTAGT TCCGTCACCT      180
```

GCGATATCAT	TGGTTTTAGA	AGCTACTTCT	GATACTAACT	TAGCACCCAT	ATTTTCAAAA	240
TGGTCTTCCA	ATTTCGATTC	TTTGGCAATG	GTCACACCGT	CATTGGTAAT	CAAGGGTGAA	300
CCGAATGACT	TTTCAAGAAC	GACATTGCGA	CCTTTTGGTC	CCAAGGTAC	TTTAACAGTG	360
TCTGCAAGAA	TATCGACACC	ACGAACCATG	GCTGAACGGG	CATCTGATGA	AAATTTAATT	420
TCTTTTGACA	TACTTACTTT	CTCCTTCTAT	TCCTCAATGA	TTGCCAAAAT	GTTAGCTTCG	480
CCTACGATGA	TGTACTTTTC	ATCGCCATCT	TTGACATCAA	GACCTGCGTG	GGCTTCAACT	540
AAGACACGAT	CTCCAGTTTT	AACACTTGGA	GCAACCAAGT	CACCGTTCAA	GGTACGAACA	600
CCTTGTCAG	TAGCCACAAC	TTGA				624

(2) INFORMATION FOR SEQ ID NO:2584:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1476 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1476

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2584:

GACTTGGCTT	CAATTAGAAA	AAGGAGAGTA	ATGATGCCAA	TTCAAAATAA	AACCATGTTG	60
ATTACCTATT	CTGATAGCCT	TGGAAATAAT	CTTAAAGACT	TATATGATAA	TTTGGAAGAG	120
CATTTTCGAG	ATGCTATTGG	AGGAGTTCAC	CTTTTACCAT	TTTTCCCATC	AACAGGTGAT	180
CGTGGATTTG	CGCCAGTTGA	CTACGACGAA	GTGGACTCAG	CTTTTGGTGA	TTGGGAGGAT	240
GTAAAGCGTT	TAGGTGAGAG	ATATTATCTT	ATGTTTGATT	TTATGATTAA	TCATATTTCT	300
CGTCAATCCA	AGTATTATAA	GGACTATCAA	GAAAAACATG	AAGCCAGTGA	ATTTAAAGCT	360
CTCTTTTTAA	ACTGGGATAA	GTTTTGGCCA	GAAAACCGTC	CGACACAGTC	TGATGTAGAT	420
TTAATTTTACA	AGCGTAAGGA	TCGTGCACCA	AAGCAAGAGA	TTGTGTTTGA	AGATGGTTCA	480
GTGGAACATT	TGTGGAATAC	CTTTGGTGAG	GAGCAGATTG	ATCTTGATGT	GACCAAAGAA	540
GTAACATATG	AATTTATCCG	TAAGACCATT	CAGCACTTGG	CAAGTAATGG	GTGTGATTTG	600
ATTCGTCTAG	ATGCCTTTGC	TTATGCAGTG	AAGAAAATTGG	ATACTAATGA	TTTCCTTTGTG	660
GAACCGATA	TTTGGGATTT	ATTGGACAAA	GTTTCGAGATA	TCGCTACTGA	GTATGGGACA	720
GAGTTTTTAC	CTGAGATTCA	TGAACACTAT	TCGATTTCAGT	TTAAAAATAGC	AGACCATGAT	780
TACTATGTTT	ATGATTTTGC	TCTTCCAATG	GTGACACTTT	ATACTCTTTA	CAGTTCCAGA	840
ACAGAGCGTT	TGGCTAAGTG	GTTAAAGATG	AGCCCGATGA	AGCAATTAC	GACGCTAGAT	900
ACCCATGATG	GGATTGGAGT	AGTAGATGTC	AAGGATATCC	TGACCGATGA	GGAGATTGAC	960
TATGCTTCAA	ATGAACTCTA	TAAGGTTGGA	GCCAATGTCA	AACGTAAGTA	CTCTAGTGCC	1020
GAGTATAACA	ACTTAGATAT	CTACCAAATC	AATTCAACCT	ACTATTCAGC	GCTTGAGAT	1080
GATGAAGTCA	AGTATTTTCT	CGCTCGTCTA	ATTCAAGCTT	TTGCCCCAGG	TATTCCTCAG	1140
GTTTACTATG	TGGGTCTATT	AGCAGGCAAG	AATGACTTGA	AATTATTAGA	AGAAACTAAA	1200
GAAGGTCGAA	ATATTAATCG	TCATTACTAT	AGCAACGAGG	AAATAGCAAA	AGAAGTGCAA	1260
CGACCTGTTG	TGAAGGCCCT	TCTCAATCTA	TTTTCTTTCC	GTAACCGTTC	AGAAGCCTTT	1320
GATCTAGAAG	GGACTACTGA	GATAGAGACA	CCAACAGCTC	ACAGCATTGT	AATCAAACGT	1380
CAAAATAAAG	ATAAGTCCGT	AACAGCAGTA	GCAGAAATTG	ATTTGCAAAA	TCAGACTTAT	1440
CGGGTAATTG	AGAATGGAGT	TGAAGTAACA	TTTTGA			1476

(2) INFORMATION FOR SEQ ID NO:2585:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 303 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...303
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2585:

ACTGCTTATT	CTTGTTTCAGC	AGCTTCTTCT	GTTGCTTCCG	CTTTTGGTGC	TTTCTCAGCT	60
TCTTCAGCTT	CAAAGGCTGC	TTTAGCCTCT	TGGGCTGCTT	TTTCGCGGGC	TTTTTCAAGG	120
TCATCTACGT	GGATGACATC	TTCGTCCATT	CCTTCATCCA	AGTCGCGAAG	TTCCACTTCT	180
TGGTCATCTT	CGTCTAGGAC	ACGCATGTCA	AGACCAAGAG	ATTGCAATTC	TTTGACAAGA	240
ACTCGGAAGG	ATTCTGGAAC	ACCTGGTTTT	GGAATTGGTT	TGCCTTTTGT	AATAGCTTCA	300
TAG						303

(2) INFORMATION FOR SEQ ID NO:2586:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 429 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...429
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2586:

AATGGAGAAT	TAAACATGTT	AGCAAATGGA	ATTACGCTTT	CTTATGGCGA	AACAAAAGAT	60
AGCTATACTA	AACTTGTTGG	ATTGAAAAGAA	GTACCAGAGT	TTGGTATTGA	ACTCGAAAAA	120
GTAGAAAATA	CTACTCTTGA	AGATACGGTG	AAGAAGTACG	AGTTTGGTAT	TGGGGACATA	180

GGAGAACTTG	AGTACAAGTT	CTCTTATAAT	AATTCAAGCG	CAACTGCTCC	TTATCGTGTA	240
TTGCGTAAGG	CAGCAGACGA	CAAGAAGAAA	CTCTACTTTG	AACAAGCTTA	TCCAGACGGT	300
ACTAAGGTCA	TTTTTGAAGG	CCAAGTATCT	GTTAAGCTTG	GCGGTGGCGG	TGTCAATGCC	360
GTTATCGATT	TCACACTTAA	GATTGCCTTG	CAGTCTAATC	TTACATTTAC	TGATGGTATT	420
GGAGGTTAA						429

(2) INFORMATION FOR SEQ ID NO:2587:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 351 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...351
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2587:

TTCGCATATT	CAGCAACATC	ATCCATCAAA	TGCGTTACCA	AGACGATGGT	CATCCCTGAC	60
TGGTGGAGTT	TTTTGAACAG	GGTCATCAAC	TCTTTTCTCC	CTAGAGGATC	TAGACCAGCT	120
GTTGGCTCAT	CTAAGACTAA	TATAGCTGGC	TCCATGGCAA	GTATGCCTGC	AATGGCAACA	180
CGTCTCATTT	GTCCCCCTGA	CAGCTCAAAC	GGACTACGAT	CAAAAAGTGA	TTCATCAATT	240
CCAACCAGAG	CCAGTTTCTC	ACGCGCAGTC	TTCACAGCAT	CTTCTTCAGA	AACTCCAAAA	300
TTTTGCGGTC	CAAAGCAAC	GTCCTTCAAA	ACCGTTTCTT	CAAAAATCTG	A	351

(2) INFORMATION FOR SEQ ID NO:2588:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 402 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2588:

AAATGTCATT	CTATGGAACC	TCAAGCGATT	GTCACCAGCC	AAGAAAGAAT	TGTTTCTTTG	60
AATATTGCGG	TGAACTATTG	CCACGATATG	AAGTTGTTCA	AAATGAGTCG	CAGAAATATC	120
GGACAAGCTG	GTAAAACTTT	GGCTGACAGT	GGTTATCAAG	GGCCCATGAA	GATATATCCT	180
CAAGCACAAA	CTCCACGTAA	ATCCAGCAAC	CTCAAGCCGC	TAATAGCTGA	AGATAAAGCC	240
TATAACCATG	CGCTATCTAA	GGAGAGAAGC	AAAGTTGAGA	ACATCTTTGC	CAAAGTAAAA	300
ACGTTTAAAA	TGTTTTC AAC	AACCTATCGA	AATCATCGTA	AACGCTTCGG	ATTACGAATG	360
AATTTGATTG	TTGGTATTAT	CAATCATGAA	CTAGGATTCT	AG		402

(2) INFORMATION FOR SEQ ID NO:2589:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 639 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...639

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2589:

ATCATGGAAT	TTAGGACAAT	TAAAGAGGAC	GGCCAAGTCC	AAGAAGAAAT	CAAAAAATCT	60
CGCTTTATCT	GCCATGCCAA	GCGTGTTTAT	AGCGAAGAAG	AGGCTCGTGA	CTTCATTACT	120
GCCATCAAAA	AAGAACACTA	CAAAGCGACA	CATAACTGCT	CTGCCTTTAT	TATTGGAGAA	180
CGTAGTGAAA	TTAAACGTAC	AAGTGATGAT	GGTGAGCCTA	GTGGTACTGC	TGGTGTTCCC	240
ATGCTTGGGG	TACTAGAAAA	TCACAATCTC	ACCAATGTCT	GTGTGGTCGT	GACACGCTAC	300
TTTGGTGGTA	TTAAACTAGG	CGCTGGAGGA	CTAATTCGTG	CTTACGCCGG	CAGTGTCGCC	360
TTAGCTGTCA	AAGAAATTGG	TATTATTGAA	ATAAAAGAAC	AGGCTGGCAT	TGCTATTCAA	420
ATGTCTTATG	CTCAGTACCA	AGAGTACAGT	AACTTCCTTA	AAGAACATGA	TCTCATGGAG	480
CTGGATACAA	ACTTTACAGA	TCAAGTCGAT	ACGATGATTT	ATGTTGATAA	GGAAGAAAAA	540
GAAACTATTA	AAGCTGCACT	TGTGGAGTTT	TTTAATGGAA	AAGTCACTTT	AACTGACCAA	600
GGTTTACGAG	AGGTTGAAGT	TCCTGTAAAC	TTAGTGTA			639

(2) INFORMATION FOR SEQ ID NO:2590:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...363

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2590:

GTAATGGAAT	TGATGAATAA	AACACGAGTA	ACAGATTCAC	TAGCAGTTGT	GATTGGACCA	60
GAATCGATTG	AAGTACTTGT	TACTGAAGGT	TTTCTATTTG	ATGTTGCGAT	TCGTTTTGTA	120
AAAGTAGACG	AAACAAATCT	TGATCAAGGA	AATGAAAAGC	CAGTATTCAC	TCCGGAATAC	180
AAGCTGGTCA	CAGTTGCTAA	ATACAAGGAA	AAACCTATCT	TTGAATCGGA	GGAAGATATT	240
CGAAAATTTG	AGAAGCAAGC	AAAAGAAGTT	AAATCGCTAT	TTGCCTTTGC	AAAGGTAAAT	300
AAACAAAATT	GGTTTAACAC	TGCCCTTTAT	CCAGGAGTGC	TGACTGAGAA	AGTTGGTGTT	360
TGA						363

(2) INFORMATION FOR SEQ ID NO:2591:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 813 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...813

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2591:

CAGATGGAAT	TGACTAAATA	CGCTTCATCT	ATGCTTCTTG	ACCCTGAGTA	TGGACTTCCA	60
GCAACTAAAG	CTCTTGATGA	AAAAGCTGGT	CTTCTCCTTG	CTTATGAAAA	AACAGGTTAT	120
GACACAACAA	GCACAAAACG	CTTGCCAGAC	TGCTTGGATG	TTTGGTCTGC	AAAACGTATT	180
AAAGAAGAAG	GTGCAGATGC	AGTTAAATTC	TTGCTTTACT	ATGATGTAGA	TAGCTCAGAC	240
GAACTCAATC	AAGAAAAACA	AGCCTACATC	GAACGCATCG	GTTCTGAGTG	TGTGGCTGAA	300
GATATCCCAT	TCTTCCTTGA	AATCCTTGCT	TACGATGAAA	AAATTGCGGA	TGCAGGTTCT	360
GTAGAATACG	CGAAAGTAAA	ACCACACAAA	GTTATCGGCG	CTATGAAAGT	CTTTTCAGAC	420
CCACGCTTTA	ACATTGATGT	CTTGAAAGTT	GAAGTTCCTG	TTAACATTAA	ATATGTTGAA	480
GGCTTCGCTG	AAGGTGAAGT	AGTTTATACA	CGTGAAGAAG	CAGCAGCCTT	CTTCAAAGCG	540
CAAGATGAAG	CAACGAACCT	GCCATACATC	TACTTGAGTG	CTGGTGTATC	AGCTAAACTC	600
TTCCAAGATA	CTCTTGATTT	TGCTCATGAA	TCAGGTGCAA	ACTTTAACGG	AGTTCTTTGT	660
GGCCGTGCTA	CATGGGCAGG	GTCAGTTGAA	GCTTACATCA	AAGATGGTGA	AGCAGCAGCT	720
CGCGAATGGC	TTCGCACAAAC	TGGATTTGAA	AACATTGATG	AGCTCAATAA	AGTTCTTCAA	780
ACAACAGCGA	CTTCATGGAA	AGAACGTGTG	TAA			813

(2) INFORMATION FOR SEQ ID NO:2592:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 204 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...204
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2592:

ACCTGCCATT CATGTAATAA AGGCTCTACT CTTAAAGGAA AACCCGTAGC ACAGACCACA	60
TACGAAGCCG TTTCTAAAGC TCTTGTGACT GCAGAAGATA CGATTATTTT AGCTGACGAG	120
AGTAAAGGAT TTTTGCTCAA TTTCTGGACT TGCTGCCGTC CCATCTCAGA CAAGGGTGCC	180
AAATCTATCC CAAATCCTAT ATAA	204

(2) INFORMATION FOR SEQ ID NO:2593:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 228 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...228
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2593:

GGAGGCCATT CTTTATCAAA GCACAAGACA GGTGTTGTTTG ATGGCATGAT GACGACAGGT	60
TGCTCTATGG GAGCCTATCA TGCACTCAAT TTCTTCCTCC AGCATCCAGA TGTCTTTACC	120
AAAGTGATTG CTCTCAGTGG TGTTTACGAC GCACGTTTCT TTGTCGGTGA TTACTACAAC	180
GATGATGCTA TTTACCAAAA CTCGCCAGTA GATTATATTT GGAACATA	228

(2) INFORMATION FOR SEQ ID NO:2594:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1137 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1137
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2594:

ATGAAACATT	CTGTTCATTT	TGGTGCCGGT	AATATCGGTC	GTGGTTTTTAT	AGGTGAAATT	60
CTATTTAAAA	ATGGTTTCCA	TATTGATTTT	GTGGATGTCA	ATAATCAGAT	AATTTATGCT	120
CTAAATGAAA	AGGGCAAGTA	TGAAATTGAA	ATTGCACAGA	AAGGACAGTC	TCGTATAGAA	180
GTAACATAATG	TGGCTGGCAT	TAATAGCAAA	GAACATCCTG	AGCAAGTCAT	TGAAGCGATT	240
CAAAAGACGG	ATATTATTAC	TACTGCAATC	GGACCTAATA	TACTCCCTTT	TATCGCTGAA	300
CTTCTAGCCA	AAGGAATCGA	AGCTCGCCGA	GTTGCAGGAA	ATACACAGGC	ATTGGATGTT	360
ATGGCCTGTG	AAAATATGAT	TGGCGGGTCT	CAATTTCTTT	ATCAAGAAGT	CAAGAAATAT	420
TTAAGTCCGG	AAGGTTTGAC	ATTTGCTGAT	AACTACATAG	GTTTTCCAAA	TGCTGCAGTA	480
GACAGGATTG	TTCCAACACA	AAGTCACGAA	GATTCCCTTT	TTGTTATGGT	CGAGCCCTTT	540
AATGAATGGG	TCGTGGAAAC	CAAGCGTCTT	AAAAATCCAG	ATTTACGTCT	AAAAGATGTG	600
CATTATGAAG	AAGATTTAGA	ACCCTTTATT	GAGCGAAAAC	TTTTTTCAGT	CAATTCCTGGA	660
CATGCAACTT	CAGCTTACAT	TGGTGCGCAT	TATGGTGCCA	AGACAATTTT	GGAAGCTCTT	720
CAAAATCCTA	ATATCAAATC	TCGGATTGAA	TCTGTATTAG	CTGAAATTCG	GAGTCTCTTG	780
ATTGCCAAAT	GGAACTTTGA	TAAAAAAGAA	TTGGAGAATT	ATCACAAAGT	CATTATAGAA	840
CGGTTTGAAA	ATCCTTTTCAT	AGTGGACGAG	GTTAGTCGCG	TAGCTCGTAC	TCCAATCCGA	900
AAATTAGGCT	ATAATGAACG	ATTCATCCGG	CCGATACGTG	AATTGAAAGA	ACTCAGTTTG	960
TCATATAAAA	ACCTACTTAA	AACAGTTGGC	TATGCCTTTG	ACTATCGCGA	TGTAAATGAT	1020
GAAGAAAAGTA	TTCGATTAGG	TGAATTGTTG	GCTAAACAAT	CAGTCAAAGA	TGTTGTTATA	1080
CAAGTTACAG	GTTTAGACGA	CCAAGAATTG	ATTGAGCAAA	TTGTAGAGTA	TATTTAA	1137

(2) INFORMATION FOR SEQ ID NO:2595:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 876 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...876

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2595:

AAAGAGGAAT	TGAAAATGGA	AAAATTAGTT	GCCTATAAAC	GCATGCCTTT	GTGGAATAAA	60
CAAACAATGC	CTGAAGCTGT	TCAGCAAAAG	CACAATACAA	AAGTTGGGAC	TTGGGGGAAA	120
ATTACTGTCT	TGAAGGGAGC	TCTCAAGTTT	ATTGAATTGA	CAGAAGAAGG	GGAAGTTCTA	180
GCTGAACACC	TCTTTGAAGC	AGGGGCAGAC	AATCCAATGG	CCCAACCTCA	AGCCTGGCAC	240
CGAGTGGAA	CTGCCACAGA	TGATGTGGAA	TGGTACTTGG	AATTTTATTG	TAAACCTGAG	300
GATTATTTTG	CTAAAAATA	CAATACCAAT	CCTGTTTCAT	CAGAGGTCCT	AGAGGCCATG	360
CAGACAGTGA	AACAAGGGAA	AGCTTTGGAT	TTGGGTTGTG	GTCAGGGGCG	TAATTCTCTT	420
TTTCTAGCCC	AGCAAGATTT	TGATGTGACG	GCTGTAGATC	AAAATGGACT	AGCTCTTGAA	480
ATCTTGCAAA	GCATTGTGGA	GCAGGAAGAT	TTGGACATGC	CTGTTGACCT	TTACGATATC	540
AATTCAGCTA	GCATTGAACA	AGAATATGAT	TTTATCGTTT	CAACAGTTGT	TCTCATGTTT	600
CTACAAGCGG	ACCGCATTCC	AGCTATTATT	CAAAATATGC	AGGAGAAAAC	CAGTGTGGGT	660
GGTTACAACC	TTATCGTTTG	TGCCATGGAC	ACGGAGGATT	ATCCTTGCTC	GGTTAACTTC	720
CCATTCACCT	TTAAAGAAGG	AGAACTGGCA	GACTATTACA	AGGATTGGGA	ATTGGTTAAG	780
TACAAATGAAA	ATCCAGGCCA	TTTGCACCGT	CGCGATGAGA	ATGGCAATCG	TATTCAACTA	840
CGCTTTGCGA	CCTTACTAGC	TAAGAAAATC	AAGTAA			876

(2) INFORMATION FOR SEQ ID NO:2596:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 486 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...486

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2596:

GGTGGTAATT	CTAGGCAAGA	CCCCTATCAC	GGACCAGGTC	AAGCGCAGGG	CTTGAGTTTT	60
TCTGTACCTG	ACTCTATCCC	AGCTCCACCA	TCCTTGCAAA	ATATCTTGAA	AGAATTGTCA	120
GATGATATCG	GAGTTAAGAA	ATCTCATGAT	TTGACAGCTT	GGGCTGAGCA	AGGAGTCTTG	180
CTTCTTAATG	CTTGTTTGAC	TGTTCCCTGCT	GGACAGGCCA	ATGGTCATGC	TGGTCAAATC	240
TGGGAGCCTT	TTACTGATGC	TGTGATTGAG	GTGGTCAATC	ATCTAGATAG	ACCAGTCGTT	300
TTTGTACTCT	GGGGAGCTTA	TGCACGTAAG	AAGAAGGCCT	TAGTTACCAA	TCCTCATCAC	360
TTGATTATCG	AATCAGCCCA	TCCAAGTCCT	TTGTCGGTTT	ATAGAGGATT	TTGGGGTTCC	420
AAGCCCTTTT	CCAAGGCCAA	TGCATTCTTA	AAAGAGACAG	GACAAGAGCC	AATCGCATTG	480
GCTTAG						486

(2) INFORMATION FOR SEQ ID NO:2597:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 300 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...300
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2597:

CATTTCAATT	CTTTTTTCAA	CCTCATACAA	GGTATGTCGA	ATAACATACA	GGCCCCAAAA	60
GGCAATGACA	AAAGTCAGAG	TGTTGATAAG	GGAAATAGTT	TGAATACTTA	TAACATTGAT	120
AAGGAATGCG	CCAGCCAGAT	TGGCGACAAT	ACGGACAACC	CTCATCAGAG	ACTGCCTGAA	180
CCCCATGGCA	TCATGCAGGT	CGTCCTTAAT	TACACTGATG	TAGAGGGCGT	TCATCATGTA	240
GGCAGACAGG	TAGCTCAAGG	TGTCAGAGAT	GAGGTTGATG	ATGACAATCA	TAATGACTGA	300

(2) INFORMATION FOR SEQ ID NO:2598:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1323 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1323
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2598:

AAGGACAATT	CAATGATTCA	TTTAATAATG	ATTAGCGCCA	TTGCTCTAGC	CATTGGAATT	60
GGTTACCGCA	CCAAAAATCAA	TATTGGCCTG	CTGGCTATTG	CTTTTTCTTA	CCTCATCGCA	120
ACCACTCTCA	TGGGATTAAG	CCCCAAAGAA	CTTCTTCATT	TTTGGCCAAC	CTCACTCTTT	180
TTTACCATT	TTAGCGTCTC	TCTCTTTTAT	AACGTTGCAA	CAACTAACGG	TACTCTTGAT	240

GTTTTGGCTC	AACACATTCT	CTACCGCACA	CGCACCCACC	CTAACGCCCT	CTACATGATT	300
TTATACCTGA	TGGCAACCCT	TTTGTCTGCT	TTAGGTGCTG	GATTTTTCAC	TACTATGGCC	360
GTTTGTCTGC	CTCTAGCGAT	TACCTCTGT	CAAAAAGCGG	ACAAACACCC	TTTGATTGGA	420
GCTCAAGCCG	TCAATTGGGG	AGCTTCAGGA	GGGGCTAATT	TGATAACCAG	TAGCTCAGGC	480
ATTGTCTTTC	AAGGCTGT	TAAGCAAATG	GGATGGGAAG	AGCAAGCTTT	TTCATTGGC	540
AATCATATCT	TTATCGTCAG	CATTATCTAC	CCACTCATCG	TCTTGCTTTT	ATTATCCTGT	600
TACAGTCACT	ATAGTAAGGG	AAGAACAAAC	TCATCCTTGA	CTATTGACCA	ACCACCACTC	660
CTCAGCAAGG	TTCAAAGACA	AACCACCTTG	CTCATGATCA	GCAGCATGGT	TTTGGTTTGG	720
CTTTTTCCCT	TGTTGCATCT	CATTTTCCCA	AACATCGCCT	GGATAGCTAC	TTATCAAAAA	780
ACATTTGATA	TTGGCTTTGT	CTCAATACTC	ATGGTCTGCC	TCGCCTTAAG	GCTCAAATTA	840
GGGAAGCAAG	AAGCCATTTT	AGCTAAGGTT	CCCTGGGCTA	CAATTATCAT	GCTCTGCGGC	900
ATGAGCTTAC	TAATGTCTCT	AGCGGTCAAG	TCAGGTTTAG	TCACACTGAT	AGGGCACCTC	960
ATGACAACAA	CCATTCTCTA	TTTCTGGTTA	CCTCTGTTCT	TTTGTGTGAT	AGCCGGAGTG	1020
ATGTCACCTCT	TTAGTTCCAC	CCTATCCGTT	GTAGCTCCAG	CCCTCTTTCC	CATCATTGCT	1080
ATCATCAGTG	CTCAAAATCC	TCAGATTGAT	ATTCACCTTAC	TCACAACAGC	CACCGTTATT	1140
GGCGCTCTAT	CTACTAATAT	CTCACCTTTT	TCATCAGCTG	GTTCTCTCAT	TCAACTCTCA	1200
CTTCCCAATA	TAGAGGAACG	TGGCCTTGCC	TTCAAAAAGC	AAATTATTCT	GGGTGTCCCC	1260
ATCAGCTTAA	GTTTGGGACT	CTTGACCACC	TGGATTCTCA	TCCTTCTAGC	TTCTTTAAGT	1320
TAG						1323

(2) INFORMATION FOR SEQ ID NO:2599:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1275 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1275

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2599:

ATAATAAATT	CCCATTTCGAT	GTGCAGACAT	AAGGAGAAAA	GTATGAAATT	ATTTTGGACA	60
AACAACATAT	ATAGACAGTT	GCTGCTAAAC	AGCTGTTTTT	CATCATTCGG	CGACAGTATT	120
TTCTACCTCG	CCATTATCAA	TTATGTGGCT	CAGTACAATT	TCGCTCCGCT	AGCGATTTTA	180
CTGATTTCCA	TTTCAGAGAT	GGTTCCCTTA	CTATCGCAAC	TCTTCTCGG	GATTCTAGGA	240
GATTTTCAAG	AAAATAGAGT	CAAACACGCA	CTCTGGATTG	CCAAAATCAA	AATCCTGCTC	300
TACGCTATTT	TGACAGTATT	TCTCGTCTTG	TCGCCCCTTT	CATTAGTTTC	AGTCATTATG	360
ATTGTCATCA	TCAACCTCAT	CTCTGACACC	TTGAGCTACC	TGTCTGCCTA	CATGATGAAC	420
GCCCTCTACA	TCAGTGTAAT	TAAGGACGAC	CTGCATGATG	CCATGGGGTT	CAGGCAGTCT	480
CTGATGAGGG	TTGTCCGTAT	TGTCGCCAAT	CTGGCTGGCG	CATTCCTTAT	CAATGTTATA	540
AGTATTCAAA	CTATTTCCCT	TATCAACACT	CTGACTTTTG	TCATTGCCTT	TTTGGGCCTG	600
TATGTTATT	GACATACCTT	GTATGAGGTT	GAAAAAGAA	TTGAAATGTC	ACATACAGCA	660
CTGAGTTTTA	AGAAATATTT	TCAACATCTT	AAACAGTCGC	TGGCTGTGCT	CCTGAGGTTA	720
AAAGATACCG	TCATACTACT	GTTTCTGACG	ACCAGTATGA	TTGCCATCTT	GGATGTGTCC	780
CCTCGGCTGA	TTGCCCTCCG	CTTCATCCAA	CAGACACTAG	CACAACTGAG	CATTGGGCAA	840

CTCCTCGCCC	TGCTCTCCAT	CATCATGTCT	TGTGGAGCTA	TCCTTGGCAA	TATGACCAGC	900
AGTAATCTAT	TTAAAAATAT	CCGTTTCACG	CACCTCTTGG	TTTTCTGTGA	GATTTCCTTA	960
TTGACTCTAA	TAAGTAGTAT	CCTTTGTCAA	GCCTATATCG	TAATTTTCAT	GACCAGTTTC	1020
ATCAGTTCTA	CGATTATCGG	CATTCTCAGC	CCTCGCCTAC	AAGCAGCTGT	CTTTGCCCCAT	1080
ATCCCCAGTG	ACAAGATGGG	GACGGTGGGC	TCTGCTCTGA	GCACAGTGGA	CATTCTCGCC	1140
CCGTCCCTGC	TCTCCCTATT	AGCCCTATCC	ATAGCATCGG	GCGTTTCGGT	GCAGTTAGCA	1200
TTGATATTTT	TGTATCTTAT	TTTAATTGCT	CTTATCTTTT	GTCAATGGTT	AGTCAAGTTC	1260
AACACTCATA	ACTAA					1275

(2) INFORMATION FOR SEQ ID NO:2600:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 618 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...618
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2600:

GTTATGAATT	CATTTAAAAA	TTTCTTAAAA	GAGTGGGGAC	TGTTCCCTCCT	AATTCTGTCA	60
TTACTAGCTT	TAAGTCGTAT	CTTTTTTTTG	AGCAATGTTT	GCGTAGAAGG	ACATTCCATG	120
GATCCGACCC	TAGCGGATGG	CGAAATTCTC	TTCGTTGTAA	AACACCTTCC	TATTGACCGT	180
TTTGATATCG	TGGTGGCCCA	TGAGGAAGAT	GGCAATAAGG	ACATCGTCAA	GCGCGTGATT	240
GGAATGCCTG	GCGACACCAT	TCGTTACGAA	AATGATAAAC	TCTACATCAA	TGACAAAGAA	300
ACGGACGAGC	CTTATCTAGC	AGACTATATC	AAACGCTTCA	AGGATGACAA	ACTCCAAAGC	360
ACTTACTCAG	GCAAGGGCTT	TGAAGGAAAT	AAAGGAACTT	TCTTTAGAAG	TATCGCTCAA	420
AAAGCCCAAG	CCTTCACAGT	TGATGTCAAC	TACAACACCA	ACTTTAGCTT	TACTGTTCCA	480
GAAGGAGAAT	ACCTTCTCCT	CGGAGATGAC	CGCTTGTTTT	CGAGCGACAG	CCGCCACGTA	540
GGTACCTTCA	AAGCAAAAGA	TATCACAGGG	GAAGCTAAAT	TCCGCTTCTG	GCCAATCACC	600
CGTATCGGAA	CATTTTAA					618

(2) INFORMATION FOR SEQ ID NO:2601:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 417 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...417

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2601:

GTATCGAATT	CCCTTGAGGA	GAAAGAAATG	AAAGTCAATA	TAGCAGATCT	TCATCCGACT	60
CAACTATATT	TATCAGAAAA	GAAAGTTGCAA	GATATTCAGA	TGCTTTACCA	GTCGGCAGAA	120
ACAATCCAAG	TCGATCCAAT	CAGTATTCTT	GCCTTTGGAG	ATTGTTTGCT	GATTACAGAT	180
GGGCATCACA	GGGCTTATCA	GGCTTTATTG	GCAGGTCGGG	ATACGATTTC	TGCTGAGTGG	240
GATAGAGATG	GTGGTGATGA	ACTATATCAT	CTCTATGCGC	AAGCTTGCGA	GGAAAGAAAG	300
ATTTACTCTG	TTTTTGATTT	AGAAGATCGT	ATCCTAGCTC	AAGATGGGTA	TGAAGCAAAA	360
TGGTATAACT	GGTGTGATGG	TTTAAATCAA	GCAGCAACTC	TTTTGTTGAA	AAGGTAG	417

(2) INFORMATION FOR SEQ ID NO:2602:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1086 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1086

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2602:

GAGAAATGATT	CGCTTGCAGT	GCTAGAAATA	GGCATTTTGA	ATAGTGAATA	TGTTATAATA	60
AGTATTAGTA	GGAGGTGTTT	TAGATTGGAG	AAGAAACTGA	CCATAAAAGA	CATTGCGGAA	120
ATGGGCTCAGA	CCTCGAAAAC	AACCGTGTCA	TTTTACCTAA	ACGGGAAATA	TGAAAAAATG	180
TCCCAAGAGA	CACGTGAAAA	GATTGAAAAA	GTTATTCATG	AAACAAATTA	CAAACCGAGC	240
ATTGTTGCGC	GTAGCTTAAA	CTCCAAACGA	ACAAAATTAA	TCGGTGTTTT	GATCGGTGAT	300
ATTACCAACA	GTTTCTCAAA	CCAAATTGTT	AAGGGAATTG	AGGATATCGC	CAGCCAGAAT	360
GGCTACCAGG	TAATGATAGG	AAATAGTAAT	TACAGCCAAG	AGAGTGAGGA	CCGGTATATT	420
GAAAGCATGC	TTCTCTTGGG	AGTAGACGGC	TTTATTATTC	AGCCGACCTC	TAATTTCCGA	480
AAATATTCTC	GTATCATCGA	TGAGAAAAAG	AAGAAAATGG	TCTTTTTTGA	TAGTCAGCTC	540
TATGAACACC	GGACTAGCTG	GGTTAAAACC	AATAACTATG	ATGCCGTTTA	TGACATGACC	600
CAGTCCTGTA	TCGAAAAAGG	TTATGAGCAT	TTTCTCTTGA	TTACAGCGGA	TACGAGTCGT	660
TTGAGTACTC	GGATTGAGCG	GGCAAGTGGT	TTTGTTGGATG	CTTTAACAGA	TGCTAATATG	720
CGTCACGCCA	GTCTAACCAT	TGAAGATAAG	CATACGAATT	TGGAACAAAT	TAAAGAATTT	780
TTACAAAAAG	AAATCGATCC	CGATGAAAAA	ACTCTGGTAT	TTATCCCTAA	CTGTTGGGCC	840
CTACCTCTAG	TCTTTACCGT	TATCAAAGAG	TTGAATTATA	ACTTGCCGCA	AGTTGGGTTG	900

ATTGGTTTTG	ACAATACGGA	GTGGACTTGC	TTTTCTTCTC	CAAGTGTTC	GACGCTGGTT	960
CAGCCCTCCT	TTGAGGAAGG	ACAACAGGCT	ACAAAGATTT	TGATTGACCA	GATTGAAGGC	1020
CGCAATCAAG	AAGAAAGGCA	ACAAGTCTTG	GATTGTAGTG	TGAATTGGAA	AGAGTCGACT	1080
TTCTAA						1086

(2) INFORMATION FOR SEQ ID NO:2603:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1059 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1059
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2603:

GCGACAGATT	CTCCATTAAA	GAAAAGGAAA	AAACAAATGA	CAAATAAAAA	TGCATATGCC	60
CAGTCGGGTG	TGGATGTTGA	AGCGGGTTAT	GAAGTTGTTG	AACGGATTAA	AAAGCACGTG	120
GCCCGTACGG	AGCGTGCAGG	TGTCATGGGA	GCTCTTGGTG	GCTTTGGTGG	TATGTTTGAC	180
CTTTCCAAGA	CTGGGGTTAA	AGAACCCGTC	TTGATTTTCAG	GGACTGACGG	TGTCGGAACC	240
AAGCTCATGT	TGGCTATCAA	GTACGACAAG	CACGATACCA	TCGGGCAGGA	CTGTGTGGCC	300
ATGTGTGTCA	ACGACATCAT	TGCTGCAGGT	GCGGAACCCC	TCTATTTTCT	CGACTACGTA	360
GCGACAGGGA	AGAAATGAAC	AGCTAAGCTA	GAACAAGTGG	TTGCTGGTGT	GGCAGAAGGT	420
TGTGTGCAGG	CTGGTGCTGC	CCTCATCGGT	GGGGAAACGG	CTGAAATGCC	GGGCATGTAC	480
GGCGAAGACG	ACTATGACTT	GGCTGGTTTT	GCGGTCGGTG	TGGCTGAAAA	ATCTCAAATC	540
ATTGACGGTT	CAAAGGTGGT	AGAGGGAGAT	GTTCTTCTCG	GACTTGCTTC	AAGTGGGATT	600
CACTCAAATG	GTTACTCTTT	GGTTCGTCGT	GTCTTTGCGG	ATTACACAGG	TGAGGAAGTC	660
CTACCAGAAAT	TGGAAGGCAA	GAAACTTAAG	GAAGTTCTAC	TTGAGCCGAC	TCGTATCTAT	720
GTCAAGGCTG	TCTTGCCGCT	CATCAAAGAA	GAGTTGGTCA	ACGGCATTGC	CCACATCACA	780
GGTGGTGGCT	TTATCGAAAA	TGTCCCTCGT	ATGTTTGCA	ATGACCTAGC	TGCTGAAATT	840
GATGAAAGCA	AAGTTCCAGT	GCTTCCAATT	TTCAAAGCCC	TTGAAAAATA	TGGTCAGATT	900
AAACACGAAG	AAATGTTTGA	AATCTTCAAT	ATGGGTGTGG	GACTTATGTT	GGCGGTCAGC	960
CCTGAAAAATG	TAGAGCGTGT	AAAAGAATTG	TTGGATGAAG	CAGTCTATGA	AATTGGTCGC	1020
ATCGTCAAGA	AAGAAAACGA	AAGTGTCATT	ATCAAATGA			1059

(2) INFORMATION FOR SEQ ID NO:2604:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 86 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...86

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2604:

Thr	Pro	Cys	Ser	Leu	Ser	Leu	Ser	Thr	Lys	Thr	Gln	Arg	Lys	Asp	Arg
1				5					10					15	
Ser	Lys	Thr	Ser	Ala	Leu	Phe	Ser	Ser	Glu	Gln	Phe	Ala	Ser	Ser	Val
			20					25					30		
His	Met	Thr	Asn	Ile	Asp	Arg	Arg	Ile	Ser	Lys	Thr	Lys	Lys	Ala	Ile
		35				40						45			
Tyr	Gln	Ala	Phe	Ile	Gln	Leu	Leu	Asn	Ala	Lys	Gly	Tyr	Glu	Ala	Thr
	50					55					60				
Thr	Val	Gln	Asp	Ile	Ile	Asp	Leu	Ala	Asp	Val	Gly	Arg	Ser	Thr	Phe
65					70					75					80
Tyr	Cys	His	Tyr	Glu	Arg										
					85										

(2) INFORMATION FOR SEQ ID NO:2605:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2605:

Trp	Ser	Cys	Ser	Ser	Gln	His	Tyr	Gly	Leu	Tyr	Leu	Lys	Glu	Glu	Ile
1				5					10					15	
Val	Met	Ser	Ile	Asn	Val	Phe	Gln	Ala	Ile	Leu	Ile	Gly	Leu	Trp	Thr
			20					25				30			
Ala	Phe	Cys	Phe	Ser	Gly	Met	Leu	Leu	Gly	Ile	Tyr	Thr	Asn	Arg	Cys
		35				40						45			
Ile	Val	Leu	Ser	Phe	Gly	Val	Gly	Ile	Ile	Leu	Gly	Asp	Leu	Pro	Thr
	50					55					60				
Ala	Leu	Ala	Met	Gly	Ala	Ile	Gly	Glu	Leu	Ala	Tyr	Met	Gly	Phe	Gly
65					70					75					80
Val	Gly	Ala	Gly	Gly	Thr	Val	Pro	Pro	Asn	Pro	Ile	Gly	Leu	Ile	Met
				85					90					95	
Arg	Gly	Ile	His	Xaa	Ser										
					100										

(2) INFORMATION FOR SEQ ID NO:2606:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...63

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2606:

Leu	Ile	Arg	Ser	His	Ser	Ile	Thr	Ile	Tyr	Tyr	Asn	Lys	Met	Met	Arg
1				5					10					15	
Val	Ile	Thr	Asn	Tyr	Arg	Phe	Glu	Lys	Ser	Leu	Ile	Ser	Phe	Ser	Ser
			20					25					30		
Ile	Leu	Thr	Asn	Ala	Ser	Ser	Leu	Val	Ser	Arg	Asn	Lys	Val	Ile	Pro
		35					40				45				
Leu	Ser	Ile	Lys	Ser	Glu	Leu	Cys	Cys	Ser	Ile	Pro	Lys	Arg	Thr	
	50					55					60				

(2) INFORMATION FOR SEQ ID NO:2607:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2607:

Phe	Ser	Ser	Ser	Phe	Val	Val	Ile	Phe	Cys	Thr	His	Ile	Pro	Leu	Lys
1				5				10						15	
Tyr	Lys	Arg	Arg	Leu	Tyr	Met	Tyr	Arg	Ile	Leu	Asn	Pro	Met	Asn	His
			20					25					30		
Asn	Val	Ser	Phe	Val	Arg	Asn	Asp	Lys	Gly	Glu	Glu	Val	Ile	Val	Ile
		35					40				45				
Gly	Lys	Gly	Ile	Ala	Phe	Gly	Lys	Lys	Lys	Gly	Asp	Leu	Ile	Ala	Glu

				85					90					95			
Asp	Val	Thr	Thr	Tyr	Leu	Asn	Tyr	Ile	Ser	Cys	Asp	Ser	Leu	Ala	Lys		
				100					105					110			
Ser	Glu	Ile	Val	Val	Pro	Met	Met	Lys	Asn	Gly	Gln	Leu	Leu	Gly	Val		
				115					120					125			
Leu	Asp	Leu	Asp	Ser	Ser	Glu	Ile	Glu	Asp	Tyr	Asp	Ala	Met	Asp	Arg		
				130					135				140				
Asp	Tyr	Leu	Glu	Gln	Phe	Val	Ala	Ile	Leu	Leu	Glu	Lys	Thr	Ala	Trp		
						150					155				160		
Asp	Phe	Thr	Met	Phe	Glu	Glu	Lys	Ser									
						165											

(2) INFORMATION FOR SEQ ID NO:2610:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...91

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2610:

Lys	Thr	Ser	Ser	Gln	Ser	Val	Thr	Pro	Val	Leu	Gln	Thr	Asn	Tyr	Tyr		
1				5					10					15			
Ile	Asp	Thr	Pro	Asp	Phe	Glu	Leu	Arg	Glu	Lys	Lys	Val	Ala	Met	Arg		
				20					25					30			
Ile	Arg	Thr	Phe	Glu	Asp	Trp	Ala	Glu	Leu	Thr	Leu	Lys	Val	Pro	Gln		
				35					40				45				
Ser	Val	Gly	Asn	Met	Glu	Tyr	Asn	Gln	Lys	Leu	Gln	Leu	Lys	Asp	Ala		
				50				55					60				
Glu	Asn	Tyr	Leu	Ser	Lys	Glu	Glu	Leu	Thr	Gln	Gly	Leu	Val	Leu	Asp		
					70					75					80		
Asp	Leu	Ala	Thr	His	Gly	Ile	Gln	Ser	Lys	Asn							
				85					90								

(2) INFORMATION FOR SEQ ID NO:2611:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2611:

```
Glu Arg Ser Ser Lys Phe Gly Ile Ile Pro Glu Leu Ile Gly Arg Leu
1          5          10          15
Pro Val Phe Ala Ala Leu Glu Gln Leu Thr Val Asp Asp Leu Val Arg
          20          25          30
Ile Leu Lys Glu Pro Arg Asn Ala Leu Val Lys Gln Tyr Gln Thr Leu
          35          40          45
Leu Ser Tyr Asp Asp Val Glu Leu Glu Phe Asp Asp Glu Ala Leu Gln
          50          55          60
Glu Ile Ala Asn Lys Ala Ile Glu Arg Lys Thr Gly Ala Arg Gly Leu
65          70          75          80
Arg Ser Ile Ile Glu Glu Thr Met Leu Asp Val Met Phe Glu Val Pro
          85          90          95
Ser Gln Glu Asn Val Lys Leu Val Arg Ile Thr Lys Glu Thr Val Asp
          100          105          110
Gly Thr Asp Lys Pro Ile Leu Glu Thr Ala
          115          120
```

(2) INFORMATION FOR SEQ ID NO:2612:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 307 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...307

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2612:

```
Lys Glu Ser Ser Met Ser Lys His Gln Glu Ile Leu Ser Tyr Leu Glu
1          5          10          15
Glu Leu Pro Val Gly Lys Arg Val Ser Val Arg Ser Ile Ser Asn His
          20          25          30
Leu Gly Val Ser Asp Gly Thr Ala Tyr Arg Ala Ile Lys Glu Ala Glu
          35          40          45
Asn Arg Gly Ile Val Glu Thr Arg Pro Arg Ser Gly Thr Ile Arg Val
          50          55          60
Lys Ser Gln Lys Val Ala Ile Glu Arg Leu Thr Phe Ala Glu Ile Ala
65          70          75          80
Glu Val Thr Ser Ser Glu Val Leu Ala Gly Gln Glu Gly Leu Glu Arg
```


50		55		60											
Lys	Val	Glu	Gln	Glu	Ser	Gly	Glu	Gln	Phe	Phe	Asn	Leu	Gly	Gln	Val
65					70				75					80	
Ser	Tyr	Gln	Asn	Lys	Lys	Thr	Gly	Leu	Val	Thr	Arg	Val	Arg	Thr	Asp
			85					90					95		
Lys	Ser	Gln	Tyr	Glu	Phe	Leu	Phe	Pro	Ser	Val	Lys	Ile	Lys	Glu	Glu
		100					105					110			
Lys	Arg	Asp	Lys	Lys	Glu	Glu	Val	Ala	Thr	Asp	Ser	Ser	Glu	Lys	Val
	115				120					125					
Glu	Lys	Lys	Lys	Ser	Glu	Glu	Lys	Pro	Glu	Lys	Lys	Glu	Asn	Ser	
130					135					140					

(2) INFORMATION FOR SEQ ID NO:2614:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...109

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2614:

Ser	Gly	Gly	Ser	Val	Trp	Lys	Gly	His	Arg	Ser	Thr	Asp	Lys	Ser	Tyr
1			5					10					15		
Pro	Gly	Asp	Asn	Arg	Leu	Ile	Ser	Pro	Lys	Ser	Ser	His	Arg	Arg	Gly
		20					25					30			
Gly	Leu	Ala	Pro	Arg	Cys	Arg	Leu	Val	Ala	Ser	Trp	Gly	Cys	Ser	Arg
	35				40				45						
Ser	Gln	Gly	Leu	Gly	Cys	Ser	Pro	Ile	Lys	Ala	Ala	Arg	Glu	Leu	Gly
50				55				60							
Ser	Glu	Arg	Arg	Glu	Thr	Val	Arg	Ser	Leu	Ser	Val	Ala	Gly	Val	Gly
65			70				75					80			
Asn	Leu	Arg	Gly	Ser	Ala	Pro	Ser	Thr	Arg	Gly	Pro	Glu	Trp	Thr	Tyr
		85					90					95			
Arg	Trp	Cys	Thr	Ser	Cys	Leu	Ala	Lys	Gly	Ile	Ala	Gly			
	100					105									

(2) INFORMATION FOR SEQ ID NO:2615:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...109

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2615:

Ser	Gly	Gly	Ser	Val	Trp	Lys	Gly	His	Arg	Ser	Thr	Asp	Lys	Ser	Tyr
1				5					10					15	
Pro	Gly	Asp	Asn	Arg	Leu	Ile	Ser	Pro	Lys	Ser	Ser	His	Arg	Arg	Gly
			20					25					30		
Gly	Leu	Ala	Pro	Arg	Cys	Arg	Leu	Val	Ala	Ser	Trp	Gly	Cys	Ser	Arg
		35					40					45			
Ser	Gln	Gly	Leu	Gly	Cys	Ser	Pro	Ile	Lys	Ala	Ala	Arg	Glu	Leu	Gly
	50					55					60				
Ser	Glu	Arg	Arg	Glu	Thr	Val	Arg	Ser	Leu	Ser	Val	Ala	Gly	Val	Gly
65					70				75						80
Asn	Leu	Arg	Gly	Ser	Ala	Pro	Ser	Thr	Arg	Gly	Pro	Glu	Trp	Thr	Tyr
			85					90						95	
Arg	Trp	Cys	Thr	Ser	Cys	Leu	Ala	Lys	Gly	Ile	Ala	Gly			
			100					105							

(2) INFORMATION FOR SEQ ID NO:2616:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 109 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...109

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2616:

Ser	Gly	Gly	Ser	Val	Trp	Lys	Gly	His	Arg	Ser	Thr	Asp	Lys	Ser	Tyr
1				5					10					15	
Pro	Gly	Asp	Asn	Arg	Leu	Ile	Ser	Pro	Lys	Ser	Ser	His	Arg	Arg	Gly
			20					25					30		
Gly	Leu	Ala	Pro	Arg	Cys	Arg	Leu	Val	Ala	Ser	Trp	Gly	Cys	Ser	Arg
		35					40					45			
Ser	Gln	Gly	Leu	Gly	Cys	Ser	Pro	Ile	Lys	Ala	Ala	Arg	Glu	Leu	Gly
	50					55					60				
Ser	Glu	Arg	Arg	Glu	Thr	Val	Arg	Ser	Leu	Ser	Val	Ala	Gly	Val	Gly
65					70				75						80
Asn	Leu	Arg	Gly	Ser	Ala	Pro	Ser	Thr	Arg	Gly	Pro	Glu	Trp	Thr	Tyr
			85					90						95	

Arg Trp Cys Thr Ser Cys Leu Ala Lys Gly Ile Ala Gly
 100 105

(2) INFORMATION FOR SEQ ID NO:2617:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...109

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2617:

Ser	Gly	Gly	Ser	Val	Trp	Lys	Gly	His	Arg	Ser	Thr	Asp	Lys	Ser	Tyr
1				5					10					15	
Pro	Gly	Asp	Asn	Arg	Leu	Ile	Ser	Pro	Lys	Ser	Ser	His	Arg	Arg	Gly
			20					25					30		
Gly	Leu	Ala	Pro	Arg	Cys	Arg	Leu	Val	Ala	Ser	Trp	Gly	Cys	Ser	Arg
		35					40					45			
Ser	Gln	Gly	Leu	Gly	Cys	Ser	Pro	Ile	Lys	Ala	Ala	Arg	Glu	Leu	Gly
	50					55				60					
Ser	Glu	Arg	Arg	Glu	Thr	Val	Arg	Ser	Leu	Ser	Val	Ala	Gly	Val	Gly
65					70				75					80	
Asn	Leu	Arg	Gly	Ser	Ala	Pro	Ser	Thr	Arg	Gly	Pro	Glu	Trp	Thr	Tyr
			85					90					95		
Arg	Trp	Cys	Thr	Ser	Cys	Leu	Ala	Lys	Gly	Ile	Ala	Gly			
			100					105							

(2) INFORMATION FOR SEQ ID NO:2618:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 510 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...510

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2618:

Gly	Glu	Gly	Ser	Phe	Gly	Ile	Phe	Lys	Gly	Asn	Asn	Met	Lys	Lys	Tyr
1				5					10					15	
Ile	Phe	Met	Arg	Val	Leu	Arg	Ser	Leu	Val	Ser	Ile	Phe	Leu	Val	Thr
			20					25					30		
Thr	Leu	Thr	Tyr	Thr	Ile	Ile	Tyr	Thr	Leu	Val	Pro	Arg	Lys	Leu	Ile
		35					40					45			
Phe	Lys	Gln	Asp	Pro	Asn	Tyr	Asn	Lys	Ile	Ala	Thr	Thr	Ala	Asp	Lys
	50					55					60				
Arg	Asp	Asn	Tyr	Glu	Asn	Thr	Val	Phe	Glu	Arg	Met	Gly	Tyr	Ile	Glu
65					70					75					80
Tyr	Tyr	Asp	Thr	Arg	Glu	Leu	Gln	Glu	Lys	Ala	Ser	Ser	Met	Asp	Ser
				85					90					95	
Ser	Val	Thr	Val	Glu	Ala	Asn	Ala	Thr	Asn	Lys	Ala	Ile	Tyr	Glu	Lys
			100					105					110		
Tyr	Ile	Asn	Gln	Leu	Gly	His	Gly	Trp	Thr	Leu	Gly	Glu	Phe	Thr	Glu
		115					120					125			
Ser	Gly	Gln	Phe	Tyr	Ala	Thr	Arg	Glu	Ile	Pro	Ile	Phe	Glu	Arg	Val
	130					135					140				
Phe	His	Phe	Tyr	Ala	Asn	Leu	Ile	Asp	Ile	Asp	His	Thr	Asn	Lys	Ile
145					150					155					160
Gln	Asp	Pro	Glu	Asn	Pro	Asp	Leu	Lys	Arg	Tyr	Leu	Arg	Phe	Glu	Asn
				165					170					175	
Asp	Pro	Ala	Ile	Gly	Trp	Ser	Leu	Val	Gly	Ser	Gly	Thr	Lys	His	Lys
			180					185					190		
Tyr	Leu	Leu	Tyr	Phe	Asn	Ser	Gln	Phe	Pro	Phe	Val	His	Gln	Asn	Phe
		195					200						205		
Val	Asn	Leu	Asn	Leu	Gly	Asp	Ser	Tyr	Pro	Thr	Tyr	Ala	Asn	Thr	Pro
	210					215						220			
Val	Leu	Gln	Val	Ile	Thr	Gln	Gly	Gln	Gly	Gln	Thr	Lys	Thr	Ala	Gln
225					230					235					240
Val	Gln	Phe	Pro	Thr	Gly	Lys	Lys	Thr	Ser	Ser	Val	Asn	Ile	Tyr	Ser
				245					250					255	
Arg	Thr	Tyr	Lys	Ser	Pro	Ser	Gln	Ala	Asp	Ser	Arg	Glu	Val	Ala	Ser
			260					265					270		
Tyr	Gly	Lys	Asp	Asp	Pro	Tyr	Thr	Ala	Thr	Glu	Ser	Asn	Tyr	Gln	Tyr
		275					280					285			
Pro	Ser	Met	Ile	Val	Ser	Ser	Ala	Ile	Thr	Gly	Leu	Ile	Gly	Leu	Val
	290					295					300				
Leu	Ala	Tyr	Ala	Leu	Ala	Val	Pro	Leu	Gly	Ser	Ala	Met	Ala	Arg	Phe
305					310					315					320
Lys	Asn	Thr	Trp	Ile	Asp	Ser	Leu	Ser	Thr	Gly	Thr	Leu	Thr	Phe	Leu
				325					330					335	
Leu	Ala	Leu	Pro	Thr	Ile	Ala	Leu	Val	Tyr	Ile	Val	Arg	Leu	Ile	Gly
			340					345					350		
Ser	Ser	Ile	Ala	Leu	Pro	Asp	Ser	Phe	Pro	Ile	Leu	Gly	Ala	Gly	Asp
		355					360					365			
Trp	Arg	Ser	Tyr	Val	Leu	Pro	Ala	Val	Ile	Leu	Gly	Leu	Leu	Gly	Ala
	370					375					380				
Pro	Val	Thr	Ala	Ile	Trp	Ile	Arg	Arg	Tyr	Met	Ile	Asp	Leu	Gln	Ser
385					390					395					400
Gln	Asp	Phe	Val	Arg	Phe	Ala	Arg	Ala	Lys	Gly	Leu	Ser	Glu	Lys	Glu
				405					410					415	
Ile	Ser	Asn	Lys	His	Ile	Phe	Lys	Asn	Ala	Met	Val	Pro	Leu	Val	Ser
		420						425					430		
Gly	Ile	Pro	Gly	Ala	Ile	Ile	Gly	Val	Ile	Gly	Gly	Ala	Thr	Leu	Thr

210		215		220
Phe Ser Ile Ile Ser	Ile Leu Val Ala Thr	Thr Leu Phe Phe Phe Ser		
225		230		240
Phe Leu Leu Gly Ser	Phe Val Val Arg Arg	Phe Ile His Gln Glu Lys		
	245	250		255
Tyr Trp Thr Leu Asp	Lys Val Leu Gln Gln Tyr	Ser Gln Leu Leu Ala		
	260	265		270
Ile Pro Ile Phe Leu	Thr Ala Ile Ala Ser	Phe Phe Ala Phe Phe Asp		
	275	280		285
Ser Leu Arg Phe Thr	Ala Leu Leu Cys Val	Ile Ser Ile Gly Ile Ile		
	290	295		300
Leu Leu Ala Ser Leu	His Ile Ile Thr Arg	Pro Ser Gln Ala Ser Glu		
305		310		320
Thr Asp Ser Phe Tyr	Gln Leu Phe Leu Ser	Val Leu Val Asn Gly Val		
	325	330		335
Ile Ile Leu Leu Phe	Phe Val Ala Glu Val	Ala Leu Ile Gly Asp Tyr		
	340	345		350
Leu Arg Ile Leu Ala	Phe Leu			
	355			

(2) INFORMATION FOR SEQ ID NO:2620:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 87 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...87
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2620:

Ile Phe Phe Ser Leu Leu Thr Ser Arg Leu Ala Val Ile Ser Ser Lys	
1	5 10 15
Ile Asn Ile Gly Ala Ser Phe Lys Lys Ala Leu Ala Ile Asp Asn Leu	
	20 25 30
Cys Leu Ser Pro Pro Asp Ser Ser Ala Pro Phe Ser Pro Ile Thr Val	
	35 40 45
Ser Lys Pro Leu Ser Ile Phe Ser Ile Lys Ser Val Gln Phe Ala Ser	
	50 55 60
Phe Ala Ala Leu Leu Thr Ser Ser Ser Leu Ala Ser Cys Leu Pro Ile	
65	70 75 80
Leu Ile Phe Ser Ile Thr Leu	
	85

(2) INFORMATION FOR SEQ ID NO:2621:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 70 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...70

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2621:

Asn	Ile	Leu	Ser	Thr	Thr	Ser	Thr	Lys	Gly	Ile	Ser	Gln	Tyr	Glu	Ile
1				5					10					15	
Lys	Lys	Arg	Leu	Glu	Ile	Thr	Ala	Arg	Ile	Ala	His	Gln	Leu	Asp	Glu
			20					25					30		
Glu	Met	Gly	Glu	Ile	Arg	Asp	Asp	Ile	Gln	Glu	Ala	Gln	Ala	Leu	Phe
		35				40						45			
Asp	Pro	Leu	Ser	Arg	Lys	Leu	Asn	Asp	Gly	Val	Gly	Asn	Ser	Asp	Asp
	50					55					60				
Thr	Asp	Glu	Glu	Tyr	Arg										
65					70										

(2) INFORMATION FOR SEQ ID NO:2622:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 124 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2622:

Thr	Leu	Ile	Ser	Phe	Ala	Ile	Ala	Ile	Val	Ile	Gly	Ile	Ile	Phe	Gly
1				5					10					15	
Met	Phe	Ser	Val	Ser	Pro	Tyr	Lys	Ser	Leu	Arg	Val	Ile	Ser	Glu	Ile
			20					25					30		
Phe	Val	Asp	Val	Ile	Arg	Gly	Ile	Pro	Leu	Met	Ile	Leu	Ala	Ala	Phe
		35				40						45			
Ile	Phe	Trp	Gly	Ile	Pro	Asn	Phe	Ile	Glu	Ser	Ile	Thr	Gly	Gln	Gln
	50					55					60				
Ser	Pro	Ile	Asn	Asp	Phe	Val	Ala	Gly	Thr	Ile	Ala	Leu	Ser	Leu	Asn
65					70				75					80	

Ala	Ala	Ala	Tyr	Ile	Ala	Glu	Ile	Val	Arg	Gly	Gly	Ile	Gln	Ala	Val
				85					90				95		
Pro	Val	Gly	Gln	Met	Glu	Ala	Ser	Arg	Ser	Leu	Gly	Ile	Ser	Tyr	Gly
			100					105					110		
Lys	Thr	Met	Arg	Lys	Ile	Ile	Leu	Pro	Gln	Ser	Asn				
		115					120								

(2) INFORMATION FOR SEQ ID NO:2623:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...331

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2623:

Leu	Gln	Ile	Ser	Met	Ile	Arg	Ser	Val	Lys	Lys	Trp	Asp	Leu	Pro	Ile
1				5				10					15		
Trp	Leu	Thr	Arg	Arg	Lys	Glu	Met	Ser	Glu	Lys	Leu	Val	Glu	Ile	Lys
			20				25					30			
Asp	Leu	Glu	Ile	Ser	Phe	Gly	Glu	Gly	Ser	Lys	Lys	Phe	Val	Ala	Val
		35				40						45			
Lys	Asn	Ala	Asn	Phe	Phe	Ile	Asn	Lys	Gly	Glu	Thr	Phe	Ser	Leu	Val
	50					55					60				
Gly	Glu	Ser	Gly	Ser	Gly	Lys	Thr	Thr	Ile	Gly	Arg	Ala	Ile	Ile	Gly
65					70				75					80	
Leu	Asn	Asp	Thr	Ser	Asn	Gly	Asp	Ile	Ile	Phe	Asp	Gly	Gln	Lys	Ile
			85					90					95		
Asn	Gly	Lys	Lys	Ser	Arg	Glu	Gln	Ala	Ala	Glu	Leu	Ile	Arg	Arg	Ile
		100					105						110		
Gln	Met	Ile	Phe	Gln	Asp	Pro	Ala	Ala	Ser	Leu	Asn	Glu	Arg	Ala	Thr
	115					120						125			
Val	Asp	Tyr	Ile	Ile	Ser	Glu	Gly	Leu	Tyr	Asn	His	Arg	Leu	Phe	Lys
	130					135					140				
Asp	Glu	Glu	Glu	Arg	Lys	Glu	Lys	Val	Gln	Asn	Ile	Ile	Arg	Glu	Val
145				150					155					160	
Gly	Leu	Leu	Ala	Glu	His	Leu	Thr	Arg	Tyr	Pro	His	Glu	Phe	Ser	Gly
			165					170					175		
Gly	Gln	Arg	Gln	Arg	Ile	Gly	Ile	Ala	Arg	Ala	Leu	Val	Met	Gln	Pro
		180				185						190			
Asp	Phe	Val	Ile	Ala	Asp	Glu	Pro	Ile	Ser	Ala	Leu	Asp	Val	Ser	Val
	195					200						205			
Arg	Ala	Gln	Val	Leu	Asn	Leu	Leu	Lys	Lys	Phe	Gln	Lys	Glu	Leu	Gly
	210				215					220					
Leu	Thr	Tyr	Leu	Phe	Ile	Ala	His	Asp	Leu	Ser	Val	Val	Arg	Phe	Ile
225					230				235						240

```

Ser Asp Arg Ile Ala Val Ile Tyr Lys Gly Val Ile Val Glu Val Ala
                245                250                255
Glu Thr Glu Glu Leu Phe Asn Asn Pro Ile His Pro Tyr Thr Gln Ala
                260                265                270
Leu Leu Ser Ala Val Pro Ile Pro Asp Pro Ile Leu Glu Arg Lys Lys
                275                280                285
Val Leu Lys Val Tyr Asp Pro Ser Gln His Asp Tyr Glu Thr Asp Lys
                290                295                300
Pro Ser Met Val Glu Ile Arg Pro Gly His Tyr Val Trp Ala Asn Gln
305                310                315                320
Thr Glu Leu Ala Arg Tyr Gln Lys Gly Leu Asn
                325                330

```

(2) INFORMATION FOR SEQ ID NO:2624:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2624:

```

Leu Ser Ser Ser Arg Ala Ser Ile Arg Val Lys Lys Gly Asp Val Phe
1          5          10          15
Asp Ser Asn Glu Ala Met Ser Thr Lys Ile Lys Gln Gly Gly Thr Thr

                20                25                30
Tyr Asp Ile Ala Ile Pro Ser Glu Tyr Met Ile Asn Lys Met Lys Asp
35          40          45
Glu Asp Leu Leu Val Pro Leu Asp Tyr Ser Lys Ile Glu Gly Ile Glu
50          55          60
Asn Ile Gly Pro Glu Phe Leu Asn Gln Ser Phe Asp Pro Gly Asn Lys
65          70          75          80
Phe Ser Ile Pro Tyr Phe Trp Gly Asp Ser Leu Cys Gly Glu Thr Phe
85          90          95
Arg His Gly Thr Thr Gln
100

```

(2) INFORMATION FOR SEQ ID NO:2625:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...66

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2625:

```
Phe Asn Ser Ser Lys Ile Ser Cys Leu Arg Ser Val Phe Asn Thr Glu
1          5          10          15
Ser Pro Pro Val Ile Val Tyr Thr Ile His Ser Ile Ile Leu Ser Phe
          20          25          30
Glu Val Lys His Phe Leu Ser Phe Ser Phe Lys Ile Tyr His Phe Phe
          35          40          45
Leu Phe Leu Glu Phe Leu Leu Gln Asp Lys Ser Leu Tyr Gly Arg Leu
50          55          60
Phe Glu
65
```

(2) INFORMATION FOR SEQ ID NO:2626:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 129 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...129

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2626:

```
Glu Asn Thr Ser Val Leu Tyr Leu Leu Phe Thr Thr Asn Thr Arg Lys
1          5          10          15
Gly Thr Glu Met Gln Glu His Tyr Thr Pro Lys Gly Lys His Leu Thr
          20          25          30
Ile Asp Asn Arg Arg Leu Ile Glu Arg Trp Lys Asn Glu Asn Lys Ser
          35          40          45
Asn Arg Glu Ile Ala Gly Leu Leu Gly Lys Ala Pro Gln Thr Ile His
50          55          60
Asn Glu Val Lys Arg Gly Thr Thr Leu Gln Gln Val Arg Lys Gly Leu
65          70          75          80
Tyr Lys Lys Val Tyr Ser Ala Asp Tyr Ala Gln Thr Val Tyr Gln Phe
          85          90          95
Asn Arg Lys Arg Ser Val Lys Lys Leu Ile Leu Thr Lys Glu Ile Arg
100          105          110
```

Glu Lys Ile Leu His Tyr His Lys His Ile Ser Lys Asn Phe Arg Leu
 115 120 125
 Lys

(2) INFORMATION FOR SEQ ID NO:2627:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 368 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...368

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2627:

Glu Asn Thr Ser Val Leu Tyr Leu Leu Phe Asn His Lys His Lys Lys
 1 5 10 15
 Gly Thr Glu Met Gln Asp Asn Tyr Thr Thr Lys Gly Lys His Leu Thr
 20 25 30
 Ile Asp Ser Arg Arg Leu Ile Glu Arg Trp Lys Lys Glu Gly Lys Ser
 35 40 45
 Asn Arg Glu Ile Ala Ser Leu Leu Gly Lys Ala Pro Gln Thr Ile His
 50 55 60
 Thr Lys Ile Lys Arg Arg Thr Val Arg Lys Cys Leu Gly Lys Gly Arg
 65 70 75 80
 Phe Lys Glu Val Tyr Ser Ala Asp Tyr Ala Gln Gln Ser Tyr Glu Asn
 85 90 95
 Asn Arg Lys Arg Ser Val Lys Lys Ser Ser Leu Thr Lys Glu Leu Lys
 100 105 110
 Glu Lys Ile Leu His Tyr His Asn Gln Lys Phe Ser Pro Glu Met Met
 115 120 125
 Val Met Ala Lys Gly Val Asn Val Gly Ile Ser Thr Ile Tyr Tyr Trp
 130 135 140
 Ile His His Gly Lys Leu Gly Leu Ser Lys Gln Asp Leu Leu Tyr Pro
 145 150 155 160
 Arg Lys Gly Lys Val Leu Lys Lys Gln Ala Ser Thr Asn Phe Lys Pro
 165 170 175
 Ala Gly Gln Ser Ile Ala Gln Arg Pro Glu Ala Ile Asn Leu Arg Leu
 180 185 190
 Glu Asn Gly His Tyr Glu Ile Asp Thr Val Leu Leu Thr Arg Ser Lys
 195 200 205
 Asn Tyr Cys Leu Leu Val Leu Thr Asp Arg Lys Ser Arg His Gln Ile
 210 215 220
 Ile Arg Leu Ile Pro Asn Lys Ser Ala Glu Val Val Asn Gln Ala Leu
 225 230 235 240
 Lys Leu Ile Leu Lys Gln His Lys Ile Leu Ser Ile Thr Ala Asp Asn

				245				250					255				
Gly	Thr	Glu	Phe	Asn	Arg	Leu	Ser	Asp	Val	Phe	Ser	Glu	Glu	His	Ile		
			260					265					270				
Tyr	Tyr	Ala	His	Pro	Tyr	Ala	Ser	Trp	Glu	Arg	Gly	Thr	Asn	Glu	Asn		
		275					280					285					
His	Asn	Arg	Leu	Ile	His	Arg	Trp	Leu	Pro	Lys	Gly	Thr	Lys	Lys	Met		
	290					295					300						
Thr	Pro	Lys	Glu	Val	Ala	Phe	Ile	Glu	Lys	Trp	Ile	Asn	Asn	Tyr	Pro		
305					310					315					320		
Lys	Lys	Cys	Leu	Asn	Tyr	Lys	Ser	Pro	Arg	Glu	Asp	Phe	Leu	Met	Ala		
			325						330				335				
Asn	Leu	Asn	Leu	Lys	Phe	Ser	Val	Arg	Asn	Lys	Ser	Arg	Asn	Arg	Phe		
		340					345					350					
Lys	Phe	Cys	Arg	Ser	Phe	Lys	Tyr	Pro	Ala	Arg	Arg	Cys	Ser	Trp	Cys		
	355					360					365						

(2) INFORMATION FOR SEQ ID NO:2628:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 129 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...129

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2628:

Glu	Asn	Thr	Ser	Val	Leu	Tyr	Leu	Leu	Phe	Thr	Thr	Asn	Thr	Arg	Lys		
1				5					10					15			
Gly	Thr	Glu	Met	Gln	Glu	His	Tyr	Thr	Pro	Lys	Gly	Lys	His	Leu	Thr		
		20					25					30					
Ile	Asp	Asn	Arg	Arg	Leu	Ile	Glu	Arg	Trp	Lys	Asn	Glu	Asn	Lys	Ser		
	35					40					45						
Asn	Arg	Glu	Ile	Ala	Gly	Leu	Gly	Lys	Ala	Pro	Gln	Thr	Ile	His			
	50				55				60								
Asn	Glu	Val	Lys	Arg	Gly	Thr	Thr	Leu	Gln	Gln	Val	Arg	Lys	Gly	Leu		
65				70				75						80			
Tyr	Lys	Lys	Val	Tyr	Ser	Ala	Asp	Tyr	Ala	Gln	Thr	Val	Tyr	Gln	Phe		
			85				90					95					
Asn	Arg	Lys	Arg	Ser	Val	Lys	Lys	Leu	Ile	Leu	Thr	Lys	Glu	Ile	Arg		
		100				105					110						
Glu	Lys	Ile	Leu	His	Tyr	His	Lys	His	Ile	Ser	Lys	Asn	Phe	Arg	Leu		
	115					120					125						

Lys

(2) INFORMATION FOR SEQ ID NO:2629:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 151 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...151
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2629:

Glu	Asn	Thr	Ser	Val	Leu	Tyr	Leu	Leu	Phe	Asn	His	Lys	His	Lys	Lys
1				5					10					15	
Gly	Thr	Glu	Met	Gln	Asp	Asn	Tyr	Thr	Thr	Lys	Gly	Lys	His	Leu	Thr
			20					25					30		
Ile	Asp	Ser	Arg	Arg	Leu	Ile	Glu	Arg	Trp	Lys	Lys	Glu	Gly	Lys	Ser
		35					40					45			
Asn	Arg	Glu	Ile	Ala	Ser	Leu	Leu	Gly	Lys	Ala	Pro	Gln	Thr	Ile	His
		50				55					60				
Thr	Lys	Ile	Lys	Arg	Arg	Thr	Val	Arg	Lys	Cys	Leu	Gly	Lys	Gly	Arg
65					70					75					80
Phe	Lys	Glu	Val	Tyr	Ser	Ala	Asp	Tyr	Ala	Gln	Gln	Ser	Tyr	Glu	Asn
				85					90					95	
Asn	Arg	Lys	His	Ser	Val	Lys	Arg	Ser	Ser	Val	Thr	Lys	Glu	Leu	Lys
			100					105					110		
Glu	Lys	Ile	Leu	His	Tyr	His	Asn	Gln	Lys	Phe	Leu	Pro	Glu	Met	Met
		115					120					125			
Val	Met	Ala	Lys	Gly	Val	Asn	Val	Gly	Ile	Ser	Thr	Ile	Tyr	Tyr	Trp
		130				135					140				
Ile	His	His	Gly	Lys	Leu	Gly									
145					150										

(2) INFORMATION FOR SEQ ID NO:2630:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 175 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2630:

Leu	Ser	Thr	Ser	Leu	Ser	Pro	Cys	Leu	Pro	Tyr	Leu	Ala	Lys	Arg	Ser
1				5					10					15	
Tyr	Ile	Ile	Met	Asn	Lys	Ser	Glu	His	Arg	His	Gln	Leu	Ile	Arg	Ala
			20					25					30		
Leu	Ile	Thr	Lys	Asn	Lys	Ile	His	Thr	Gln	Ala	Glu	Leu	Gln	Ala	Leu
		35					40					45			
Leu	Ala	Glu	Asn	Asp	Ile	Gln	Val	Thr	Gln	Ala	Thr	Leu	Ser	Arg	Asp
	50					55					60				
Ile	Lys	Asn	Met	Asn	Leu	Ser	Lys	Val	Arg	Glu	Glu	Asp	Ser	Ala	Tyr
65					70				75						80
Tyr	Val	Leu	Asn	Asn	Gly	Ser	Ile	Ser	Lys	Trp	Glu	Lys	Arg	Leu	Glu
			85						90					95	
Leu	Tyr	Met	Glu	Asp	Ala	Leu	Val	Trp	Met	Arg	Pro	Val	Gln	His	Gln
			100					105					110		
Val	Leu	Leu	Lys	Thr	Leu	Pro	Gly	Leu	Ala	Gln	Ser	Phe	Gly	Ser	Ile
		115					120						125		
Ile	Asp	Thr	Leu	Ser	Phe	Pro	Asp	Ala	Ile	Ala	Thr	Leu	Cys	Gly	Asn
	130					135					140				
Asp	Val	Cys	Leu	Ile	Ile	Cys	Glu	Asp	Ala	Asp	Thr	Ala	Gln	Lys	Cys
145					150					155					160
Phe	Glu	Glu	Leu	Lys	Lys	Phe	Ala	Pro	Pro	Phe	Phe	Phe	Glu	Glu	
				165					170						175

(2) INFORMATION FOR SEQ ID NO:2631:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...77

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2631:

Ala	Ser	Ala	Ser	Ser	Gly	Cys	Gln	Leu	Thr	Ser	Leu	Glu	Gln	Phe	Ile
1				5					10					15	
Asn	Gln	Gly	Met	Ile	Ala	Arg	Gln	Leu	Met	Val	Phe	Phe	Ser	Thr	Asn
			20					25					30		
Gln	Ala	Asp	Thr	Arg	Ile	Thr	Asn	Met	Ser	Ile	Asp	Ser	Leu	Ile	Ile
		35					40					45			
Asn	Asn	Ser	Lys	Asp	Phe	Gln	Ser	Ser	Ser	His	Ala	Ser	Val	Ser	Phe
	50					55					60				
Ile	Leu	Thr	Lys	Leu	Val	Asn	Leu	Leu	Ile	Phe	Asn	Phe			
65					70					75					

(2) INFORMATION FOR SEQ ID NO:2632:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 595 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...595

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2632:

Val	Leu	Ala	Ser	Gly	Phe	His	Leu	Gln	Ser	Glu	Arg	Asp	Phe	Met	Ser
1				5				10						15	
Ile	Ile	Gln	Lys	Leu	Trp	Trp	Phe	Phe	Lys	Leu	Glu	Lys	Arg	Arg	Tyr
			20					25					30		
Leu	Val	Gly	Ile	Val	Ala	Leu	Val	Leu	Val	Ser	Val	Leu	Asn	Leu	Ile
		35					40					45			
Pro	Pro	Met	Val	Met	Gly	Arg	Val	Ile	Asp	Ala	Ile	Thr	Ser	Gly	Gln
		50				55					60				
Leu	Thr	Gln	Gln	Asp	Leu	Leu	Leu	Ser	Leu	Phe	Tyr	Leu	Leu	Leu	Ala
65					70					75					80
Ala	Phe	Gly	Met	Tyr	Tyr	Leu	Arg	Tyr	Val	Trp	Arg	Met	Tyr	Ile	Leu
			85						90					95	
Gly	Thr	Ser	Tyr	Cys	Leu	Gly	Gln	Ile	Met	Arg	Ser	Arg	Leu	Phe	Lys
			100					105					110		
His	Phe	Thr	Lys	Met	Ser	Ser	Ala	Phe	Tyr	Gln	Thr	Tyr	Arg	Thr	Gly
		115					120					125			
Asp	Leu	Met	Ala	His	Ala	Thr	Asn	Asp	Ile	Asn	Ala	Leu	Thr	Arg	Leu
		130				135					140				
Ala	Gly	Gly	Gly	Val	Met	Ser	Ala	Val	Asp	Ala	Ser	Ile	Thr	Ala	Leu
145					150					155					160
Val	Thr	Leu	Leu	Thr	Met	Leu	Phe	Ser	Ile	Ser	Trp	Gln	Met	Thr	Leu
				165					170					175	
Val	Ala	Ile	Leu	Pro	Leu	Pro	Phe	Met	Ala	Tyr	Ala	Thr	Ser	Arg	Leu
			180					185					190		
Gly	Arg	Lys	Thr	His	Lys	Ala	Phe	Gly	Glu	Ser	Gln	Ala	Ala	Phe	Ser
		195				200						205			
Glu	Leu	Asn	Asn	Lys	Val	Gln	Glu	Ser	Val	Ser	Gly	Ile	Lys	Val	Thr
	210					215					220				
Lys	Ser	Phe	Gly	Tyr	Gln	Ala	Asp	Glu	Leu	Lys	Ser	Phe	Gln	Ala	Val
225					230					235					240
Asn	Glu	Leu	Thr	Phe	Gln	Lys	Asn	Leu	Gln	Thr	Met	Lys	Tyr	Asp	Ser
			245						250					255	
Leu	Phe	Asp	Pro	Met	Val	Leu	Leu	Phe	Val	Gly	Ser	Ser	Tyr	Val	Leu
		260						265					270		
Thr	Leu	Leu	Val	Gly	Ser	Leu	Val	Val	Gln	Glu	Gly	Gln	Ile	Thr	Val
	275					280						285			
Gly	Asn	Leu	Val	Thr	Phe	Ile	Ser	Tyr	Leu	Asp	Met	Leu	Val	Trp	Pro

290		295		300											
Leu	Met	Ala	Ile	Gly	Phe	Leu	Phe	Asn	Thr	Thr	Gln	Arg	Gly	Lys	Val
305					310					315					320
Ser	Tyr	Gln	Arg	Ile	Glu	Asn	Leu	Leu	Ser	Gln	Glu	Ser	Pro	Val	Gln
				325						330					335
Asp	Pro	Glu	Phe	Pro	Leu	Asp	Gly	Ile	Glu	Asn	Gly	Arg	Leu	Glu	Tyr
			340					345					350		
Ala	Ile	Asp	Ser	Phe	Ala	Phe	Glu	Asn	Glu	Glu	Thr	Leu	Thr	Asp	Ile
		355					360					365			
His	Phe	Ser	Leu	Ala	Lys	Gly	Gln	Thr	Leu	Gly	Leu	Val	Gly	Gln	Thr
	370					375					380				
Gly	Ser	Gly	Lys	Thr	Ser	Leu	Ile	Lys	Leu	Leu	Leu	Arg	Glu	Tyr	Asp
385					390				395						400
Val	Asp	Lys	Gly	Ala	Ile	Tyr	Leu	Asn	Gly	His	Asp	Ile	Arg	Asp	Tyr
			405					410					415		
Arg	Leu	Thr	Asp	Leu	Arg	Ser	Leu	Met	Gly	Tyr	Val	Pro	Gln	Asp	Gln
		420					425					430			
Phe	Leu	Phe	Ala	Thr	Ser	Ile	Leu	Asp	Asn	Ile	Arg	Phe	Gly	Asn	Pro
	435					440					445				
Asn	Leu	Pro	Leu	Ser	Ala	Val	Glu	Glu	Ala	Thr	Lys	Leu	Ala	Arg	Val
450					455						460				
Tyr	Gln	Asp	Ile	Val	Asp	Met	Pro	Gln	Gly	Phe	Asp	Thr	Leu	Ile	Gly
465				470					475						480
Glu	Lys	Gly	Val	Ser	Leu	Ser	Gly	Gly	Gln	Lys	Gln	Arg	Leu	Ala	Met
			485					490					495		
Ser	Arg	Ala	Met	Ile	Leu	Asp	Pro	Asp	Ile	Leu	Ile	Leu	Asp	Asp	Ser
		500					505					510			
Leu	Ser	Ala	Val	Asp	Ala	Lys	Thr	Glu	Tyr	Ala	Ile	Ile	Asp	Asn	Leu
	515					520						525			
Lys	Glu	Thr	Arg	Lys	Asp	Lys	Thr	Thr	Ile	Ile	Thr	Ala	His	Arg	Leu
530				535					540						
Ser	Ala	Val	Val	His	Ala	Asp	Leu	Ile	Leu	Val	Leu	Gln	Asn	Gly	Gln
545				550					555						560
Ile	Ile	Glu	Arg	Gly	Arg	His	Glu	Asp	Leu	Leu	Ala	Leu	Asp	Gly	Trp
			565				570						575		
Tyr	Ala	Gln	Thr	Tyr	Gln	Ser	Gln	Gln	Leu	Glu	Met	Lys	Gly	Glu	Glu
		580				585						590			
Asp	Ala	Glu													
	595														

(2) INFORMATION FOR SEQ ID NO:2633:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 102 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2633:

```
Leu Phe Arg Phe Thr Thr Asn Pro Glu Phe Pro Ser Met Ile Glu
1      5      10      15
Leu Phe Ser Ile Leu Pro Glu Tyr Pro Leu Lys Lys Asp Gly Arg Glu
      20      25      30
Ile Pro Leu His Phe Asp Gln Asp Ala Ser Leu Ser Ala Leu Leu Leu
      35      40      45
Asp Glu Asp Tyr Tyr Asn Ile Leu Val His Glu Lys Glu Thr Ile Gln
      50      55      60
Gly Tyr Ser Val Leu Ser Asn Cys Gly Leu Tyr Ser Ser Lys Ile Ser
65      70      75      80
Ser Asn His Val Ser Phe His Leu Gln Pro Gln Asn Ser Val Leu Ser
      85      90      95
Ser Leu Gln Leu Ala Ser
      100
```

(2) INFORMATION FOR SEQ ID NO:2634:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 112 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2634:

```
Phe Leu Tyr Ser Ser Lys Ile Ser Ser Asn His Val Ser Val Ala Leu
1      5      10      15
Pro Tyr Val Trp Leu Leu Thr Ser Ser Val Ser Ser Thr Ile Ser Lys
      20      25      30
Pro Cys Phe Glu Leu Thr Ser Ser Val Ser Ser Thr Thr Ser Lys Pro
      35      40      45
Cys Phe Glu Leu Thr Ser Ser Val Ser Ser Thr Thr Ser Glu Pro Cys
      50      55      60
Phe Glu Leu Thr Ser Ser Val Ser Ser Thr Thr Ser Lys Pro Cys Phe
65      70      75      80
Glu Leu Thr Ser Ser Val Ser Ser Thr Thr Ser Lys Leu Cys Phe Glu
      85      90      95
Gln Pro Ala Ala Ser Phe Leu Val Cys Ser Leu Ile Phe Ile Glu Tyr
      100      105      110
```

(2) INFORMATION FOR SEQ ID NO:2635:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 157 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...157

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2635:

Arg	Ala	His	Ser	Arg	Phe	Met	Pro	Leu	Ser	Phe	Arg	Tyr	Gln	Val	Ser
1				5					10					15	
Ala	Leu	Asp	Tyr	Ile	Asp	Lys	Ala	Leu	Ser	Ala	Glu	Glu	Phe	Glu	Ser
			20					25					30		
Arg	Ile	Glu	Thr	Ala	Leu	Leu	Tyr	Ala	Asn	Gly	Gln	Asp	Ser	Lys	Ser
		35					40					45			
Leu	Ala	Glu	Asp	Cys	Phe	Tyr	Phe	Lys	Ser	Lys	Phe	Ala	Gln	Phe	Gln
	50					55					60				
Tyr	Pro	Phe	Lys	Glu	Val	Tyr	Tyr	Leu	Glu	Thr	Ser	Thr	Arg	Pro	His
65					70					75				80	
Arg	Val	Ile	Leu	Tyr	Thr	Lys	Thr	Asp	Arg	Leu	Glu	Phe	Thr	Ala	Ser
				85					90					95	
Leu	Glu	Glu	Val	Leu	Lys	Gln	Glu	Pro	Arg	Phe	Leu	Gln	Cys	His	Arg
			100					105					110		
Ser	Phe	Leu	Ile	Asn	Pro	Ala	Asn	Val	Val	His	Leu	Asp	Lys	Lys	Glu
		115					120					125			
Lys	Leu	Leu	Phe	Phe	Pro	Asn	Gly	Gly	Ser	Cys	Leu	Ile	Ala	Arg	Tyr
	130					135					140				
Lys	Val	Arg	Glu	Val	Ser	Glu	Ala	Ile	Asn	Asn	Leu	His			
145					150					155					

(2) INFORMATION FOR SEQ ID NO:2636:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 256 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...256

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2636:

Leu	Leu	Pro	Leu	Ser	Ile	Gln	Lys	Gly	Lys	Gly	Phe	Leu	Arg	Ile	Ile
1				5					10					15	
Pro	Phe	Leu	Phe	Ala	Ile	Ile	Gly	Gly	Tyr	Leu	Phe	Ala	Leu	Thr	Leu
		20					25						30		
Gly	Leu	Val	Asp	Phe	Thr	Pro	Val	Leu	Lys	Ala	Asn	Trp	Phe	Glu	Ser
	35					40					45				
Pro	Gly	Phe	Tyr	Leu	Pro	Phe	Ser	Thr	Gly	Gly	Ala	Phe	Lys	Glu	Tyr
	50				55						60				
Asn	Leu	Tyr	Phe	Gly	Pro	Glu	Ala	Ile	Ala	Ile	Leu	Pro	Ile	Ala	Ile
65					70					75					80
Val	Thr	Ile	Ser	Glu	His	Ile	Gly	Asp	His	Thr	Val	Leu	Gly	Gln	Ile
			85						90					95	
Cys	Gly	Arg	Gln	Phe	Leu	Lys	Glu	Pro	Gly	Leu	His	Arg	Thr	Leu	Ile
		100						105					110		
Gly	Asp	Gly	Ile	Ala	Thr	Ser	Val	Ser	Ala	Phe	Leu	Gly	Gly	Pro	Ala
	115					120						125			
Asn	Thr	Thr	Tyr	Gly	Glu	Asn	Thr	Gly	Val	Ile	Gly	Met	Thr	Arg	Ile
	130					135					140				
Ala	Ser	Val	Ser	Val	Ile	Arg	Asn	Ala	Ala	Phe	Ile	Ala	Ile	Ala	Leu
145					150					155					160
Ser	Phe	Leu	Gly	Lys	Phe	Thr	Ala	Leu	Ile	Ser	Thr	Ile	Pro	Asn	Ala
			165					170					175		
Val	Leu	Gly	Gly	Met	Ser	Ile	Leu	Leu	Tyr	Gly	Val	Ile	Ala	Ser	Asn
		180						185					190		
Gly	Leu	Lys	Val	Leu	Ile	Lys	Glu	Arg	Val	Asp	Phe	Ala	Gln	Met	Arg
	195					200						205			
Asn	Leu	Ile	Ile	Ala	Ser	Ala	Met	Leu	Val	Leu	Gly	Leu	Gly	Gly	Ala
	210					215					220				
Ile	Leu	Lys	Leu	Gly	Pro	Val	Thr	Leu	Ser	Gly	Thr	Ala	Leu	Ser	Ala
225					230					235					240
Met	Thr	Gly	Ile	Ile	Leu	Asn	Leu	Ile	Leu	Pro	Tyr	Glu	Asn	Lys	Asp
			245					250						255	

(2) INFORMATION FOR SEQ ID NO:2637:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 67 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...67
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2637:

Asn	Ile	Asn	Ser	Met	Lys	Ile	Lys	Glu	Gln	Thr	Arg	Lys	Leu	Ala	Ala
1				5					10					15	
Gly	Cys	Ser	Lys	His	Ser	Phe	Glu	Val	Val	Asp	Lys	Thr	Asp	Glu	Val
		20						25					30		

Ser Ser Lys His Gly Phe Glu Val Val Asp Glu Thr Asp Glu Val Ser
 35 40 45
 Asn His Ile Tyr Gly Lys Ala Thr Leu Thr Lys Phe Glu Leu Asp Phe
 50 55 60
 Arg Arg Val
 65

(2) INFORMATION FOR SEQ ID NO:2638:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 154 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...154
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2638:

Leu Pro Asn Ser Arg Lys Asn Thr Glu Arg Arg Glu Gln Lys Pro Ser
 1 5 10 15
 Leu Lys Ala Cys Ser Leu Arg Asn Lys Ala Ser Ile Arg Val Thr Asp
 20 25 30
 Leu Ser Arg Lys Glu Glu Ile Gln Ala Leu Leu Glu Ala Asn Asp Ser
 35 40 45
 Leu Leu Ala Thr Thr Arg Leu Val Lys Glu Gln Gly His Phe Ala Gly
 50 55 60
 His Asn Leu Phe Ala Asp Gly Ala Ile Thr Ile Gln Asp Glu Ser Ser
 65 70 75 80
 Gln Leu Val Ala Pro Thr Leu Asp Leu Gln Gly Asp Glu Arg Val Leu
 85 90 95
 Asp Pro Val Arg Leu Gln Val Glu Asn Ser Pro Tyr Ser Leu Leu Ser
 100 105 110
 Tyr Asp Arg Ser Gly Tyr Cys Ser Gly Leu Val Arg Pro Gln Val Gly
 115 120 125
 Phe Asn Ser Arg Lys Cys Pro Thr Ser Gly Ser Cys Arg Ser Gly Ser
 130 135 140
 Asn Ser Lys Ile Gly Cys Gln Lys Gly Ala
 145 150

(2) INFORMATION FOR SEQ ID NO:2639:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 255 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2639:

Lys	Glu	Asn	Ser	Ala	Ile	Ser	Cys	Lys	Met	Gln	Arg	Val	Glu	Phe	Phe
1				5					10					15	
Leu	Arg	Gln	Ile	Trp	Tyr	Asn	Ser	Phe	Asn	Lys	Glu	Glu	Phe	Leu	Met
			20					25					30		
Ile	Lys	Ile	Leu	Leu	Val	Glu	Asp	Asp	Leu	Gly	Leu	Ser	Asn	Ser	Val
		35					40					45			
Phe	Asp	Phe	Leu	Asp	Asp	Phe	Ala	Asp	Val	Met	Gln	Val	Phe	Asp	Gly
	50					55					60				
Glu	Glu	Gly	Leu	Tyr	Glu	Ala	Glu	Ser	Gly	Val	Tyr	Asp	Leu	Ile	Leu
65					70				75					80	
Leu	Asp	Leu	Met	Leu	Pro	Glu	Lys	Asn	Gly	Phe	Gln	Val	Leu	Lys	Glu
			85						90					95	
Leu	Arg	Glu	Lys	Gly	Ile	Thr	Thr	Pro	Val	Leu	Ile	Met	Thr	Ala	Lys
		100						105					110		
Glu	Ser	Leu	Asp	Asp	Lys	Gly	His	Gly	Phe	Glu	Leu	Gly	Ala	Asp	Asp
		115				120						125			
Tyr	Leu	Thr	Lys	Pro	Phe	Tyr	Leu	Glu	Glu	Leu	Lys	Met	Arg	Ile	Gln
	130					135						140			
Ala	Leu	Leu	Lys	Arg	Ser	Gly	Lys	Phe	Asn	Glu	Asn	Thr	Leu	Thr	Tyr
145				150					155						160
Gly	Asn	Ile	Val	Val	Asn	Leu	Ser	Thr	Asn	Thr	Val	Lys	Val	Glu	Asp
			165					170						175	
Thr	Pro	Val	Glu	Leu	Leu	Gly	Lys	Glu	Phe	Asp	Leu	Leu	Val	Tyr	Phe
		180						185					190		
Leu	Gln	Asn	Gln	Asn	Val	Ile	Leu	Pro	Lys	Thr	Gln	Ile	Phe	Asp	Arg
		195					200					205			
Leu	Trp	Gly	Phe	Asp	Ser	Asp	Thr	Thr	Ile	Ser	Val	Val	Glu	Val	Tyr
	210					215					220				
Val	Ser	Lys	Val	Arg	Lys	Lys	Leu	Lys	Gly	Thr	Thr	Phe	Ala	Glu	Asn
225				230					235						240
Leu	Gln	Thr	Leu	Arg	Ser	Val	Gly	Tyr	Leu	Leu	Lys	Asp	Val	Gln	
			245						250					255	

(2) INFORMATION FOR SEQ ID NO:2640:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 317 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...317

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2640:

Ile	Met	Asn	Ser	Ile	Arg	Lys	Thr	Leu	Asn	Lys	Asn	Gln	Asn	Lys	Lys
1				5					10					15	
Lys	Lys	Asp	Ala	Ser	Ile	Ser	Leu	His	Lys	Pro	Ile	Arg	Gly	Asn	Ser
			20					25					30		
His	Leu	Ser	Asn	Asn	Ile	Phe	Ile	Lys	Ile	Lys	Arg	Ile	Met	Lys	Ser
		35				40						45			
Leu	Lys	Glu	Asp	Phe	Ser	Val	Arg	Ala	Glu	Lys	Tyr	Glu	Asn	Tyr	Gln
	50					55					60				
Glu	Thr	Phe	Gln	Gly	Pro	Asn	Ser	Phe	Ser	Lys	Thr	Asp	Pro	Asp	Ala
65					70					75					80
Thr	Phe	Met	Arg	Met	Lys	Glu	Asp	His	Met	Lys	Asn	Gly	Gln	Leu	Lys
				85					90					95	
Ala	Ala	Tyr	Asn	Leu	Gln	Ile	Ala	Thr	Glu	Asn	Gln	Phe	Val	Leu	His
		100						105					110		
Tyr	Asp	Val	Phe	Ser	Asn	Pro	Thr	Asp	Thr	Lys	Thr	Leu	Leu	Pro	Phe
	115						120					125			
Leu	Glu	Thr	Tyr	Pro	His	Asp	Leu	Lys	Thr	Val	Val	Ala	Asp	Ala	Gly
	130					135					140				
Tyr	Gly	Ser	Glu	Glu	Asn	Leu	Leu	Arg	Leu	Asp	Glu	Lys	Glu	Val	Asn
145					150					155					160
His	Leu	Ile	Lys	Tyr	Ala	Met	Phe	Asp	Lys	Glu	Gln	Lys	Arg	Gly	Tyr
				165				170						175	
Lys	Gln	Ser	Ala	Arg	Asn	Leu	Ala	Asn	Trp	His	Tyr	Asn	Asp	Lys	Glu
			180					185					190		
Asp	Ser	Tyr	Thr	His	Pro	Asp	Gly	Trp	Tyr	Tyr	Arg	Phe	His	His	Thr
	195						200					205			
Lys	His	Gln	Lys	Thr	Gln	Thr	Asp	Phe	Gln	Gln	Glu	Ile	Lys	Val	Tyr
	210						215					220			
Tyr	Ala	Asp	Glu	Pro	Glu	Ser	Ala	Pro	Gln	Lys	Gly	Leu	Tyr	Met	Asn
225					230					235					240
Glu	Gly	Tyr	Gln	Asn	Leu	Lys	Ala	Lys	Glu	Cys	Gln	Ala	Leu	Leu	Ser
				245					250					255	
Pro	Gln	Gly	Arg	Gln	Ile	Phe	Ala	Gln	Arg	Lys	Ile	Asp	Val	Glu	Pro
			260					265					270		
Val	Phe	Gly	Gln	Ile	Lys	Ala	Cys	Leu	Gly	Tyr	Lys	Arg	Cys	Asn	Leu
	275						280					285			
Arg	Gly	Lys	Arg	Gln	Val	Arg	Ile	Asp	Met	Gly	Leu	Val	Leu	Met	Ala
	290					295					300				
Asn	Asn	Leu	Leu	Lys	Tyr	Asn	Lys	Arg	Thr	Thr	Gln	Asn			
305					310						315				

(2) INFORMATION FOR SEQ ID NO:2641:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...65

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2641:

Phe	Gln	Asn	Ser	Leu	Leu	Leu	Ser	Ser	Ile	Leu	Leu	Tyr	Asn	Val	Lys
1				5					10					15	
Thr	Arg	Thr	Met	Thr	Val	Ala	Ile	Tyr	Thr	Glu	Val	Leu	Arg	Gly	Asn
			20					25					30		
Tyr	Gly	Val	Ala	Ala	Ala	Leu	Ser	Thr	Ile	Leu	Thr	Val	Leu	Thr	Val
		35					40					45			
Gly	Ser	Leu	Leu	Leu	Phe	Met	Lys	Ile	Ser	Lys	Ser	Asn	Ser	Ile	Thr
	50					55					60				
Leu															
65															

(2) INFORMATION FOR SEQ ID NO:2642:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 587 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...587

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2642:

Ser	Leu	Arg	Leu	Phe	Gln	Val	Lys	Lys	Glu	Phe	Asp	Met	Ser	Asn	Gly
1				5					10					15	
Gln	Leu	Ile	Tyr	Leu	Met	Val	Ala	Ile	Ala	Val	Ile	Leu	Val	Leu	Ala
			20					25					30		
Tyr	Val	Val	Ala	Ile	Phe	Leu	Arg	Lys	Arg	Asn	Glu	Gly	Arg	Leu	Glu
		35					40					45			
Ala	Leu	Glu	Glu	Arg	Lys	Glu	Glu	Leu	Tyr	Asn	Leu	Pro	Val	Asn	Asp
	50					55					60				
Glu	Val	Glu	Ala	Val	Lys	Asn	Met	His	Leu	Ile	Gly	Gln	Ser	Gln	Val
65					70					75					80
Ala	Phe	Arg	Glu	Trp	Asn	Gln	Lys	Trp	Val	Asp	Leu	Ser	Leu	Asn	Ser
			85					90					95		
Phe	Ala	Asp	Ile	Glu	Asn	Asn	Leu	Phe	Glu	Ala	Glu	Gly	Tyr	Asn	His
			100					105					110		

Ser	Phe	Arg	Phe	Leu	Lys	Ala	Ser	His	Gln	Ile	Asp	Gln	Ile	Glu	Ser
		115					120					125			
Gln	Ile	Thr	Leu	Ile	Glu	Glu	Asp	Ile	Ala	Ala	Ile	Arg	Asn	Ala	Leu
	130					135					140				
Ala	Asp	Leu	Glu	Lys	Gln	Glu	Ser	Lys	Asn	Ser	Gly	Arg	Val	Leu	His
145					150					155					160
Ala	Leu	Asp	Leu	Phe	Glu	Glu	Leu	Gln	His	Arg	Val	Ala	Glu	Asn	Ser
				165					170						175
Glu	Gln	Tyr	Gly	Gln	Ala	Leu	Asp	Glu	Ile	Glu	Lys	Gln	Leu	Glu	Asn
			180					185					190		
Ile	Gln	Ser	Glu	Phe	Ser	Gln	Phe	Val	Thr	Leu	Asn	Ser	Ser	Gly	Asp
	195						200					205			
Pro	Val	Glu	Ala	Ala	Val	Ile	Leu	Asp	Asn	Thr	Glu	Asn	His	Ile	Leu
	210					215					220				
Ala	Leu	Ser	His	Ile	Val	Asp	Arg	Val	Pro	Ala	Leu	Val	Thr	Thr	Leu
225					230					235					240
Ser	Thr	Glu	Leu	Pro	Asp	Gln	Leu	Gln	Asp	Leu	Glu	Ala	Gly	Tyr	Arg
				245					250						255
Lys	Leu	Ile	Asp	Ala	Asn	Tyr	His	Phe	Val	Glu	Thr	Asp	Ile	Glu	Ala
			260					265					270		
Arg	Phe	His	Leu	Leu	Tyr	Glu	Ala	Phe	Lys	Lys	Asn	Gln	Glu	Asn	Ile
	275						280					285			
Arg	Gln	Leu	Glu	Leu	Asp	Asn	Ala	Glu	Tyr	Glu	Asn	Gly	Gln	Ala	Gln
	290					295					300				
Glu	Glu	Ile	Asn	Ala	Leu	Tyr	Asp	Ile	Phe	Thr	Arg	Glu	Ile	Ala	Ala
305					310					315					320
Gln	Lys	Val	Val	Glu	Asn	Leu	Leu	Ala	Thr	Leu	Pro	Thr	Tyr	Leu	Gln
				325					330					335	
His	Met	Lys	Glu	Asn	Asn	Thr	Leu	Leu	Gly	Glu	Asp	Ile	Ala	Arg	Leu
			340					345					350		
Asn	Lys	Thr	Tyr	Leu	Leu	Pro	Glu	Thr	Ala	Ala	Ser	His	Val	Arg	Arg
		355					360					365			
Ile	Gln	Thr	Glu	Leu	Glu	Ser	Phe	Glu	Ala	Ala	Ile	Val	Glu	Val	Thr
	370					375					380				
Ser	Asn	Gln	Glu	Glu	Pro	Thr	Gln	Ala	Tyr	Ser	Val	Leu	Glu	Glu	Asn
385					390					395					400
Leu	Glu	Asp	Leu	Gln	Thr	Gln	Leu	Lys	Asp	Ile	Glu	Asp	Glu	Gln	Ile
				405					410					415	
Ser	Val	Ser	Glu	Arg	Leu	Thr	Gln	Ile	Glu	Lys	Asp	Asp	Ile	Asn	Ala
			420					425					430		
Arg	Gln	Lys	Ala	Asn	Val	Tyr	Val	Asn	Arg	Leu	His	Thr	Ile	Lys	Arg
		435					440					445			
Tyr	Met	Glu	Lys	Arg	Asn	Leu	Pro	Gly	Ile	Pro	Gln	Thr	Phe	Leu	Lys
	450					455					460				
Leu	Phe	Phe	Thr	Ala	Ser	Asn	Asn	Thr	Glu	Asp	Leu	Met	Val	Glu	Leu
465					470					475					480
Glu	Gln	Lys	Met	Ile	Asn	Ile	Glu	Ser	Val	Thr	Arg	Val	Leu	Glu	Ile
				485					490					495	
Ala	Thr	Asn	Asp	Met	Glu	Ala	Leu	Glu	Thr	Glu	Thr	Tyr	Asn	Ile	Val
			500					505					510		
Gln	Tyr	Ala	Thr	Leu	Thr	Glu	Gln	Leu	Leu	Gln	Tyr	Ser	Asn	Arg	Tyr
		515					520					525			
Arg	Ser	Phe	Asp	Glu	Arg	Ile	Gln	Glu	Ala	Phe	Asn	Glu	Ala	Leu	Asp
	530					535					540				
Ile	Phe	Glu	Lys	Glu	Phe	Asp	Tyr	His	Ala	Ser	Phe	Asp	Lys	Ile	Ser
545					550					555					560
Gln	Ala	Leu	Glu	Val	Ala	Glu	Pro	Gly	Val	Thr	Asn	Arg	Phe	Val	Thr

565 570 575
 Ser Tyr Glu Lys Thr Arg Glu Thr Ile Arg Phe
 580 585

(2) INFORMATION FOR SEQ ID NO:2643:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...90

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2643:

Leu	Pro	Cys	Ser	Met	Ile	Phe	Pro	Ser	Phe	Met	Thr	Lys	Ile	Lys	Ser
1				5					10					15	
Ala	Phe	Arg	Met	Ile	Asp	Lys	Arg	Trp	Ala	Met	Thr	Lys	Asp	Val	Arg
			20					25					30		
Pro	Ser	Ile	Lys	Arg	Ser	Met	Ala	Phe	Trp	Ile	Asn	Ser	Ser	Val	Arg
			35				40					45			
Val	Ser	Thr	Glu	Glu	Val	Ala	Ser	Ser	Lys	Ile	Lys	Ser	Asp	Ala	Ser
			50			55					60				
Leu	Arg	Arg	Ala	Gln	Ala	Ile	Val	Asn	Ser	Cys	Phe	Cys	Pro	Thr	Asp
65				70					75					80	
Lys	Val	Thr	Val	Ser	Ser	Lys	Met	Val	Ser						
			85					90							

(2) INFORMATION FOR SEQ ID NO:2644:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...76

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2644:

Ser	Thr	Cys	Ser	Gln	Ile	Arg	Gly	Leu	Trp	Val	Ala	Ile	Ile	Met	Val
1				5					10					15	
Arg	Phe	Gly	Phe	Phe	Arg	Asp	Ser	Arg	Met	Glu	Ser	Asn	Ser	Ser	Glu
			20					25					30		
Phe	Leu	Gly	Ser	Ser	Glu	Ala	Val	Gly	Ser	Ser	Ala	Arg	Ile	Lys	Gly
		35					40					45			
Gly	Ser	Phe	Lys	Ile	Ile	Phe	Ala	Asn	Ala	Thr	Arg	Cys	Ala	Ser	Pro
	50					55					60				
Pro	Asp	Asn	Ser	Asn	Ile	Gly	Cys	Phe	Lys	Ser	Lys				
65					70						75				

(2) INFORMATION FOR SEQ ID NO:2645:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...74

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2645:

Gln	Lys	Cys	Ser	Glu	Met	Thr	Ser	Asn	His	Phe	Arg	Ala	Arg	Lys	Lys
1				5					10					15	
His	Lys	Tyr	Thr	Phe	Ile	Phe	Phe	His	Pro	Asp	Tyr	Thr	Val	Gly	Phe
			20					25					30		
Gly	Ile	Ser	Pro	Asn	His	Ala	Phe	Arg	Leu	Val	Gly	Tyr	Thr	Thr	Gly
		35					40					45			
Arg	Glu	Leu	His	Pro	Ala	Leu	Lys	Ile	Val	Ile	Gln	Leu	Gln	Met	Ile
	50					55					60				
Ile	Val	Leu	Asn	Phe	Glu	Tyr	Val	Asn	Arg						
65					70										

(2) INFORMATION FOR SEQ ID NO:2646:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 359 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...359

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2646:

Pro	Trp	Cys	Ser	Gly	Cys	Gln	Asp	Glu	Arg	Trp	Trp	Ala	Arg	Arg	Leu			
1				5					10					15				
Tyr	His	Ser	Leu	Gly	Asn	Gln	Phe	Asp	Thr	Arg	Thr	Arg	Thr	Ser	Arg			
			20					25					30					
Lys	Ile	Arg	Arg	Glu	Arg	Ser	Cys	Ser	Asp	Met	Asp	Arg	Glu	Pro	Val			
			35				40					45						
Thr	Val	Arg	Ser	Tyr	Ala	Asn	Ile	Ala	Ile	Ile	Lys	Tyr	Trp	Gly	Lys			
	50					55					60							
Lys	Lys	Glu	Lys	Glu	Met	Val	Pro	Ala	Thr	Ser	Ser	Ile	Ser	Leu	Thr			
65					70					75				80				
Leu	Glu	Asn	Met	Tyr	Thr	Glu	Thr	Thr	Leu	Ser	Pro	Leu	Pro	Ala	Asn			
			85						90					95				
Val	Thr	Ala	Asp	Glu	Phe	Tyr	Ile	Asn	Gly	Gln	Leu	Gln	Asn	Glu	Val			
			100					105					110					
Glu	His	Ala	Lys	Met	Ser	Lys	Ile	Ile	Asp	Arg	Tyr	Arg	Pro	Ala	Gly			
	115						120					125						
Glu	Gly	Phe	Val	Arg	Ile	Asp	Thr	Gln	Asn	Asn	Met	Pro	Thr	Ala	Ala			
	130					135					140							
Gly	Leu	Ser	Ser	Ser	Ser	Ser	Gly	Leu	Ser	Ala	Leu	Val	Lys	Ala	Cys			
145					150					155				160				
Asn	Ala	Tyr	Phe	Lys	Leu	Gly	Leu	Asp	Arg	Ser	Gln	Leu	Ala	Gln	Glu			
			165						170					175				
Ala	Lys	Phe	Ala	Ser	Gly	Ser	Ser	Ser	Arg	Ser	Phe	Tyr	Gly	Pro	Leu			
			180					185					190					
Gly	Ala	Trp	Asp	Lys	Asp	Ser	Gly	Glu	Ile	Tyr	Pro	Val	Glu	Thr	Asp			
	195						200					205						
Leu	Lys	Leu	Ala	Met	Ile	Met	Leu	Val	Leu	Glu	Asp	Lys	Lys	Lys	Pro			
	210					215					220							
Ile	Ser	Ser	Arg	Asp	Gly	Met	Lys	Leu	Cys	Val	Glu	Thr	Ser	Thr	Thr			
225					230					235				240				
Phe	Asp	Asp	Trp	Val	Arg	Gln	Ser	Glu	Lys	Asp	Tyr	Gln	Asp	Met	Leu			
			245						250					255				
Ile	Tyr	Leu	Lys	Glu	Asn	Asp	Phe	Ala	Lys	Ile	Gly	Glu	Leu	Thr	Glu			
		260					265						270					
Lys	Asn	Ala	Leu	Ala	Met	His	Ala	Thr	Thr	Lys	Thr	Ala	Ser	Pro	Ala			
	275					280						285						
Phe	Ser	Tyr	Leu	Thr	Asp	Ala	Ser	Tyr	Glu	Ala	Met	Asp	Phe	Val	Arg			
	290					295					300							
Gln	Leu	Arg	Glu	Lys	Gly	Glu	Ala	Cys	Tyr	Phe	Thr	Met	Asp	Ala	Gly			
305					310					315				320				
Pro	Asn	Val	Lys	Val	Phe	Cys	Gln	Glu	Lys	Asp	Leu	Glu	His	Leu	Ser			
			325						330					335				
Glu	Ile	Phe	Gly	Gln	Arg	Tyr	Arg	Leu	Ile	Val	Ser	Lys	Thr	Lys	Asp			
		340						345					350					
Leu	Ser	Gln	Asp	Asp	Cys	Cys												
		355																

(2) INFORMATION FOR SEQ ID NO:2647:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 133 amino acids
(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...133

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2647:

```

Leu Lys Ser Ser Met Glu Asn Pro Leu Arg Lys Val Phe Ala Pro Leu
1      5      10      15
Asp Asn Ser Thr Phe Leu Arg Lys Ser Leu His Leu Arg Lys Met Glu
      20      25      30
Met Phe Pro Val Glu Thr Glu Glu Ile Thr Tyr Lys Arg Lys Lys Ser
      35      40      45
Lys Gly Lys Arg Gln Ala Leu Leu Ala Gln Phe Asp Ser Glu Glu Val
      50      55      60
His His Gln Val Glu Glu Arg Ile Cys Pro Asp Cys Gln Gly Asp Leu
65      70      75      80
Lys Glu Ile Gly Gly Ser Leu Gln Gly Gln Glu Leu Val Phe Ile Pro
      85      90      95
Ala Gln Leu Lys Arg Ile Asp His Ile Gln His Ala Tyr Lys Cys Gln
      100     105     110
Ala Cys Ser Asp Lys Asn Pro Ser Asp Lys Ile Val Lys Ala Pro Ile
      115     120     125
Pro Lys Ala Pro Leu
      130

```

(2) INFORMATION FOR SEQ ID NO:2648:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 107 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...107

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2648:

```

Ser Lys Ser Ser His Ile Ile Leu Tyr Val Ser Asp Met Tyr Gly Ala
1      5      10      15
Thr Ile Leu Val Pro Leu Ile Leu Gly Met Pro Val Ser Val Ala Leu

```

		20					25					30					
Phe	Ala	Ser	Gly	Val	Gly	Thr	Leu	Ile	Tyr	Met	Ile	Ala	Thr	Gly	Phe		
		35					40					45					
Lys	Val	Pro	Val	Tyr	Leu	Gly	Ser	Ser	Phe	Ala	Phe	Ile	Thr	Ala	Met		
		50					55				60						
Ser	Leu	Ala	Met	Lys	Glu	Met	Gly	Gly	Asp	Val	Ser	Ala	Ala	Gln	Thr		
65					70					75					80		
Gly	Val	Ile	Leu	Thr	Gly	Met	Val	Tyr	Val	Leu	Val	Ala	Thr	Ser	Ile		
				85					90					95			
Arg	Tyr	Val	Arg	Thr	Lys	Trp	Ile	Asp	Lys	Leu							
		100						105									

(2) INFORMATION FOR SEQ ID NO:2649:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...305

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2649:

Thr	His	Gly	Ser	Pro	Phe	Gly	His	Phe	Tyr	Ala	Lys	Ile	Val	Ala	Met		
1				5					10					15			
Asp	Lys	Ile	Ile	Lys	Thr	Ile	Ser	Glu	Ser	Gly	Ala	Phe	Arg	Ala	Phe		
			20					25					30				
Val	Leu	Asp	Ser	Thr	Glu	Thr	Val	Arg	Thr	Ala	Gln	Glu	Lys	His	Gln		
		35					40				45						
Thr	Gln	Ala	Ser	Ser	Thr	Val	Ala	Leu	Gly	Arg	Thr	Leu	Ile	Ala	Ser		
		50				55					60						
Gln	Ile	Leu	Ala	Ala	Asn	Glu	Lys	Gly	Asn	Thr	Lys	Leu	Thr	Val	Lys		
65					70				75						80		
Val	Leu	Gly	Ser	Ser	Ser	Leu	Gly	Ala	Ile	Ile	Thr	Val	Ala	Asp	Thr		
				85				90						95			
Lys	Gly	Asn	Val	Lys	Gly	Tyr	Val	Gln	Asn	Pro	Gly	Val	Asp	Ile	Lys		
		100						105					110				
Lys	Thr	Ala	Thr	Gly	Glu	Val	Leu	Val	Gly	Pro	Phe	Val	Gly	Asn	Gly		
		115					120					125					
Gln	Phe	Leu	Val	Ile	Thr	Asp	Tyr	Gly	Thr	Gly	Asn	Pro	Tyr	Asn	Ser		
		130				135					140						
Ile	Thr	Pro	Leu	Ile	Ser	Gly	Glu	Ile	Gly	Glu	Asp	Leu	Ala	Phe	Tyr		
145					150					155					160		
Leu	Thr	Glu	Ser	Gln	Gln	Thr	Pro	Ser	Ala	Val	Gly	Leu	Asn	Val	Leu		
				165				170						175			
Leu	Asp	Glu	Glu	Asp	Lys	Val	Lys	Val	Ala	Gly	Gly	Phe	Leu	Val	Gln		
		180					185					190					
Val	Leu	Pro	Gly	Ala	Lys	Lys	Glu	Glu	Ile	Ala	Arg	Phe	Glu	Lys	Arg		

Val	Ala	Ile	Gly	Tyr	Tyr	Met	Pro	Ala	Leu	Leu	Phe	Phe	Val	Gly	Ile
				165					170					175	
Gly	Met	Trp	His	Phe	Phe	Ile	Ser	Asp	Met	Leu	Glu	Pro	Val	Tyr	Glu
			180					185					190		
Ile	Ile	His	Glu	Lys	Leu	Ala	Thr	Lys							
		195					200								

(2) INFORMATION FOR SEQ ID NO:2651:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 307 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...307
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2651:

Thr	Gln	Pro	Leu	Lys	Gln	Cys	Leu	Ser	Gly	Lys	Tyr	Lys	Ser	Trp	Arg
1				5					10					15	
Leu	Ile	Val	Glu	Lys	Ile	Ile	Lys	Glu	Lys	Ile	Ser	Ser	Leu	Leu	Ser
			20					25					30		
Gln	Glu	Glu	Glu	Val	Leu	Ser	Val	Glu	Gln	Leu	Gly	Gly	Met	Thr	Asn
			35				40					45			
Gln	Asn	Tyr	Leu	Ala	Lys	Thr	Thr	Asn	Lys	Gln	Tyr	Ile	Val	Lys	Phe
	50				55					60					
Phe	Gly	Lys	Gly	Thr	Glu	Lys	Leu	Ile	Asn	Arg	Gln	Asp	Glu	Lys	Tyr
65				70				75						80	
Asn	Leu	Glu	Leu	Leu	Lys	Asp	Leu	Gly	Leu	Asp	Val	Lys	Asn	Tyr	Leu
			85				90						95		
Phe	Asp	Ile	Glu	Ala	Gly	Ile	Lys	Val	Asn	Glu	Tyr	Ile	Glu	Ser	Ala
			100				105						110		
Ile	Thr	Leu	Asp	Ser	Thr	Ser	Ile	Lys	Thr	Lys	Phe	Asp	Lys	Ile	Ala
		115				120						125			
Pro	Ile	Leu	Gln	Thr	Ile	His	Thr	Ser	Ala	Lys	Glu	Leu	Arg	Gly	Glu
		130			135						140				
Phe	Ala	Pro	Phe	Glu	Glu	Ile	Lys	Lys	Tyr	Glu	Ser	Leu	Ile	Glu	Glu
145				150					155					160	
Gln	Ile	Pro	Tyr	Ala	Asn	Tyr	Glu	Ser	Val	Arg	Asn	Ala	Val	Phe	Ser
			165				170							175	
Leu	Glu	Lys	Arg	Leu	Ala	Asp	Leu	Gly	Val	Asp	Arg	Lys	Ser	Cys	His
			180				185						190		
Ile	Asp	Leu	Val	Pro	Glu	Asn	Phe	Ile	Glu	Ser	Pro	Gln	Gly	Arg	Leu
		195				200						205			
Tyr	Leu	Ile	Asp	Trp	Glu	Tyr	Ser	Ser	Met	Asn	Asp	Pro	Met	Trp	Asp
	210					215					220				
Leu	Ala	Ala	Leu	Phe	Leu	Glu	Ser	Glu	Phe	Thr	Ser	Gln	Glu	Glu	Glu
225					230					235					240

Thr	Phe	Leu	Ser	His	Tyr	Glu	Ser	Asp	Gln	Thr	Pro	Val	Ser	His	Glu
				245					250					255	
Lys	Ile	Ala	Ile	Tyr	Lys	Ile	Leu	Gln	Asp	Thr	Ile	Trp	Ser	Leu	Trp
		260						265					270		
Thr	Val	Tyr	Lys	Glu	Glu	Gln	Gly	Ala	Asp	Phe	Gly	Tyr	Tyr	Gly	Val
		275					280					285			
Asn	Arg	Tyr	Gln	Arg	Ala	Val	Lys	Gly	Leu	Ala	Ser	Tyr	Gly	Gly	Ser
	290					295					300				
Asp	Glu	Lys													
305															

(2) INFORMATION FOR SEQ ID NO:2652:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...105
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2652:

Asn	Asp	Arg	Phe	Leu	Asn	Arg	Asn	Lys	Ile	Met	Phe	Gly	Phe	Phe	Lys
1				5					10					15	
Lys	Asp	Lys	Ala	Val	Glu	Val	Glu	Val	Pro	Thr	Gln	Val	Pro	Ala	His
		20						25					30		
Ile	Gly	Ile	Ile	Met	Asp	Gly	Asn	Gly	Arg	Trp	Ala	Lys	Lys	Arg	Met
		35				40						45			
Gln	Pro	Arg	Val	Phe	Gly	His	Lys	Ala	Gly	Met	Glu	Ala	Leu	Gln	Thr
	50				55					60					
Val	Thr	Lys	Ala	Ala	Asn	Lys	Leu	Gly	Val	Lys	Val	Ile	Thr	Val	Tyr
65				70					75					80	
Ala	Phe	Ser	Tyr	Gly	Lys	Leu	Asp	Pro	Ser	Arg	Ser	Gly	Ser	Gln	Val
			85					90						95	
Tyr	His	Glu	Leu	Ala	Ser	Arg	Val	Leu							
			100					105							

(2) INFORMATION FOR SEQ ID NO:2653:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 77 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...77

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2653:

His	Thr	Arg	Leu	Trp	Leu	Trp	His	Ala	Trp	Val	Arg	Ser	Pro	Ser	Leu
1				5					10					15	
Ala	Tyr	Phe	Ile	Leu	Gly	Tyr	Ser	Gln	Ala	Val	Arg	Gln	Gly	Thr	Leu
			20					25					30		
Thr	Pro	Ser	Cys	Val	Gly	Ser	Asn	Pro	Ala	Thr	Pro	Val	Thr	Ile	Cys
		35					40					45			
Arg	Arg	Gly	Gly	Ile	Gly	Arg	Arg	Ala	Gly	Leu	Lys	Ile	Gln	Cys	Pro
	50					55					60				
Gln	Gly	Arg	Ala	Gly	Ser	Thr	Pro	Ala	Ala	Gly	Ile	Val			
65					70					75					

(2) INFORMATION FOR SEQ ID NO:2654:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 74 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...74

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2654:

Val	Leu	Arg	Phe	Ser	Gly	Leu	Arg	Gln	Ala	Met	Lys	Met	Asn	Lys	Lys
1				5					10					15	
Ser	Ser	Tyr	Val	Ile	Asn	Arg	Leu	Leu	Val	Ile	Ile	Val	Leu	Ile	
			20					25				30			
Leu	Gly	Thr	Leu	Ala	Leu	Gly	Ile	Gly	Leu	Met	Val	Gly	Tyr	Gly	Ile
		35					40					45			
Leu	Gly	Lys	Gly	Gln	Asp	Pro	Trp	Ala	Ile	Leu	Ser	Pro	Ala	Lys	Trp
	50					55					60				
Gln	Glu	Leu	Ile	His	Lys	Phe	Thr	Gly	Asn						
65					70										

(2) INFORMATION FOR SEQ ID NO:2655:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 215 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...215
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2655:

```

Ser Asp Leu Ser Met Phe Thr Gly Ile Ile Glu Glu Ile Gly Lys Val
1      5      10
Glu Arg Ile Gln Lys Asp Ser Arg Asn Cys Lys Leu Ser Ile Lys Ala
      20      25      30
Ser Lys Ile Leu Thr Asp Ile His Leu Gly Asp Ser Ile Ala Val Asn
      35      40      45
Gly Ile Cys Leu Thr Val Thr His Phe Asn His Gln Ser Phe Thr Val
      50      55      60
Asp Val Met Asn Glu Thr Trp Ser Arg Thr Ala Leu Thr Leu Leu Lys
      65      70      75      80
His Gly Ser Glu Val Asn Leu Glu Arg Ala Leu Ser Val Asn Gly Arg
      85      90      95
Leu Gly Gly His Val Val Thr Gly His Ile Asp Gly Thr Gly Lys Ile
      100     105     110
Ser Ser Ile Lys Lys Asp Asp Asn Ala Val Trp Tyr Gln Ile Asn Thr
      115     120     125
Gln Lys Glu Ile Leu Asp Leu Ile Val Glu Lys Gly Ser Ile Thr Ile
      130     135     140
Asp Gly Ile Ser Leu Thr Val Ala Lys Val Ser Lys Val Asn Phe Ser
      145     150     155     160
Val Ser Val Ile Pro His Thr Leu Glu Gln Thr Ile Leu Lys Ser Lys
      165     170     175
Gln Val Gly Ser Thr Val Asn Leu Glu Asn Asp Ile Leu Gly Lys Tyr
      180     185     190
Val Gln Lys Leu Met Asp Asn Ser Pro Lys Ser Glu Ile Ser Lys Glu
      195     200     205
Leu Leu Tyr Gln Asn Gly Phe
      210     215

```

(2) INFORMATION FOR SEQ ID NO:2656:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 131 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2656:

```
Thr Ser Leu Ser Ser Ser Thr Tyr Pro Thr Phe Ile Val Ile Lys Ile
1          5          10          15
Tyr Leu Lys Leu Tyr Lys Glu Asn Ser Ile Met Asn Arg Glu Glu Val
          20          25          30
Thr Leu Leu Gly Phe Glu Ile Val Ala Tyr Ala Gly Asp Ala Arg Ser
          35          40          45
Lys Leu Leu Glu Ala Leu Lys Ala Ala Glu Ala Gly Asp Phe Glu Lys
          50          55          60
Ala Asp Ala Leu Val Glu Glu Ala Gly Ser Cys Ile Ala Glu Ala His
65          70          75          80
His Ala Gln Thr Ser Leu Leu Thr Lys Glu Ala Ser Gly Glu Asp Leu
          85          90          95
Ala Tyr Ser Val Thr Met Met His Gly Gln Asp His Leu Met Thr Thr
          100         105         110
Ile Leu Leu Lys Asp Leu Met His His Leu Ile Glu Leu Tyr Lys Arg
          115         120         125
Gly Val Lys
          130
```

(2) INFORMATION FOR SEQ ID NO:2657:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 181 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...181

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2657:

```
Lys Pro Leu Ser Val Ser Thr Lys Thr Gly Thr Tyr Ile Gly Arg Arg
1          5          10          15
Arg Asn Met Thr Met Pro Asn Ile Ile Met Thr Arg Ile Asp Glu Arg
          20          25          30
Leu Ile His Gly Gln Gly Gln Leu Trp Val Lys Tyr Leu Gly Cys Asn
          35          40          45
Thr Val Ile Val Ala Asn Asp Glu Val Ser Thr Asp Lys Met Gln Gln
          50          55          60
Thr Leu Met Lys Thr Val Val Pro Asp Ser Val Ala Met Arg Phe Phe
65          70          75          80
Pro Leu Gln Lys Val Ile Asp Ile Ile His Lys Ala Asn Pro Ala Gln
```

				85					90					95			
Thr	Ile	Phe	Ile	Val	Val	Lys	Asn	Val	Lys	Asp	Ala	Leu	Thr	Leu	Val		
			100					105					110				
Glu	Gly	Gly	Val	Pro	Ile	Lys	Glu	Ile	Asn	Ile	Gly	Asn	Ile	His	Asn		
		115					120					125					
Ala	Thr	Gly	Lys	Glu	Gln	Val	Thr	Arg	Ser	Ile	Phe	Leu	Gly	Glu	Glu		
	130					135					140						
Asp	Lys	Val	Ala	Leu	Lys	Glu	Leu	Ser	Gln	Thr	His	Gln	Val	Thr	Phe		
145					150					155					160		
Asn	Thr	Lys	Thr	Thr	Pro	Thr	Gly	Asn	Asp	Gly	Ala	Val	Gln	Val	Asn		
			165					170						175			
Ile	Met	Asp	Tyr	Ile													
			180														

(2) INFORMATION FOR SEQ ID NO:2658:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 470 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...470

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2658:

Asp	Ser	Leu	Ser	Ala	Gln	Cys	Trp	Tyr	Pro	Val	Phe	Trp	Asp	Trp	Gly		
1				5				10					15				
Phe	Ser	Gly	Ile	Lys	Val	Pro	Cys	Leu	Trp	Gln	Arg	Cys	Asn	Trp	Ser		
		20					25					30					
Ser	Leu	Leu	Phe	Tyr	Phe	Met	Asp	Cys	Thr	Leu	Ala	Gly	Ile	Ser	Thr		
	35					40					45						
Leu	Leu	Ser	Val	Val	Tyr	Leu	Leu	Gly	Leu	Gln	Glu	Asn	Ser	Leu	Val		
	50				55					60							
Asp	Leu	Leu	Lys	Gly	Lys	Leu	Pro	Leu	Lys	Arg	Met	Met	Thr	Leu	Met		
65				70				75						80			
Met	Val	Gly	Gln	Leu	Leu	Ala	Val	Leu	Val	Val	Gly	Ser	Ser	Ala	Thr		
			85				90						95				
Arg	Leu	Leu	Pro	His	Tyr	Arg	Glu	Met	Gln	Glu	Met	Glu	Arg	Ala	Ser		
	100					105					110						
Asn	Lys	Trp	Ser	Gln	Ser	Ser	Asp	Arg	Tyr	Arg	Leu	Ser	Phe	Gly	Trp		
	115					120					125						
Ser	Ser	Ala	Phe	Ala	Asp	Glu	Glu	Gly	Thr	Arg	Lys	Asp	Asn	Arg	Glu		
	130				135					140							
Trp	Gln	Thr	Phe	Thr	Glu	Glu	Arg	Leu	Ala	Asn	Thr	Asp	Ser	Phe	Tyr		
145				150				155						160			
Ile	Met	Ser	Asn	Val	Asp	Asn	Phe	Ser	Asp	Gly	Ala	Glu	Val	Asp	Leu		
			165				170						175				
Asp	Gly	Asn	Arg	Leu	Ser	Asp	Tyr	Thr	Pro	Ser	Gly	Asn	Val	Ile	Tyr		

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2659:

Gln	Lys	Leu	Ser	Val	Pro	Val	Leu	Asp	Thr	Ile	Lys	Pro	Asp	Pro	Phe
1				5					10					15	
Pro	Glu	Gln	Tyr	Phe	Leu	Glu	Ile	Thr	Ser	Pro	Gly	Leu	Glu	Arg	Pro
		20						25					30		
Leu	Lys	Thr	Lys	Asp	Ala	Val	Ala	Gly	Ala	Val	Gly	Lys	Tyr	Ile	His
		35					40					45			
Val	Gly	Leu	Tyr	Gln	Ala	Ile	Asp	Lys	Gln	Lys	Val	Phe	Glu	Gly	Thr
	50					55					60				
Leu	Leu	Ala	Phe	Glu	Glu	Asp	Glu	Leu	Thr	Met	Glu	Tyr	Met	Asp	Lys
65					70					75					80
Thr	Arg	Lys	Lys	Thr	Val	Arg	Ile	Pro	Tyr	Ser	Leu	Val	Ser	Lys	Ala
				85					90					95	
Arg	Leu	Ala	Val	Lys	Leu										
				100											

(2) INFORMATION FOR SEQ ID NO:2660:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 123 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...123
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2660:

Lys	Lys	Leu	Ser	Glu	Val	Ser	His	Met	Ala	Phe	Glu	Lys	Ile	Ile	Gln
1				5					10					15	
Leu	Lys	Asn	Cys	Arg	Tyr	Asp	Tyr	Thr	Leu	Ser	Pro	Ser	Val	Lys	Lys
		20						25					30		
Phe	Thr	Leu	Lys	Asp	Asn	Thr	Phe	Phe	Glu	Thr	Lys	Val	Gly	Asn	Tyr
		35					40					45			
Glu	Leu	Thr	Arg	Leu	Leu	Glu	Lys	Val	Pro	Asn	Ser	Gly	Glu	Gly	Phe
	50					55					60				
Gln	Leu	Lys	Ile	Ile	Ile	Asn	Lys	Glu	Leu	Thr	Gly	Ala	Lys	Ile	Asn
65					70					75					80
Ile	Thr	Asp	Lys	Phe	Gly	Leu	Arg	Leu	Val	Asp	Ile	Phe	Lys	Ser	Glu
				85					90					95	
Asp	His	His	Ile	His	Gln	Glu	Lys	Phe	Tyr	Phe	Leu	Met	Asp	Ser	Leu
			100					105					110		
Val	Glu	Arg	Gly	Ile	Phe	Thr	Lys	Ser	Glu	Arg					
		115					120								

(2) INFORMATION FOR SEQ ID NO:2661:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 75 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...75

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2661:

Ser	Gly	Leu	Ser	Leu	Ala	Glu	Arg	Pro	Arg	Ile	Arg	Phe	Phe	Leu	Ala
1				5					10					15	
His	Cys	Trp	Glu	Arg	Leu	His	His	Ala	Arg	Val	Gly	Pro	Val	Asp	Asn
			20					25					30		
Gly	Ala	Trp	Asp	Val	Gly	Gly	Gly	Trp	Asn	Ala	Glu	Thr	Tyr	Ala	Ala
		35				40						45			
Val	Glu	Leu	Ile	Glu	Ser	His	Ser	Thr	Lys	Glu	Glu	Phe	Ile	Arg	Arg
	50				55						60				
Thr	Thr	Ala	Phe	Ile	Ser	Asn	Ser	Tyr	Ala	Ile					
65					70					75					

(2) INFORMATION FOR SEQ ID NO:2662:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 332 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...332

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2662:

Phe	Trp	Leu	Ser	Tyr	Gln	Thr	Cys	Leu	Gln	Asp	Glu	Ser	Ile	Gln	Thr
1				5					10					15	
Gln	Leu	Cys	Ser	Arg	Lys	Glu	Glu	Asn	Met	Ala	Lys	Lys	Lys	Ile	Lys
			20					25					30		
Lys	Glu	Lys	Ile	Asp	Asn	Val	Gly	Ile	His	Ser	Phe	Ser	Lys	Lys	Ala
		35				40						45			
Asp	Ile	Phe	Phe	Ser	Ile	Ile	Ser	Gly	Leu	Ile	Ala	Leu	Ser	Cys	Ile
	50				55					60					
Leu	Pro	Phe	Val	Phe	Val	Ile	Ile	Ile	Ser	Val	Thr	Asp	Glu	Lys	Ser
65					70					75					80

```

Leu Leu Gln Tyr Gly Tyr Ser Phe Phe Pro Ser Gln Phe Gly Leu Asp
      85          90          95
Gly Phe Glu Phe Leu Ala Gln Phe Lys Asp Lys Ile Leu Gln Ala Leu
      100        105        110
Phe Ile Ser Val Phe Val Thr Val Val Gly Thr Leu Thr Asn Val Phe
      115        120        125
Ile Thr Thr Thr Tyr Ala Tyr Ala Ile Ser Arg Thr Thr Phe Lys Tyr
      130        135        140
Arg Arg Phe Phe Thr Ile Phe Val Leu Leu Ser Met Leu Phe Asn Ala
      145        150        155        160
Gly Leu Val Pro Gly Tyr Ile Met Val Thr Arg Val Leu Gln Leu Gly
      165        170        175
Asp Thr Val Trp Ala Leu Ile Val Pro Met Leu Leu Ser Pro Phe Asn
      180        185        190
Ile Ile Leu Met Arg Ser Phe Phe Lys Lys Thr Ile Pro Glu Ala Ile
      195        200        205
Leu Glu Ser Ala Arg Ile Asp Gly Ala Ser Glu Ala Arg Ile Phe Phe
      210        215        220
Gln Ile Cys Leu Pro Leu Ser Leu Pro Gly Ile Ala Thr Ile Thr Leu
      225        230        235        240
Leu Thr Ala Leu Gly Phe Trp Asn Asp Trp Phe Asn Ala Leu Leu Tyr
      245        250        255
Ile Lys Ser Asp Asn Leu Tyr Pro Leu Gln Tyr Leu Leu Met Gln Ile
      260        265        270
Gln Gln Asn Met Asp Tyr Ile Ala Lys Ala Val Gly Leu Thr Gly Gln
      275        280        285
Leu Gly Val Ala Leu Pro Lys Glu Thr Gly Arg Met Ala Met Val Val
      290        295        300
Val Ala Thr Leu Pro Ile Ala Ile Leu Tyr Pro Phe Phe Gln Arg Tyr
      305        310        315        320
Phe Val Lys Gly Leu Thr Ile Gly Gly Val Lys Glu
      325        330

```

(2) INFORMATION FOR SEQ ID NO:2663:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 306 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...306
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2663:

```

Leu Ser Leu Ser Leu Ser Ser Gln Ser Leu Trp Leu His Ser Arg Asn
1          5          10          15
Tyr Thr His Leu Ile Trp Arg Thr Ser Lys Met Asn Asn Ser Ile Lys
      20          25          30

```

Leu	Lys	Arg	Arg	Leu	Thr	Gln	Ser	Leu	Thr	Tyr	Leu	Tyr	Leu	Ile	Gly
		35					40					45			
Leu	Ser	Ile	Val	Ile	Ile	Tyr	Pro	Leu	Leu	Ile	Thr	Ile	Met	Ser	Ala
	50					55					60				
Phe	Lys	Ala	Gly	Asn	Val	Ser	Ala	Phe	Lys	Leu	Asp	Thr	Asn	Ile	Asp
65				70						75					80
Leu	Asn	Phe	Asp	Asn	Phe	Lys	Gly	Leu	Phe	Thr	Glu	Thr	Leu	Tyr	Gly
			85						90					95	
Thr	Trp	Tyr	Leu	Asn	Thr	Leu	Ile	Ile	Ala	Leu	Ile	Thr	Met	Ala	Val
			100					105					110		
Gln	Thr	Ser	Ile	Ile	Val	Leu	Ala	Gly	Tyr	Ala	Tyr	Ser	Arg	Tyr	Asn
		115					120					125			
Phe	Leu	Ala	Arg	Lys	Gln	Ser	Leu	Val	Phe	Phe	Leu	Ile	Ile	Gln	Met
	130					135					140				
Val	Pro	Thr	Met	Ala	Ala	Leu	Thr	Ala	Phe	Phe	Val	Met	Ala	Leu	Met
145					150					155					160
Leu	Asn	Ala	Leu	Asn	His	Asn	Trp	Phe	Leu	Ile	Phe	Leu	Tyr	Val	Gly
				165					170					175	
Gly	Gly	Ile	Pro	Met	Asn	Ala	Trp	Leu	Met	Lys	Gly	Tyr	Phe	Asp	Thr
		180					185						190		
Val	Pro	Met	Ser	Leu	Asp	Glu	Ser	Ala	Lys	Leu	Asp	Gly	Ala	Gly	His
	195						200					205			
Phe	Arg	Arg	Phe	Trp	Gln	Ile	Val	Leu	Pro	Leu	Val	Arg	Pro	Met	Val
	210				215						220				
Ala	Val	Gln	Ala	Leu	Trp	Ala	Phe	Met	Gly	Pro	Phe	Gly	Asp	Tyr	Ile
225					230				235						240
Leu	Ser	Ser	Phe	Leu	Leu	Arg	Glu	Lys	Glu	Tyr	Phe	Thr	Val	Ala	Val
			245						250					255	
Gly	Leu	Gln	Thr	Phe	Val	Asn	Asn	Ala	Lys	Asn	Leu	Lys	Ile	Ala	Tyr
		260					265						270		
Phe	Ser	Ala	Gly	Ala	Ile	Leu	Ile	Ala	Leu	Pro	Leu	Cys	Ile	Leu	Phe
	275						280					285			
Phe	Phe	Leu	Gln	Lys	Asn	Phe	Val	Ser	Gly	Leu	Thr	Ser	Gly	Gly	Asp
	290					295					300				
Lys	Gly														
305															

(2) INFORMATION FOR SEQ ID NO:2664:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 423 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...423
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2664:

Leu	Gln	Leu	Ser	Lys	Arg	Asn	Cys	Gln	Asn	Ala	Lys	Gly	Lys	Pro	Met
1				5					10					15	
Leu	Asp	Val	Glu	Ala	Ile	Arg	Lys	Asp	Phe	Pro	Ile	Leu	Asp	Gln	Ile
			20					25					30		
Val	Asn	Asp	Glu	Pro	Leu	Val	Tyr	Leu	Asp	Asn	Ala	Ala	Thr	Thr	Gln
		35					40					45			
Lys	Pro	Leu	Val	Val	Leu	Lys	Ala	Ile	Asn	Ser	Tyr	Tyr	Glu	Gln	Asp
	50					55					60				
Asn	Ala	Asn	Val	His	Arg	Gly	Val	His	Thr	Leu	Ala	Glu	Arg	Ala	Thr
65					70					75					80
Ala	Ser	Tyr	Glu	Ala	Ala	Arg	Glu	Thr	Ile	Arg	Lys	Phe	Ile	Asn	Ala
				85					90					95	
Gly	Ser	Thr	Lys	Glu	Val	Leu	Phe	Thr	Arg	Gly	Thr	Thr	Thr	Ser	Leu
			100					105					110		
Asn	Trp	Val	Ala	Arg	Phe	Ala	Glu	Glu	Ile	Leu	Ala	Glu	Gly	Asp	Arg
		115					120					125			
Val	Leu	Ile	Ser	Val	Met	Glu	His	His	Ser	Asn	Ile	Ile	Pro	Trp	Gln
	130					135					140				
Glu	Ala	Cys	Arg	Lys	Thr	Gly	Ala	Glu	Leu	Val	Tyr	Val	Tyr	Leu	Lys
145					150					155					160
Asp	Gly	Ala	Leu	Asp	Met	Glu	Asp	Leu	Arg	Ala	Lys	Leu	Thr	Asp	Lys
				165					170					175	
Val	Lys	Phe	Val	Ser	Leu	Ala	His	Ala	Ser	Asn	Val	Leu	Gly	Val	Val
			180					185					190		
Asn	Pro	Ile	Lys	Glu	Ile	Thr	Gln	Leu	Ala	His	Gln	Val	Gly	Ala	Ile
		195					200					205			
Met	Val	Val	Asp	Gly	Ala	Gln	Ser	Thr	Pro	His	Met	Lys	Ile	Asp	Val
	210					215					220				
Gln	Asp	Leu	Asp	Leu	Asp	Phe	Phe	Ala	Phe	Ser	Gly	His	Lys	Met	Ala
225					230					235					240
Gly	Pro	Thr	Gly	Ile	Gly	Val	Leu	Tyr	Gly	Lys	Glu	Lys	Tyr	Leu	Glu
				245					250					255	
Gln	Met	Ser	Pro	Val	Glu	Phe	Gly	Gly	Glu	Met	Ile	Asp	Phe	Val	Tyr
			260					265					270		
Glu	Gln	Phe	Ala	Ser	Trp	Lys	Glu	Leu	Pro	Trp	Lys	Phe	Glu	Ala	Gly
		275					280					285			
Thr	Pro	Asn	Met	Ala	Gly	Ala	Ile	Gly	Leu	Ala	Thr	Ala	Val	Asp	Tyr
	290				295						300				
Leu	Glu	Lys	Ile	Gly	Met	Asp	Ala	Val	Glu	Ala	His	Glu	Gln	Glu	Leu
305					310					315					320
Ile	Ala	Tyr	Val	Tyr	Pro	Lys	Leu	Gln	Ala	Ile	Glu	Gly	Leu	Thr	Ile
				325					330					335	
Tyr	Gly	Ser	Gln	Asp	Leu	Ala	Gln	Arg	Ser	Gly	Val	Ile	Ala	Phe	Asn
			340					345					350		
Leu	Gly	Asp	Leu	His	Pro	His	Asp	Leu	Ala	Thr	Ala	Leu	Asp	Tyr	Glu
	355						360					365			
Gly	Val	Ala	Val	Arg	Ala	Gly	His	His	Cys	Ala	Gln	Pro	Leu	Leu	Gln
	370					375					380				
Tyr	Leu	Glu	Val	Pro	Ala	Thr	Ala	Arg	Ala	Ser	Phe	Tyr	Ile	Tyr	Asn
385					390					395					400
Thr	Lys	Ala	Asp	Cys	Asp	Lys	Leu	Val	Asp	Ala	Leu	Gln	Lys	Thr	Lys
				405					410					415	
Glu	Phe	Phe	Asn	Gly	Thr	Phe									
			420												

(2) INFORMATION FOR SEQ ID NO:2665:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 70 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...70
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2665:

```

Lys Met Leu Ser Val Asn Thr Ile Leu Glu Lys Phe Tyr Lys Glu His
1          5          10          15
Gln Val Lys Pro Phe Ile Ser Pro Glu Arg Glu Leu Asp Thr Trp Leu
          20          25          30
Leu Ser Pro Lys Pro Val Pro Lys Arg Asn Met Asp Leu Leu Val Asp
          35          40          45
Asp Ser Leu Ala Gly Asp Ile Ile Leu Leu Trp Arg Ile Gln Phe Gly
          50          55          60
Thr Phe Thr Thr Glu Thr
65          70

```

(2) INFORMATION FOR SEQ ID NO:2666:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 64 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...64
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2666:

```

Thr Leu Ile Ser Asn Ser Phe Asn Ile Glu Ala Ser Val Arg Asp Ala
1          5          10          15
Asp Val Val Ile Gly Ala Ile Leu Ile Pro Gly Ala Lys Ala Pro Glu
          20          25          30
Leu Val Thr Asp Glu Met Val Lys Gln Met Arg Pro Gly Ser Val Ser
          35          40          45
Leu Thr Leu Leu Leu Thr Lys Val Ala Leu Ser Lys Gln Leu Thr Val
          50          55          60

```

(2) INFORMATION FOR SEQ ID NO:2667:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...109

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2667:

Leu	Glu	Arg	Leu	Ala	Lys	Ser	Leu	Gly	Ile	Ala	Tyr	Phe	Thr	Ala	Asn
1				5					10					15	
Gln	Leu	Glu	Val	Lys	Glu	Gly	Leu	Leu	Thr	Gly	Lys	Leu	Val	Gly	Gln
			20					25					30		
Ile	Ile	Ser	Pro	Gln	Val	Lys	Lys	Glu	Thr	Leu	Glu	Lys	Trp	Arg	Lys
		35				40						45			
Lys	Leu	Lys	Leu	Ser	Lys	Glu	Arg	Thr	Val	Ala	Ile	Gly	Asp	Gly	Val
	50					55					60				
Asn	Asn	Leu	Leu	Met	Leu	Lys	Ser	Ala	Glu	Leu	Gly	Ile	Ala	Phe	Cys
65				70					75					80	
Ala	Lys	Glu	Val	Leu	Lys	Lys	Glu	Ile	Pro	His	His	Val	Asp	Lys	Arg
			85					90					95		
Asp	Phe	Leu	Glu	Val	Leu	Pro	Leu	Ile	Asp	Cys	Leu	Glu			
			100					105							

(2) INFORMATION FOR SEQ ID NO:2668:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...88

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2668:

Pro Ser Val Ser Val Lys Trp Val Ser Ile Ala Ser Arg Val Val Pro

1				5					10					15			
Ala	Thr	Gly	Leu	Ala	Ile	Thr	Arg	Ser	Ser	Pro	Lys	Ile	Ala	Leu	Ile		
			20					25					30				
Lys	Leu	Asp	Phe	Pro	Thr	Phe	Gly	Arg	Pro	Ile	Arg	Leu	Asn	Leu	Met		
		35					40					45					
Thr	Ser	Gly	Phe	Ser	Ser	Ser	Tyr	Ser	Phe	Gly	Arg	Phe	Ser	Thr	Ile		
	50					55					60						
Ala	Ser	Ser	Thr	Ser	Pro	Val	Pro	Ile	Pro	Trp	Thr	Asp	Glu	Ile	Gly		
65					70					75					80		
Ser	Gly	Ser	Pro	Lys	Pro	Arg	Ala										
				85													

(2) INFORMATION FOR SEQ ID NO:2669:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 202 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...202

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2669:

Lys	Gly	Val	Ser	Ala	Met	Thr	Arg	Thr	Glu	Tyr	Leu	Thr	Gln	Leu	Glu		
1				5					10				15				
Leu	Tyr	Leu	Lys	Lys	Leu	Pro	Glu	Ala	Asp	Arg	Ile	Glu	Ala	Met	Asp		
			20					25					30				
Tyr	Phe	Arg	Glu	Leu	Phe	Asp	Asp	Ala	Gly	Val	Glu	Gly	Glu	Glu	Glu		
		35				40					45						
Leu	Ile	Ala	Ser	Leu	Gly	Thr	Pro	Lys	Glu	Val	Ala	His	Glu	Val	Leu		
	50				55					60							
Ser	Asn	Leu	Leu	Asp	Lys	Lys	Ile	Asn	Glu	Ala	Pro	Ala	Gln	Lys	Asn		
65				70					75						80		
Asn	Arg	Gln	Ile	Leu	His	Ile	Ala	Leu	Leu	Ala	Leu	Leu	Ala	Ala	Pro		
				85					90					95			
Ile	Gly	Ile	Pro	Leu	Gly	Ile	Ala	Ile	Leu	Val	Thr	Leu	Phe	Ala	Ile		
			100					105					110				
Leu	Val	Ala	Ala	Leu	Thr	Val	Ile	Leu	Ala	Phe	Phe	Ala	Val	Ser	Ile		
		115					120					125					
Leu	Gly	Ile	Ile	Gly	Gly	Phe	Leu	Phe	Leu	Val	Glu	Ser	Phe	Thr	Val		
	130					135					140						
Leu	Ala	Gln	Ala	Lys	Ser	Ala	Phe	Ile	Leu	Ile	Phe	Gly	Ser	Gly	Leu		
145				150					155					160			
Leu	Ala	Ile	Gly	Ala	Ser	Ser	Leu	Val	Leu	Leu	Gly	Ile	Ser	Tyr	Val		
			165					170					175				

Ala Arg Phe Phe Gly Leu Leu Ile Val Arg Leu Val Gln Phe Val Leu

	180		185		190
Lys	Lys	Gly	Lys	Arg	Gly
			Asn	Gln	His
	195		200		Ala

(2) INFORMATION FOR SEQ ID NO:2670:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...118

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2670:

Lys	Leu	Val	Ser	Ser	Cys	Gln	Ser	Val	Tyr	Ala	Thr	Arg	Ala	Ser	Phe
1				5					10					15	
Leu	Asp	Gly	Gln	Gly	Ile	Thr	Val	Asp	Glu	Met	Ala	Trp	Ile	Ile	Arg
			20					25					30		
Gly	Ile	Val	Asn	Ala	Leu	Ile	Gly	Arg	Tyr	Ile	Lys	Leu	Gly	Thr	Tyr
		35					40					45			
Ala	Ala	Lys	Tyr	Gly	Ile	Ser	Met	Ala	Arg	Ser	Ile	Leu	Asn	Arg	Ala
		50				55					60				
Ala	Ala	Thr	Ala	Ala	Ala	Arg	Val	Gly	Leu	Leu	Thr	Lys	Ile	Phe	Gly
65					70				75					80	
Trp	Ile	Leu	Arg	Ile	Ala	Val	Leu	Ala	Ala	Asp	Val	Tyr	Gly	Asn	Phe
			85					90						95	
Ala	Asn	Asn	Ile	Ala	Val	Ala	Trp	Asp	Ala	His	Asp	Lys	Ile	Pro	Asn
		100					105						110		
Asn	Gly	Arg	Ile	Asn	Phe										
					115										

(2) INFORMATION FOR SEQ ID NO:2671:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...77

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2671:

```
Asn Val Val Ser Leu Gln Asn Arg Lys Asp Arg Ala Lys Met Phe Glu
1          5          10          15
Leu Thr Tyr Lys Asp Cys Tyr His Val Glu Arg Thr Leu Lys Tyr Glu
          20          25          30
Asp His Glu Ala Leu Met Leu Thr Leu Ser Gly Cys Cys Thr Pro Tyr
          35          40          45
Xaa Asp Thr Leu Tyr Val Thr Ser Leu Thr Phe Arg Gly Gln Lys Val
          50          55          60
Tyr Gln Gly Leu Ser Glu Thr Ser Thr Val Phe Tyr Leu
65          70          75
```

(2) INFORMATION FOR SEQ ID NO:2672:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 97 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...97

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2672:

```
Ile Ile Ser Ser Lys Leu Leu Pro Asn Val Ile Leu Pro Arg Leu Ile
1          5          10          15
Ile Phe Ser Val Met Tyr Thr Asn Ser Lys Gly Thr Leu Ile Asn Ile
          20          25          30
Ser Val Lys Arg Val Ile Leu Ser Leu Phe Leu Arg Lys Lys Leu Phe
          35          40          45
Ser Ile Ser Ile Gly Phe Thr Leu Ser Pro Val Phe Leu Pro Lys Ala
          50          55          60
Ile Pro Leu Pro Lys Arg Arg Ile Ser Ile Ser Phe Leu Leu Cys Ala
65          70          75          80
Ile Thr Ala Leu Trp Phe Ser Ile Arg Phe Met Ile Ile Lys Phe Pro
          85          90          95
Phe
```

(2) INFORMATION FOR SEQ ID NO:2673:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 71 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...71
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2673:

```

Ala Ile Ser Ser Arg Val Ile Phe Ser Ser Ala Ser Ser Asn Asp Ile
1           5           10           15
Gly Val Lys Trp Leu Lys Lys Leu Val Glu Ala Ala Lys Ser Gln Thr
          20           25           30
Lys Gly Leu Thr Ser Phe Pro Ile Pro Met Ile Thr Gly Ala Val Arg
          35           40           45
Ile Arg Lys Ala Ser Phe Arg Leu Arg Ala Ile Leu Leu Gly Tyr Asn
          50           55           60
Ser Pro Lys Thr Met Glu Ile
65           70

```

(2) INFORMATION FOR SEQ ID NO:2674:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 104 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...104
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2674:

```

Thr Tyr Ser Ser Ser Gln Glu Lys Gln Ser Asp Trp Lys Val Gln Tyr
1           5           10           15
Thr Arg Cys Leu Asp Ile Ile Phe Pro Glu Leu Asp Lys Ile Val Gly
          20           25           30
Lys His Ser Glu Tyr Thr Tyr Gln Leu Leu Thr Arg Tyr Pro Asn Pro
          35           40           45
Gln Lys Arg Ile Glu Ala Gly Phe Asp Lys Leu Ile Glu Ile Lys Arg
          50           55           60
Leu Thr Ala Ser Asn Ser Arg Ala Phe Cys Arg Ala Leu Lys Ser Ser
65           70           75           80
Pro Asn His Gln Ile Glu Ile Arg Asn Ser Leu Asp Lys Thr Ile Asp

```

	85	90	95
Phe Ser Tyr Ser Leu Ser Phe Ser			
100			

(2) INFORMATION FOR SEQ ID NO:2675:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2675:

Phe	Asn	Ser	Ser	Ser	Leu	His	Leu	Glu	Phe	Phe	Tyr	Thr	Phe	His	Leu
1				5					10					15	
Ser	Lys	Leu	Met	Thr	Lys	Leu	Leu	Asn	Lys	Lys	Trp	Lys	Val	Lys	Ile
			20					25					30		
Met	Lys	Gln	Ile	Leu	Leu	Val	Cys	Asn	Ala	Gly	Met	Ser	Thr	Ser	Met
		35					40				45				
Leu	Val	Lys	Lys	Met	Gln	Gln	Ser	Ala	Thr	Glu	Arg	Gly	Ile	Glu	Ile
	50					55				60					
Ser	Ile	Gln	Ala	Lys	Ser	Met	Thr	Glu	Ala	Lys	Lys	Asn	Ile	His	Glu
65					70					75				80	
Ala	Asp	Val	Ile	Leu	Ile	Gly	Pro	Gln	Ile	Arg	Tyr	Glu	Leu	Leu	Ala
			85					90					95		
Val	Lys	Glu	Ile	Ala	Gly	Asn	Ile	Pro	Val	Asp	Thr	Ile	Asp	Met	Arg
		100						105				110			
Asp	Tyr	Gly	Met	Met	Asn	Gly	Ala	Lys	Val	Leu	Glu	Gln	Ala	Leu	Ala
	115					120						125			
Trp	Ile	Gly	Glu	Ile	Arg										
130															

(2) INFORMATION FOR SEQ ID NO:2676:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...233

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2676:

Thr	Leu	Ser	Ser	Asn	Ser	Arg	Leu	Asn	Arg	Ser	Tyr	Ser	Arg	Gly	Gly
1				5				10						15	
Asn	Pro	Met	Asn	Thr	Ser	Leu	Lys	Leu	Ser	Lys	Gln	Leu	Ser	Phe	Gly
			20				25					30			
Glu	Glu	Ile	Ala	Asn	Ser	Val	Thr	His	Ala	Val	Gly	Ala	Val	Ile	Met
		35				40					45				
Leu	Ile	Leu	Leu	Pro	Ile	Ser	Ser	Ile	Tyr	Ser	Tyr	Glu	Ala	His	Gly
	50				55					60					
Phe	Leu	Ser	Ser	Ile	Gly	Val	Ser	Ile	Phe	Val	Ile	Ser	Leu	Phe	Leu
65				70					75					80	
Met	Phe	Leu	Ser	Ser	Thr	Ile	Tyr	His	Ser	Met	Ala	Tyr	Gly	Ser	Thr
			85					90					95		
His	Lys	Tyr	Val	Leu	Arg	Ile	Ile	Asp	His	Ser	Met	Ile	Tyr	Val	Ala
		100					105					110			
Ile	Ala	Gly	Ser	Tyr	Thr	Pro	Val	Val	Leu	Thr	Leu	Met	Asn	Asn	Trp
	115					120					125				
Phe	Gly	Tyr	Leu	Ile	Ile	Val	Ile	His	Trp	Gly	Thr	Thr	Ile	Phe	Gly
	130			135						140					
Thr	Leu	Tyr	Lys	Ile	Phe	Ala	Ile	Asn	Val	Asn	Asp	Lys	Phe	Ser	Leu
145				150				155						160	
Ala	Leu	Tyr	Leu	Ile	Met	Gly	Trp	Leu	Val	Leu	Ala	Ile	Ile	Pro	Ala
			165					170						175	
Ile	Ile	Asn	Gln	Thr	Thr	Pro	Val	Phe	Trp	Ser	Leu	Met	Val	Thr	Gly
		180					185					190			
Gly	Leu	Cys	Tyr	Thr	Val	Gly	Ala	Gly	Phe	Tyr	Ala	Lys	Lys	Lys	Pro
	195					200				205					
Tyr	Phe	His	Met	Ile	Trp	His	Leu	Phe	Ile	Leu	Ala	Ala	Ser	Val	Leu
	210			215						220					
Gln	Tyr	Ile	Ala	Ile	Val	Tyr	Tyr	Met							
225				230											

(2) INFORMATION FOR SEQ ID NO:2677:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2677:

Arg	Gln	Ser	Ser	Leu	Tyr	Ile	Ile	Phe	Gln	Gly	Gly	Arg	Met	Lys	Ile
1				5					10					15	
Leu	Pro	Phe	Ile	Ala	Arg	Gly	Thr	Ser	Tyr	Tyr	Leu	Lys	Met	Ser	Val
			20					25					30		
Lys	Lys	Leu	Val	Pro	Phe	Leu	Val	Val	Gly	Leu	Met	Leu	Ala	Ala	Gly
		35					40					45			
Asp	Ser	Val	Tyr	Ala	Tyr	Ser	Arg	Gly	Asn	Gly	Ser	Ile	Ala	Arg	Gly
	50					55					60				
Asp	Asp	Tyr	Pro	Ala	Tyr	Tyr	Lys	Asn	Gly	Ser	Gln	Glu	Ile	Asp	Gln
65					70					75				80	
Trp	Arg	Met	Tyr	Ser	Arg	Gln	Cys	Thr	Ser	Phe	Val	Ala	Phe	Arg	Leu
				85				90					95		
Ser	Asn	Val	Asn	Gly	Phe	Glu	Ile	Pro	Ala	Ala	Tyr	Gly	Asn	Ala	Asn
			100					105					110		
Glu	Trp	Gly	His	Arg	Ala	Arg	Arg	Glu	Gly	Tyr	Arg	Val	Asp	Asn	Thr
		115					120					125			
Pro	Thr	Ile	Gly	Ser	Ile	Thr	Cys	Ser	Thr	Ala	Gly	Thr	Asn	Val	His
	130					135					140				
Gly	Ala	Trp	Val	Ser	Lys										
145					150										

(2) INFORMATION FOR SEQ ID NO:2678:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 280 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...280

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2678:

Ser	Ser	Ser	Ser	Pro	Ile	Trp	Arg	Ser	Leu	Gly	Gly	Asn	Met	Thr	Gln
1				5					10					15	
Asp	Leu	Gln	Lys	Arg	Thr	Leu	Phe	Ala	Gly	Ile	Ala	Leu	Ala	Ile	Phe
			20					25					30		
Leu	Pro	Ile	Leu	Met	Ile	Gly	Gly	Leu	Leu	Leu	Gln	Ile	Ala	Ile	Gly
		35				40						45			
Ile	Ile	Ala	Met	Leu	Ala	Met	His	Glu	Leu	Leu	Lys	Met	Arg	Gly	Leu
	50					55					60				
Glu	Thr	Met	Thr	Met	Glu	Gly	Leu	Leu	Thr	Leu	Phe	Ala	Thr	Phe	Ala
65					70					75				80	
Leu	Thr	Ile	Pro	Leu	Glu	Asn	Tyr	Leu	Thr	Phe	Leu	Pro	Val	Asp	Gly
			85					90					95		
Asn	Val	Val	Ala	Tyr	Ser	Val	Leu	Ile	Ser	Ile	Met	Leu	Gly	Thr	Thr
			100				105						110		

Val	Phe	Ser	Lys	Ser	Tyr	Thr	Ile	Glu	Asp	Ala	Val	Phe	Pro	Leu	Ala
		115					120					125			
Met	Ser	Phe	Tyr	Val	Gly	Phe	Gly	Phe	Asn	Ala	Leu	Leu	Asp	Ala	Arg
	130				135						140				
Val	Ala	Gly	Leu	Asp	Lys	Ala	Leu	Leu	Ala	Leu	Cys	Ile	Val	Trp	Ala
145					150					155					160
Thr	Asp	Ser	Gly	Ala	Tyr	Leu	Val	Gly	Met	Asn	Tyr	Gly	Lys	Arg	Lys
			165						170					175	
Leu	Ala	Pro	Arg	Val	Ser	Pro	Asn	Lys	Thr	Leu	Glu	Gly	Ala	Leu	Gly
			180					185					190		
Gly	Ile	Leu	Gly	Ala	Ile	Leu	Val	Thr	Ile	Ile	Phe	Met	Ile	Val	Asp
	195						200					205			
Ser	Thr	Val	Ala	Leu	Pro	Tyr	Gly	Ile	Tyr	Lys	Met	Ser	Val	Phe	Ala
	210					215					220				
Ile	Phe	Phe	Ser	Ile	Ala	Gly	Gln	Phe	Gly	Asp	Leu	Leu	Glu	Ser	Ser
225					230					235					240
Ile	Lys	Arg	His	Phe	Gly	Val	Lys	Asp	Ser	Gly	Lys	Phe	Ile	Pro	Gly
			245					250						255	
His	Gly	Gly	Val	Leu	Asp	Arg	Phe	Asp	Ser	Met	Leu	Leu	Val	Phe	Pro
			260					265					270		
Ile	Met	His	Leu	Phe	Gly	Leu	Phe								
	275					280									

(2) INFORMATION FOR SEQ ID NO:2679:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 81 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...81

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2679:

Ser	Asn	Gly	Leu	Lys	Leu	His	Val	Ser	Ala	Val	Arg	Phe	Arg	Leu	Ala
1			5					10						15	
Pro	Phe	Ile	Tyr	Phe	Gly	Arg	Val	Ala	Lys	Arg	Leu	Asn	Ala	Ala	Asp
			20					25					30		
Cys	Lys	Ser	Ala	Pro	Ser	Gly	Ser	Gly	Val	Arg	Ile	Pro	Pro	Leu	Pro
	35					40					45				
Phe	Tyr	Gly	His	Ser	Leu	Lys	Val	Glu	Leu	Arg	Ser	Pro	Lys	Pro	Ser
	50					55				60					
Val	Trp	Val	Gln	Phe	Leu	Leu	Pro	Val	Leu	Ile	Glu	Leu	Trp	Arg	Val
65					70					75				80	
Trp															

(2) INFORMATION FOR SEQ ID NO:2680:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 139 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...139

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2680:

```

Pro Phe Pro Ser Ile Pro Ala Ile Pro Thr Ile Ser Pro Ala Arg Thr
1      5      10      15
Ser Lys Asp Arg Phe Leu Thr Ala Gly Thr Pro Arg Phe Ser Leu Thr
20      25      30
Thr Lys Ser Leu Ile Asp Lys Thr Ser Phe Gly Leu Glu Ala Cys
35      40      45
Phe Ser Val Leu Lys Glu Thr Glu Arg Pro Thr Ile Ile Ser Ala Lys
50      55      60
Ser Ala Leu Val Ala Pro Ala Ile Ser Thr Val Ser Ile Asp Phe Pro
65      70      75      80
Arg Arg Ile Thr Val Thr Arg Ser Glu Thr Ala Arg Ile Ser Ser Asn
85      90      95
Leu Trp Val Ile Lys Ile Ile Asp Phe Pro Ser Leu Thr Arg Phe Phe
100     105     110
Ile Ile Ala Ile Asn Ser Ser Ile Ser Asp Gly Val Lys Thr Ala Val
115     120     125
Gly Ser Ser Lys Ile Arg Ile Ser Ala Pro Leu
130     135

```

(2) INFORMATION FOR SEQ ID NO:2681:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 169 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...169

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2681:

Thr	Leu	Pro	Ser	Val	Gln	Leu	Phe	Val	Lys	Gln	Phe	Gln	Lys	Glu	Trp
1				5					10					15	
Lys	Cys	Leu	Val	Ser	Met	Thr	Asp	Met	Leu	Val	Trp	Leu	Pro	Val	Lys
			20					25					30		
Ile	His	Pro	Leu	Asn	Ala	Ala	Ser	Val	Gly	Asp	Ile	Ile	Ser	Arg	Gly
			35				40					45			
Gly	Thr	Phe	Leu	His	Ser	Ala	Arg	Tyr	Pro	Asn	Phe	Ala	Gln	Leu	Glu
	50					55					60				
Gly	Gln	Leu	Lys	Gly	Ile	Glu	Gln	Leu	Lys	Lys	His	Gly	Ile	Glu	Gly
65					70					75				80	
Val	Val	Val	Ile	Gly	Gly	Asp	Gly	Ser	Tyr	His	Gly	Ala	Met	Arg	Leu
				85				90						95	
Thr	Glu	His	Gly	Phe	Pro	Ala	Ile	Gly	Leu	Pro	Gly	Thr	Ile	Asp	Asn
			100					105					110		
Asp	Ile	Val	Gly	Thr	Asp	Phe	Thr	Ile	Gly	Phe	Asp	Thr	Ala	Val	Thr
		115					120					125			
Thr	Ala	Met	Asp	Ala	Ile	Asn	Lys	Ile	Arg	Asp	Thr	Ser	Ser	Ile	His
	130					135					140				
Arg	Arg	Thr	Phe	Val	Ile	Glu	Phe	Met	Gly	Arg	Asn	Ala	Gly	Asp	Ile
145					150					155					160
Ala	Leu	Trp	Ala	Gly	Ile	Ala	Thr	Gly							
				165											

(2) INFORMATION FOR SEQ ID NO:2682:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 183 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2682:

Asn	Thr	Thr	Ser	Gly	Gly	Thr	Pro	Met	Leu	Tyr	Val	Gly	Ile	Asp	Val
1				5					10					15	
Ala	Lys	Asn	Lys	His	Asp	Val	Thr	Ala	Leu	Asn	Val	Pro	Gly	Lys	Thr
			20					25					30		
Val	Leu	Lys	Pro	Leu	Thr	Phe	Ser	Asn	Asn	Lys	Ala	Gly	Phe	Glu	Leu
		35				40						45			
Leu	Asp	Leu	Ser	Leu	Arg	Gln	Leu	Asn	Gln	Asp	Cys	Leu	Ile	Ala	Leu
	50					55				60					
Glu	Asn	Thr	Gly	His	Tyr	Ala	Phe	Asn	Leu	Leu	Asn	Phe	Leu	His	Glu
65				70						75				80	
Gln	Gly	Tyr	Lys	Val	Tyr	Thr	Tyr	Asn	Pro	Leu	Leu	Ile	Lys	Glu	Phe
			85					90					95		
Ala	Lys	Ser	Leu	Ser	Leu	Arg	Lys	Thr	Lys	Thr	Asp	Lys	Lys	Asp	Ala

		100					105				110				
His	Gly	Ile	Ala	Leu	Lys	Leu	Leu	Ser	Asp	Pro	Asn	Arg	Glu	Gln	Phe
		115					120					125			
Gln	His	Asp	Asn	Arg	Gln	Val	Glu	Leu	Lys	Ile	Leu	Ala	Arg	His	Ile
		130					135					140			
His	Arg	Leu	Lys	Lys	Asn	Ser	Leu	Ile	Gly	Lys	Tyr	Asn	Thr	Leu	Val
		145				150				155					160
Val	Leu	Ile	Ser	Ser	Phe	Leu	Ser	Trp	Ile	Lys	Ser	Leu	Glu	Ser	Ile
			165					170						175	
Gln	Asn	Ile	Pro	Thr	Asn	Ser									
			180												

(2) INFORMATION FOR SEQ ID NO:2683:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...110

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2683:

Arg	Lys	Thr	Ser	Met	Val	Asp	Met	Leu	Thr	Glu	Asp	Asp	Phe	Lys	Glu
1				5					10					15	
Leu	Thr	Lys	Val	Lys	Thr	Val	Gly	Glu	Ile	Cys	Cys	Arg	Phe	Phe	Asp
		20					25						30		
Ser	Lys	Gly	Lys	Glu	Val	Tyr	Glu	Asn	Leu	Gln	Glu	Arg	Thr	Ile	Ala
		35				40					45				
Ile	Ser	Leu	Glu	Asp	Leu	Lys	Asn	Ile	Pro	Gln	Ser	Leu	Ala	Val	Ala
	50				55					60					
Tyr	Gly	Asp	Thr	Lys	Val	Ser	Ser	Ile	Leu	Ser	Val	Leu	Arg	Ala	Asn
65				70					75						80
Leu	Val	Asn	His	Leu	Ile	Thr	Asp	Lys	Asn	Thr	Ile	Leu	Lys	Val	Leu
			85				90							95	
Glu	Glu	Asp	Gly	Asp	Leu	Thr	Phe	Arg	Glu	Ile	Leu	Gly	Glu		
		100					105						110		

(2) INFORMATION FOR SEQ ID NO:2684:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2684:

Val	Trp	Ala	Ser	Ile	Ser	Leu	Ile	Ile	Arg	Ala	Gly	Thr	Pro	Ala	Thr
1				5					10					15	
Thr	Thr	Phe	Ser	Gly	Thr	Ser	Trp	Val	Thr	Ile	Ala	Pro	Ala	Ala	Thr
			20					25					30		
Thr	Glu	Pro	Leu	Pro	Ile	Trp	Thr	Pro	Ser	Ile	Thr	Thr	Ala	Leu	Ala
		35				40						45			
Pro	Ile	Arg	Thr	Leu	Ser	Pro	Thr	Arg	Thr	Gly	Ser	Ala	Leu	Ala	Gly
	50					55				60					
Ser	Ile	Thr	Pro	Ala	Lys	Thr	Ala	His	Ala	Pro	Thr	Trp	Leu	Phe	Tyr
65					70					75					80
Pro	Thr	Met	Ala	Arg	Pro	Pro	Arg	Met	Ala	Pro	Met	Ser	Ile	Met	Val
			85					90					95		
Pro	Ala	Pro	Ile	Ser	Ala	Pro	Ile	Leu	Ile	Thr	Ala	Pro	Ile	Met	Ile
		100						105					110		
Thr	Ala	Leu	Ser	Pro	Ile	Ser	Thr	Trp	Ser	Arg	Ile	Ile	Ala	Pro	Gly
		115				120						125			
Ser	Ile	Arg	Ala	Leu	Ile	Ala	Arg	Leu	Ser	Ser	Lys	Gly	Thr	Ala	Glu
	130					135					140				
Leu	Arg	Ala	Ser	Cys	Ser	Thr	Thr								
145					150										

(2) INFORMATION FOR SEQ ID NO:2685:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 184 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...184

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2685:

Ile	Lys	Gly	Leu	Ile	Asn	Gln	Lys	Glu	Gly	Asp	Phe	Leu	Arg	Thr	Tyr
1				5					10					15	
Glu	Asn	Lys	Glu	Glu	Leu	Lys	Ala	Glu	Ile	Glu	Lys	Thr	Phe	Glu	Lys
		20						25					30		
Tyr	Ile	Leu	Glu	Phe	Asp	Asn	Ile	Pro	Glu	Asn	Leu	Lys	Asp	Lys	Arg

		35					40				45				
Ala	Asp	Glu	Val	Asp	Arg	Thr	Pro	Ala	Glu	Asn	Leu	Ala	Tyr	Gln	Val
	50					55				60					
Gly	Trp	Thr	Asn	Leu	Val	Leu	Lys	Trp	Glu	Glu	Asp	Glu	Arg	Lys	Gly
65					70				75					80	
Leu	Gln	Val	Lys	Thr	Pro	Ser	Asp	Lys	Phe	Lys	Trp	Asn	Gln	Leu	Gly
			85						90					95	
Glu	Leu	Tyr	Gln	Trp	Phe	Thr	Asp	Thr	Tyr	Ala	His	Leu	Ser	Leu	Gln
		100						105					110		
Glu	Leu	Lys	Ala	Lys	Leu	Asn	Glu	Asn	Ile	His	Ser	Ile	Ser	Ala	Met
		115					120					125			
Ile	Asp	Ser	Leu	Ser	Glu	Glu	Glu	Leu	Phe	Glu	Pro	His	Met	Arg	Lys
	130					135				140					
Trp	Ala	Asp	Glu	Ala	Thr	Lys	Thr	Ala	Thr	Trp	Glu	Val	Tyr	Lys	Phe
145					150					155				160	
Ile	His	Val	Asn	Thr	Val	Ala	Pro	Phe	Gly	Thr	Phe	Arg	Thr	Lys	Ile
			165						170					175	
Arg	Lys	Trp	Lys	Lys	Ile	Val	Leu								
			180												

(2) INFORMATION FOR SEQ ID NO:2686:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...430

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2686:

Asp	Met	Gly	Leu	Phe	Asp	Arg	Leu	Phe	Gly	Lys	Lys	Glu	Glu	Pro	Lys
1			5						10					15	
Ile	Glu	Glu	Val	Val	Lys	Glu	Ala	Leu	Glu	Asn	Leu	Asp	Leu	Ser	Glu
		20					25					30			
Asp	Ile	Glu	Pro	Ala	Phe	Thr	Glu	Ala	Glu	Glu	Val	Ser	Gln	Glu	Glu
	35					40					45				
Ala	Glu	Val	Glu	Ser	Ser	Glu	Glu	Ser	Val	Phe	Gln	Glu	Glu	Asp	Ser
	50					55				60					
Gln	Asp	Thr	Val	Glu	Glu	Asn	Leu	Asp	Leu	Glu	Pro	Val	Val	Glu	Val
65				70					75					80	
Ser	Gln	Glu	Glu	Val	Glu	Glu	Phe	Pro	Asn	Ser	Gln	Glu	Val	Thr	Glu
			85					90						95	
Glu	Glu	Lys	Leu	Glu	His	Glu	Gly	Thr	Val	Glu	Glu	Asn	Asn	Phe	Glu
		100					105					110			
Val	Leu	Glu	Pro	Glu	Ala	Pro	Gln	Thr	Glu	Glu	Thr	Val	Gln	Glu	Lys
		115					120					125			
Tyr	Asp	Arg	Ser	Leu	Lys	Lys	Thr	Arg	Thr	Gly	Phe	Gly	Ala	Arg	Leu

130		135		140											
Asn	Ala	Phe	Phe	Ala	Asn	Phe	Arg	Ser	Val	Asp	Glu	Glu	Phe	Phe	Glu
145					150					155					160
Glu	Leu	Glu	Glu	Leu	Leu	Ile	Met	Ser	Asp	Val	Gly	Val	Gln	Val	Ala
				165						170					175
Ser	Asn	Leu	Thr	Glu	Glu	Leu	Arg	Tyr	Glu	Ala	Lys	Leu	Glu	Asn	Ala
			180					185					190		
Lys	Lys	Pro	Asp	Ala	Leu	Arg	Arg	Val	Ile	Ile	Glu	Lys	Leu	Val	Glu
		195					200					205			
Leu	Tyr	Glu	Lys	Asp	Gly	Ser	Tyr	Asp	Glu	Ser	Ile	His	Phe	Gln	Asp
	210					215					220				
Asn	Leu	Thr	Val	Met	Leu	Phe	Val	Gly	Val	Asn	Gly	Val	Gly	Lys	Thr
225					230					235					240
Thr	Ser	Ile	Gly	Lys	Leu	Ala	His	Arg	Tyr	Lys	Arg	Ala	Gly	Lys	Lys
			245					250					255		
Val	Met	Leu	Val	Ala	Ala	Asp	Thr	Phe	Arg	Ala	Gly	Ala	Val	Ala	Gln
		260					265						270		
Leu	Ala	Glu	Trp	Gly	Arg	Arg	Val	Asp	Val	Pro	Val	Val	Thr	Gly	Pro
	275					280					285				
Glu	Lys	Ala	Asp	Pro	Ala	Ser	Val	Val	Phe	Asp	Gly	Met	Glu	Arg	Ala
	290					295				300					
Val	Ala	Glu	Gly	Ile	Asp	Ile	Leu	Met	Ile	Asp	Thr	Ala	Gly	Arg	Leu
305				310						315					320
Gln	Asn	Lys	Asp	Asn	Leu	Met	Ala	Glu	Leu	Glu	Lys	Ile	Gly	Arg	Ile
			325					330					335		
Ile	Lys	Arg	Val	Pro	Glu	Ala	Pro	His	Glu	Thr	Phe	Leu	Ala	Leu	
		340					345					350			
Asp	Ala	Ser	Thr	Gly	Gln	Asn	Ala	Leu	Val	Gln	Ala	Lys	Glu	Phe	Ser
	355					360					365				
Lys	Ile	Thr	Pro	Leu	Thr	Gly	Ile	Val	Leu	Thr	Lys	Ile	Asp	Gly	Thr
	370					375					380				
Ala	Arg	Gly	Gly	Val	Val	Leu	Ala	Ile	Arg	Glu	Glu	Leu	Asn	Ile	Pro
385				390						395					400
Val	Lys	Leu	Ile	Gly	Phe	Gly	Glu	Lys	Ile	Asp	Asp	Ile	Gly	Glu	Phe
			405					410					415		
Asn	Ser	Glu	Asn	Phe	Met	Lys	Gly	Leu	Leu	Glu	Gly	Leu	Ile		
		420					425					430			

(2) INFORMATION FOR SEQ ID NO:2687:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 126 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...126
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2687:

Tyr	Ala	Gly	Leu	Arg	Asn	Asp	Glu	Trp	Ser	Lys	Ser	Ser	Gly	Thr	Ser
1				5					10					15	
Thr	Cys	Met	Asp	Arg	Arg	Asn	Lys	Met	Thr	Glu	Glu	Met	Glu	Tyr	Ile
			20					25					30		
Cys	Phe	Gln	Leu	Ile	Ala	Asn	Ser	Gly	Ala	Ala	Lys	Ser	Ser	Phe	Ile
		35					40					45			
Glu	Ala	Ile	Gln	Leu	Ala	Lys	Ala	Gly	Asn	Leu	Lys	Glu	Ala	Lys	Ile
	50					55					60				
Lys	Val	Glu	Glu	Ala	Glu	Asp	Ser	Leu	Val	Glu	Ala	His	Lys	Ile	His
65					70					75					80
Ser	Asn	Leu	Ile	Gln	Lys	Glu	Ala	Thr	Gly	Glu	Lys	Ile	Gly	Phe	Ser
				85					90					95	
Leu	Leu	Phe	Met	His	Ala	Glu	Asp	Gln	Met	Ala	Ser	Thr	Glu	Ile	Ile
			100					105					110		
Gln	Leu	Leu	Ser	Lys	Glu	Phe	Ile	Asp	Leu	Tyr	Gln	Asn	Lys		
		115						120					125		

(2) INFORMATION FOR SEQ ID NO:2688:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...194

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2688:

His	Leu	Lys	Ser	Ser	Asn	Leu	Leu	Thr	Met	Thr	Arg	Lys	Ile	Phe	Lys
1					5				10					15	
Thr	Val	Asn	Lys	Ser	Val	Glu	Ala	Gly	Phe	Tyr	Gln	Ala	Ile	Leu	Asp
			20					25					30		
Ala	Val	Ser	Asp	Leu	Leu	Ala	Ser	Lys	Thr	Thr	Ile	Thr	Ile	Leu	
		35					40					45			
Asp	Ile	Gly	Cys	Gly	Glu	Gly	Phe	Tyr	Ser	Arg	Lys	Leu	Gln	Glu	Ser
	50					55					60				
His	Ser	Glu	Lys	Thr	Phe	Tyr	Ala	Phe	Asp	Ile	Ser	Lys	Asp	Ser	Val
65					70					75					80
Gln	Ile	Ala	Ala	Lys	Ser	Glu	Pro	Asn	Trp	Ala	Val	Asn	Trp	Phe	Val
				85					90					95	
Gly	Asp	Leu	Ala	Arg	Leu	Pro	Ile	Lys	Asp	Ala	Ser	Met	Asp	Ile	Leu
		100						105					110		
Leu	Asp	Ile	Phe	Ser	Pro	Ala	Asn	Tyr	Gly	Glu	Phe	Arg	Arg	Val	Leu
		115					120					125			
Ser	Lys	Asp	Gly	Ile	Leu	Ile	Lys	Val	Ile	Pro	Thr	Glu	Asn	His	Leu
	130					135					140				
Lys	Glu	Ile	Arg	Gln	Arg	Val	Gln	Asp	Gln	Leu	Thr	Asn	Lys	Glu	Tyr

145		150		155		160									
Ser	Asn	Gln	Asp	Ile	Lys	Glu	His	Phe	Gln	Glu	His	Phe	Thr	Ile	Leu
		165		170		175									
Ser	Ser	Gln	Thr	Ala	Ser	Leu	Thr	Lys	Thr	Ile	Thr	Ala	Glu	Lys	Leu
		180				185							190		
Gln	Ala														

(2) INFORMATION FOR SEQ ID NO:2689:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...60
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2689:

Thr	Ile	Lys	Ser	Ser	Thr	Lys	Arg	Glu	Asn	Ile	Leu	Leu	Phe	Ile	Thr
1				5					10					15	
Leu	Leu	Ala	Leu	Lys	Ile	Leu	Phe	Asn	Arg	Thr	Phe	Ile	Val	Val	Ser
		20					25					30			
Thr	Gln	Ile	Phe	Ile	Lys	Lys	Ile	Arg	Ala	Asn	Thr	Pro	Ala	Ala	Ala
	35					40					45				
Pro	Ile	Ser	Gln	Pro	Pro	Arg	Pro	Pro	Thr	Leu	Ile				
50					55					60					

(2) INFORMATION FOR SEQ ID NO:2690:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 65 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...65
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2690:

Ala	Tyr	Lys	Ser	Ser	Gln	Ile	Thr	Leu	Leu	Ile	Gly	Gly	Pro	Asn	Leu
1				5					10					15	
Gln	Cys	Arg	Gly	Ser	Phe	Tyr	Ile	Gly	Leu	Cys	Ala	Phe	Trp	Asp	Ser
			20					25					30		
Lys	Pro	Phe	Trp	Gln	Ile	Leu	Gln	Asn	Leu	Ser	Asp	Asn	Cys	Leu	Phe
		35				40					45				
Leu	Ile	Leu	His	Leu	Asp	Phe	Phe	Asn	Tyr	Lys	His	His	Lys	Phe	Leu
	50					55					60				
Ser															
65															

(2) INFORMATION FOR SEQ ID NO:2691:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2691:

Phe	Ile	Lys	Ser	Tyr	Phe	Ser	Val	Lys	Ala	Ala	Ser	Cys	Gly	Arg	Thr
1				5					10					15	
Leu	Pro	Ser	Arg	Ser	Ser	Ile	Asp	Ala	Pro	Pro	Pro	Val	Leu	Ile	His
			20					25				30			
Glu	Asn	Leu	Ser	Ala	Arg	Pro	Arg	Leu	Ile	Ala	Ala	Ala	Ala	Glu	Ser
	35					40					45				
Pro	Pro	Pro	Met	Ile	Asp	Leu	Thr	Pro	Gly	Cys	Phe	Thr	Ile	Ala	Ser
	50				55					60					
Ile	Thr	Pro	Ile	Val	Pro	Ala	Trp	Lys	Ser	Gly	Phe	Ser	Asn	Thr	Pro
65				70					75					80	
Ile	Gly	Pro	Phe	His	Thr	Thr	Val	Leu	Ala	Pro	Val	Lys	Ala	Ser	Ser
			85					90					95		
Asn	Leu	Ala	Ile	Asp	Phe	Gly	Pro	Met	Ser	Arg	Pro	Arg	Lys	Pro	Ser
		100					105					110			
Glu	Thr	Ala	Ser	Pro	Ser	Val	Ser	Arg	Thr	Ser	Val				
	115					120									

(2) INFORMATION FOR SEQ ID NO:2692:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...109

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2692:

```
Lys Ile Lys Ser Glu Glu Ile Gln Met Ile Lys Ile Leu Ala Ala Cys
1           5           10           15
Gly Ala Gly Val Asn Ser Ser His Gln Ile Lys Ser Ala Leu Glu Glu
          20           25           30
Glu Leu Ser Asn Arg Gly Tyr Asp Val His Cys Asp Ala Val Met Val
          35           40           45
Lys Asp Val Asn Glu Asp Leu Met Lys Gly Tyr Asp Ile Phe Thr Pro
          50           55           60
Ile Ala Ala Thr Asp Leu Gly Phe Glu Pro Gly Ile Pro Val Ile Glu
65           70           75           80
Ala Gly Pro Ile Leu Phe Arg Ile Pro Ala Met Ser Ala Pro Val Phe
          85           90           95
Asp Asn Ile Glu Ala Ala Ile Lys Glu His Gly Leu Ser
          100          105
```

(2) INFORMATION FOR SEQ ID NO:2693:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...108

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2693:

```
Lys Ile Lys Ser Glu Glu Ile Gln Met Ile Lys Ile Leu Ala Ala Cys
1           5           10           15
Gly Ala Gly Val Asn Ser Ser His Gln Ile Lys Ser Ala Leu Glu Glu
          20           25           30
Glu Leu Ser Asn Arg Gly Tyr Asp Val His Cys Asp Ala Val Met Val
          35           40           45
Lys Asp Val Asn Glu Asp Leu Met Lys Gly Tyr Asp Ile Phe Thr Pro
          50           55           60
Ile Ala Ala Thr Asp Leu Gly Phe Glu Pro Gly Ile Pro Val Ile Glu
65           70           75           80
Ala Gly Pro Ile Leu Phe Cys Ile Pro Ala Met Ser Val Pro Val Phe
```


	85	90	95
Asp Asn Ile Ile Leu Pro Ala Lys Gln Asn Met Val			
	100	105	

(2) INFORMATION FOR SEQ ID NO:2694:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...83

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2694:

Ser	Thr	Lys	Ser	Ala	Trp	Glu	Thr	Lys	Arg	Ile	Phe	Tyr	Val	Ser	Lys
1				5					10					15	
His	Leu	Pro	Glu	Lys	Val	Asn	Asn	Ile	Gly	Gln	Thr	Val	Gly	Ile	Asn
			20					25					30		
His	Glu	Gly	Lys	Gly	Phe	Gly	Gln	Asn	Asp	Asp	Gly	His	Val	Ala	Leu
		35					40					45			
Glu	Thr	His	Leu	Gly	Gln	Gly	Ser	Gln	His	Thr	Glu	Lys	Val	Ser	Trp
	50					55				60					
Ala	Asn	Gly	Pro	Asn	His	His	Lys	Asn	Lys	Glu	Ala	Val	Lys	Thr	Ile
65					70					75					80
Ala	Leu	Ile													

(2) INFORMATION FOR SEQ ID NO:2695:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...76

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2695:

Leu	Pro	Lys	Ser	Arg	Arg	Phe	Pro	Arg	Lys	Leu	Tyr	Gln	His	His	Arg
1			5						10					15	
Glu	Arg	Leu	Gly	Gln	Leu	Gly	Arg	Pro	Ser	Leu	Phe	Arg	Asn	Arg	Gly
		20						25					30		
Lys	Phe	Ile	Pro	Arg	Gly	Gly	Met	Ser	Ile	Asp	Pro	Tyr	Tyr	Asn	Tyr
	35						40					45			
Gly	Lys	Gln	Gly	Asn	Lys	Tyr	Glu	Xaa	Leu	Ala	Glu	Gln	Arg	Val	Phe
	50					55					60				
Gln	His	Asp	Val	Tyr	Pro	Glu	Lys	Ile	Asp	Asn	Arg				
65					70					75					

(2) INFORMATION FOR SEQ ID NO:2696:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...206

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2696:

Lys	Arg	Lys	Ser	Ile	Met	Lys	Phe	Leu	Glu	Leu	Asn	Lys	Lys	Arg	His
1			5						10					15	
Ala	Thr	Lys	His	Phe	Thr	Asp	Lys	Pro	Val	Asp	Pro	Lys	Asp	Val	Arg
		20						25				30			
Thr	Ala	Ile	Glu	Ile	Ala	Thr	Leu	Ala	Pro	Ser	Ala	His	Asn	Ser	Gln
	35					40						45			
Pro	Trp	Lys	Phe	Val	Val	Val	Arg	Glu	Lys	Asn	Ala	Glu	Leu	Ala	Lys
	50					55					60				
Leu	Ala	Tyr	Gly	Ser	Asn	Phe	Glu	Gln	Val	Ser	Ser	Ala	Pro	Val	Thr
65				70					75					80	
Ile	Ala	Leu	Phe	Thr	Asp	Thr	Asp	Leu	Ala	Lys	Arg	Ala	Arg	Lys	Ile
		85						90						95	
Ala	Arg	Val	Gly	Gly	Ala	Asn	Asn	Phe	Ser	Glu	Glu	Gln	Leu	Gln	Tyr
		100						105					110		
Phe	Met	Lys	Asn	Leu	Pro	Ala	Glu	Phe	Ala	Arg	Tyr	Ser	Glu	Gln	Gln
	115						120					125			
Val	Ser	Asp	Tyr	Leu	Ala	Leu	Asn	Ala	Gly	Leu	Val	Ala	Met	Asn	Leu
	130						135				140				
Val	Leu	Ala	Leu	Thr	Asp	Gln	Gly	Ile	Gly	Ser	Asn	Ile	Ile	Leu	Gly
145				150					155					160	
Phe	Asp	Lys	Ser	Lys	Val	Asn	Glu	Val	Leu	Glu	Ile	Lys	Asp	Arg	Phe
		165						170						175	
Arg	Pro	Glu	Leu	Leu	Ile	Thr	Val	Gly	Tyr	Thr	Asp	Glu	Lys	Leu	Glu
		180					185					190			
Pro	Ser	Tyr	Arg	Leu	Pro	Val	Asp	Glu	Ile	Ile	Glu	Lys	Arg		
	195						200					205			

(2) INFORMATION FOR SEQ ID NO:2697:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 539 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...539

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2697:

Lys	Glu	Glu	Ser	Met	Ser	Thr	Lys	Tyr	Ile	Phe	Val	Thr	Gly	Gly	Val
1				5					10					15	
Val	Ser	Ser	Ile	Gly	Lys	Gly	Ile	Val	Ala	Ala	Ser	Leu	Gly	Arg	Leu
			20					25					30		
Leu	Lys	Asn	Arg	Gly	Leu	Lys	Val	Thr	Ile	Gln	Lys	Phe	Asp	Pro	Tyr
		35					40					45			
Ile	Asn	Ile	Asp	Pro	Gly	Thr	Met	Ser	Pro	Tyr	Gln	His	Gly	Glu	Val
	50					55					60				
Phe	Val	Thr	Asp	Asp	Gly	Ala	Glu	Thr	Asp	Leu	Asp	Leu	Gly	His	Tyr
65					70					75					80
Glu	Arg	Phe	Ile	Asp	Ile	Asn	Leu	Asn	Lys	Tyr	Ser	Asn	Val	Thr	Thr
			85					90					95		
Gly	Lys	Ile	Tyr	Ser	Glu	Val	Leu	Arg	Lys	Glu	Arg	Arg	Gly	Glu	Tyr
			100					105					110		
Leu	Gly	Ala	Thr	Val	Gln	Val	Ile	Pro	His	Ile	Thr	Asp	Ala	Leu	Lys
	115						120					125			
Glu	Lys	Ile	Lys	Arg	Ala	Ala	Leu	Thr	Thr	Asp	Ser	Asp	Val	Ile	Ile
	130					135					140				
Thr	Glu	Val	Gly	Gly	Thr	Val	Gly	Asp	Ile	Glu	Ser	Leu	Pro	Phe	Leu
145						150				155					160
Glu	Ala	Leu	Arg	Gln	Met	Lys	Ala	Asp	Val	Gly	Ala	Asp	Asn	Val	Met
			165						170					175	
Tyr	Ile	His	Thr	Thr	Leu	Leu	Pro	Tyr	Leu	Lys	Ala	Ala	Gly	Glu	Met
			180					185					190		
Lys	Thr	Lys	Pro	Thr	Gln	His	Ser	Val	Lys	Glu	Leu	Arg	Gly	Leu	Gly
	195						200						205		
Ile	Gln	Pro	Asn	Met	Leu	Val	Ile	Arg	Thr	Glu	Glu	Pro	Ala	Gly	Gln
	210					215						220			
Gly	Ile	Lys	Asn	Lys	Leu	Ala	Gln	Phe	Cys	Asp	Val	Ala	Pro	Glu	Ala
225					230					235					240
Val	Ile	Glu	Ser	Leu	Asp	Val	Glu	His	Leu	Tyr	Gln	Ile	Pro	Leu	Asn
			245						250					255	
Leu	Gln	Ala	Gln	Gly	Met	Asp	Gln	Ile	Val	Cys	Asp	His	Leu	Lys	Leu
		260						265					270		
Asp	Ala	Pro	Ala	Ala	Asp	Met	Thr	Glu	Trp	Ser	Ala	Met	Val	Asp	Lys
		275					280						285		

```

Val Met Asn Leu Lys Lys Gln Val Lys Ile Ser Leu Val Gly Lys Tyr
290                295                300
Val Glu Leu Gln Asp Ala Tyr Ile Ser Val Val Glu Ala Leu Lys His
305                310                315                320
Ser Gly Tyr Val Asn Asp Val Glu Val Lys Ile Asn Trp Val Asn Ala
                325                330                335
Asn Asp Val Thr Ala Glu Asn Val Ala Glu Leu Leu Ser Asp Ala Asp
                340                345                350
Gly Ile Ile Val Pro Gly Gly Phe Gly Gln Arg Gly Thr Glu Gly Lys
                355                360                365
Ile Gln Ala Ile Arg Tyr Ala Arg Glu Asn Asp Val Pro Met Leu Gly
                370                375                380
Val Cys Leu Gly Met Gln Leu Thr Cys Ile Glu Phe Ala Arg His Val
385                390                395                400
Leu Gly Leu Glu Gly Ala Asn Ser Ala Glu Leu Ala Pro Glu Thr Lys
                405                410                415
Tyr Pro Ile Ile Asp Ile Met Arg Asp Gln Ile Asp Ile Glu Asp Met
                420                425                430
Gly Gly Thr Leu Arg Leu Gly Leu Tyr Pro Ser Lys Leu Lys Arg Gly
                435                440                445
Ser Lys Ala Ala Ala Ala Tyr His Asn Gln Glu Val Val Gln Arg Arg
                450                455                460
His Arg His Arg Tyr Glu Phe Asn Asn Ala Phe Arg Glu Gln Phe Glu
465                470                475                480
Ala Ala Gly Phe Val Phe Ser Gly Val Ser Pro Asp Asn Arg Leu Val
                485                490                495
Glu Ile Val Glu Ile Pro Glu Asn Lys Phe Phe Val Ala Cys Gln Tyr
                500                505                510
His Pro Glu Leu Ser Ser Arg Pro Asn Arg Pro Glu Glu Leu Tyr Thr
                515                520                525
Ala Phe Val Thr Ala Ala Val Glu Asn Ser Asn
                530                535

```

(2) INFORMATION FOR SEQ ID NO:2698:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 368 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...368
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2698:

```

Lys Thr Arg Ser Leu Val Ala Ser Thr Val Lys Thr Ile Arg Leu Leu
1                5                10                15
Leu Val Leu Ala Ser Ile Ser Leu Met Leu Lys Leu Thr Ser Phe Gln
                20                25                30

```

His	Lys	Val	Ile	Glu	Ile	Gln	Ala	Gly	Asp	Glu	Lys	Gln	Glu	Leu	Thr	35	40	45
Ala	Glu	Thr	Ile	Val	Ile	Asn	Thr	Gly	Ala	Val	Ser	Asn	Val	Leu	Pro	50	55	60
Ile	Pro	Gly	Leu	Ala	Thr	Ser	Lys	Asn	Val	Phe	Asp	Ser	Thr	Gly	Ile	65	70	75
Gln	Ser	Leu	Asp	Lys	Leu	Pro	Glu	Lys	Leu	Gly	Val	Leu	Gly	Gly	Gly	85	90	95
Asn	Ile	Gly	Leu	Glu	Phe	Ala	Gly	Leu	Tyr	Asn	Lys	Leu	Gly	Ser	Lys	100	105	110
Val	Thr	Val	Leu	Asp	Ala	Leu	Asp	Thr	Phe	Leu	Pro	Arg	Ala	Glu	Pro	115	120	125
Ser	Ile	Ala	Ala	Leu	Ala	Lys	Gln	Tyr	Leu	Glu	Glu	Asp	Gly	Ile	Glu	130	135	140
Leu	Leu	Gln	Asn	Ile	His	Thr	Thr	Glu	Ile	Lys	Asn	Asp	Gly	Asp	Gln	145	150	155
Val	Leu	Val	Val	Thr	Glu	Asp	Glu	Thr	Tyr	Arg	Phe	Asp	Ala	Leu	Leu	165	170	175
Tyr	Ala	Thr	Gly	Arg	Lys	Pro	Asn	Val	Glu	Pro	Leu	Gln	Leu	Glu	Asn	180	185	190
Thr	Asp	Ile	Glu	Leu	Thr	Glu	Arg	Gly	Ala	Ile	Lys	Val	Asp	Lys	His	195	200	205
Cys	Gln	Thr	Asn	Val	Pro	Gly	Val	Phe	Ala	Val	Gly	Asp	Val	Asn	Gly	210	215	220
Gly	Leu	Gln	Phe	Thr	Tyr	Ile	Ser	Leu	Asp	Asp	Phe	Arg	Val	Val	Tyr	225	230	235
Ser	Tyr	Leu	Ala	Gly	Asp	Gly	Ser	Tyr	Thr	Leu	Glu	Asp	Arg	Leu	Asn	245	250	255
Val	Pro	Asn	Thr	Met	Phe	Ile	Thr	Pro	Ala	Leu	Ser	Gln	Val	Gly	Leu	260	265	270
Thr	Glu	Ser	Gln	Ala	Ala	Asp	Leu	Lys	Leu	Pro	Tyr	Ala	Val	Lys	Glu	275	280	285
Ile	Pro	Val	Ala	Ala	Met	Pro	Arg	Gly	His	Val	Asn	Gly	Asp	Leu	Arg	290	295	300
Gly	Ala	Phe	Lys	Ala	Val	Val	Asn	Thr	Glu	Thr	Lys	Glu	Ile	Leu	Gly	305	310	315
Ala	Ser	Ile	Phe	Ser	Glu	Gly	Ser	Gln	Glu	Ile	Ile	Asn	Ile	Ile	Thr	325	330	335
Val	Ala	Met	Asp	Asn	Lys	Ile	Pro	Tyr	Thr	Tyr	Phe	Thr	Lys	Gln	Ile	340	345	350
Phe	Thr	His	Pro	Thr	Leu	Ala	Glu	Asn	Leu	Asn	Asp	Leu	Phe	Ala	Ile	355	360	365

(2) INFORMATION FOR SEQ ID NO:2699:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...287

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2699:

Gly	Gly	Arg	Ser	Leu	Met	Gln	Thr	Gln	Glu	Lys	His	Ser	Gln	Ala	Ala
1				5				10						15	
Val	Leu	Gly	Leu	Gln	His	Leu	Leu	Ala	Met	Tyr	Ser	Gly	Ser	Ile	Leu
			20					25					30		
Val	Pro	Ile	Met	Ile	Ala	Thr	Ala	Leu	Gly	Tyr	Ser	Ala	Glu	Gln	Leu
		35				40						45			
Thr	Tyr	Leu	Ile	Ser	Thr	Asp	Ile	Phe	Met	Cys	Gly	Val	Ala	Thr	Phe
	50				55					60					
Leu	Gln	Leu	Gln	Leu	Asn	Lys	Tyr	Phe	Gly	Ile	Gly	Leu	Pro	Val	Val
65				70					75					80	
Leu	Gly	Val	Ala	Phe	Gln	Ser	Val	Ala	Pro	Leu	Ile	Met	Ile	Gly	Gln
			85					90					95		
Ser	His	Gly	Ser	Gly	Ala	Met	Phe	Gly	Ala	Leu	Ile	Ala	Ser	Gly	Ile
		100				105						110			
Tyr	Val	Val	Leu	Val	Ser	Gly	Ile	Phe	Ser	Lys	Val	Ala	Asn	Leu	Phe
	115					120						125			
Pro	Ser	Ile	Val	Thr	Gly	Ser	Val	Ile	Thr	Thr	Ile	Gly	Leu	Thr	Leu
	130				135						140				
Ile	Pro	Val	Ala	Ile	Gly	Asn	Met	Gly	Asn	Asn	Val	Pro	Glu	Pro	Thr
145				150					155					160	
Gly	Gln	Ser	Leu	Leu	Leu	Ser	Ala	Ile	Thr	Val	Leu	Ile	Ile	Leu	Leu
			165					170						175	
Ile	Asn	Ile	Phe	Thr	Lys	Gly	Phe	Ile	Lys	Ser	Ile	Ser	Ile	Leu	Ile
	180					185						190			
Gly	Leu	Val	Val	Gly	Thr	Ala	Ile	Ala	Ala	Ser	Met	Gly	Leu	Val	Asp
	195					200					205				
Phe	Ser	Pro	Val	Ala	Ala	Ala	Pro	Val	Val	His	Val	Pro	Thr	Pro	Phe
	210				215					220					
Tyr	Phe	Gly	Met	Pro	Thr	Phe	Glu	Ile	Ser	Ser	Ile	Val	Met	Met	Cys
225				230					235					240	
Ile	Ile	Ala	Thr	Val	Ser	Met	Val	Glu	Ser	Thr	Gly	Leu	Phe	Ile	Trp
		245				250						255			
Pro	Cys	Leu	Ile	Ser	Gln	Arg	Ile	Gln	Ser	Thr	Ala	Pro	Pro	Ala	Gln
	260					265						270			
Arg	Ile	Pro	Arg	Arg	Arg	Phe	Gly	Leu	Asn	Phe	Trp	Gly	Asp	Phe	
	275					280						285			

(2) INFORMATION FOR SEQ ID NO:2700:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 777 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...777

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2700:

Thr	Val	Leu	Ser	Ser	Ser	Lys	Thr	Ser	Ser	Val	Ser	Tyr	Phe	Tyr	Phe
1				5					10					15	
Ala	Phe	Asp	Val	Leu	Gly	Ile	Leu	Ile	Phe	Val	Gly	Lys	Ala	Tyr	Asn
			20					25					30		
Phe	Ile	Asn	Pro	Lys	Gly	Ile	Lys	Met	Ala	Lys	Gln	Val	Phe	Gln	Thr
		35					40					45			
Thr	Phe	Ala	Gly	Arg	Glu	Leu	Ile	Val	Glu	Thr	Gly	Gln	Val	Ala	Lys
	50					55					60				
Gln	Ala	Asn	Gly	Ser	Val	Val	Val	Arg	Tyr	Gly	Glu	Ser	Thr	Val	Leu
65					70					75					80
Thr	Ala	Ala	Val	Met	Ser	Lys	Lys	Met	Ala	Thr	Gly	Asp	Phe	Phe	Pro
				85					90					95	
Leu	Gln	Val	Asn	Tyr	Glu	Glu	Lys	Met	Tyr	Ala	Ala	Gly	Lys	Phe	Pro
			100					105					110		
Gly	Gly	Phe	Met	Lys	Arg	Glu	Gly	Arg	Pro	Ser	Thr	Asp	Ala	Thr	Leu
	115						120					125			
Thr	Ala	Arg	Leu	Ile	Asp	Arg	Pro	Ile	Arg	Pro	Met	Phe	Ala	Glu	Gly
	130					135					140				
Phe	Arg	Asn	Glu	Val	Gln	Val	Ile	Asn	Thr	Val	Leu	Ser	Tyr	Asp	Glu
145					150					155					160
Asn	Ala	Ser	Ala	Pro	Met	Ala	Ala	Met	Phe	Gly	Ser	Ser	Leu	Ala	Leu
				165					170					175	
Ser	Ile	Ser	Asp	Ile	Pro	Phe	Asp	Gly	Pro	Ile	Ala	Gly	Val	Gln	Val
			180					185					190		
Gly	Tyr	Val	Asp	Gly	Gln	Ile	Ile	Ile	Asn	Pro	Ser	Gln	Glu	Gln	Ala
	195						200					205			
Glu	Gln	Ser	Leu	Leu	Glu	Leu	Thr	Val	Ala	Gly	Thr	Lys	His	Ala	Val
	210					215					220				
Asn	Met	Val	Glu	Ser	Gly	Ala	Lys	Glu	Leu	Ser	Glu	Glu	Ile	Met	Leu
225					230					235					240
Glu	Ala	Leu	Leu	Lys	Gly	His	Glu	Ala	Val	Lys	Glu	Leu	Ile	Ala	Phe
				245					250					255	
Gln	Glu	Glu	Ile	Val	Ala	Ala	Val	Gly	Lys	Glu	Lys	Ala	Glu	Val	Glu
			260					265					270		
Leu	Leu	His	Val	Asp	Ala	Glu	Leu	Gln	Ala	Glu	Ile	Ile	Ala	Ala	Tyr
	275						280					285			
Asn	Ser	Asp	Leu	Gln	Lys	Ala	Val	Gln	Val	Glu	Glu	Lys	Leu	Ala	Arg
	290					295					300				
Glu	Ala	Ala	Thr	Gln	Val	Val	Lys	Asp	Gln	Val	Thr	Ala	Val	Tyr	Glu
305					310					315					320
Glu	Lys	Tyr	Ala	Asp	His	Glu	Glu	Phe	Asp	Arg	Ile	Met	Arg	Asp	Val
				325					330					335	
Ala	Glu	Ile	Leu	Glu	Gln	Met	Glu	His	Ala	Glu	Val	Arg	Arg	Leu	Ile
			340					345					350		
Thr	Glu	Asp	Lys	Val	Arg	Pro	Asp	Gly	Arg	Lys	Val	Asp	Glu	Ile	Arg
	355						360					365			
Pro	Leu	Asp	Ala	Val	Val	Asp	Phe	Leu	Pro	Arg	Val	His	Gly	Ser	Gly
	370					375					380				
Leu	Phe	Thr	Arg	Gly	Gln	Thr	Gln	Ala	Leu	Ser	Val	Leu	Thr	Leu	Ala
385					390					395					400
Pro	Met	Gly	Glu	Thr	Gln	Ile	Ile	Asp	Gly	Leu	Asp	Pro	Glu	Tyr	Lys

				405				410					415			
Lys	Arg	Phe	Met	His	His	Tyr	Asn	Phe	Pro	Gln	Tyr	Ser	Val	Gly	Glu	
			420					425					430			
Thr	Gly	Arg	Tyr	Gly	Ala	Pro	Gly	Arg	Arg	Glu	Ile	Gly	His	Gly	Ala	
		435					440					445				
Leu	Gly	Glu	Arg	Ala	Leu	Ala	Gln	Val	Leu	Pro	Ser	Leu	Glu	Glu	Phe	
	450					455					460					
Pro	Tyr	Ala	Ile	Arg	Leu	Val	Ala	Glu	Val	Leu	Glu	Ser	Asn	Gly	Ser	
465					470					475					480	
Ser	Ser	Gln	Ala	Ser	Ile	Cys	Ala	Gly	Thr	Leu	Ala	Leu	Met	Ala	Gly	
			485					490					495			
Gly	Val	Pro	Ile	Lys	Ala	Pro	Val	Ala	Gly	Ile	Ala	Met	Gly	Leu	Ile	
		500						505					510			
Ser	Asp	Gly	Asn	Asn	Tyr	Thr	Val	Leu	Thr	Asp	Ile	Gln	Gly	Leu	Glu	
	515						520					525				
Asp	His	Phe	Gly	Asp	Met	Asp	Phe	Lys	Val	Ala	Gly	Thr	Arg	Asp	Gly	
	530					535					540					
Ile	Thr	Ala	Leu	Gln	Met	Asp	Ile	Lys	Ile	Gln	Gly	Ile	Thr	Ala	Glu	
545					550					555					560	
Ile	Leu	Thr	Glu	Ala	Leu	Ala	Gln	Ala	Lys	Lys	Ala	Arg	Phe	Glu	Ile	
			565					570						575		
Leu	Asp	Val	Ile	Glu	Ala	Thr	Ile	Pro	Glu	Val	Arg	Leu	Glu	Leu	Ala	
		580						585					590			
Pro	Thr	Ala	Pro	Lys	Ile	Asp	Thr	Ile	Lys	Ile	Asp	Val	Asp	Lys	Ile	
	595						600					605				
Lys	Ile	Val	Ile	Gly	Lys	Gly	Glu	Thr	Ile	Asp	Lys	Ile	Ile	Ala		
	610					615				620						
Glu	Thr	Gly	Val	Lys	Ile	Asp	Ile	Asp	Glu	Glu	Gly	Asn	Val	Ser	Ile	
625					630					635					640	
Tyr	Ser	Ser	Asp	Gln	Asp	Ala	Ile	Asn	Arg	Ala	Lys	Glu	Ile	Ile	Ala	
			645					650						655		
Gly	Leu	Val	Arg	Glu	Ala	Lys	Val	Asp	Glu	Val	Tyr	Arg	Ala	Lys	Val	
		660					665						670			
Val	Arg	Ile	Glu	Lys	Phe	Gly	Ala	Phe	Val	Asn	Leu	Phe	Asp	Lys	Thr	
	675					680						685				
Asp	Ala	Leu	Val	His	Ile	Ser	Glu	Met	Ala	Trp	Thr	Arg	Thr	Asn	Arg	
	690					695					700					
Val	Glu	Asp	Leu	Val	Glu	Ile	Gly	Asp	Glu	Val	Asp	Val	Lys	Val	Ile	
705					710					715					720	
Lys	Ile	Asp	Glu	Lys	Gly	Arg	Ile	Asp	Ala	Ser	Met	Lys	Ala	Leu	Leu	
			725					730					735			
Pro	Arg	Pro	Pro	Lys	Pro	Glu	His	Asp	Glu	Lys	Gly	Glu	Lys	Ser	Glu	
		740						745					750			
Arg	Pro	His	Arg	Pro	Arg	His	His	Lys	Asp	His	Lys	Pro	Lys	Lys	Glu	
		755				760						765				
Phe	Thr	Glu	Thr	Pro	Lys	Asp	Ser	Glu								
	770					775										

(2) INFORMATION FOR SEQ ID NO:2701:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...357

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2701:

Asp	Cys	Leu	Ser	Gln	Leu	Cys	Asp	Ser	Ala	Leu	Glu	Leu	Ile	Leu	Arg
1				5					10					15	
Val	Leu	Glu	Val	Gly	Pro	Gly	Asp	Glu	Val	Ile	Val	Pro	Ala	Met	Thr
			20					25					30		
Tyr	Thr	Ala	Ser	Cys	Ser	Val	Ile	Thr	His	Val	Gly	Ala	Thr	Pro	Val
		35					40					45			
Met	Val	Asp	Ile	Gln	Ala	Asp	Thr	Phe	Glu	Met	Asp	Tyr	Asp	Leu	Leu
	50					55				60					
Glu	Gln	Ala	Ile	Thr	Glu	Lys	Thr	Lys	Val	Ile	Ile	Pro	Val	Glu	Leu
65					70					75				80	
Ala	Gly	Ile	Val	Cys	Asp	Tyr	Asp	Arg	Leu	Phe	Gln	Val	Val	Glu	Lys
				85					90					95	
Lys	Arg	Asp	Phe	Thr	Ala	Ser	Ser	Lys	Trp	Gln	Lys	Ala	Phe	Asn	
		100					105					110			
Arg	Ile	Val	Ile	Val	Ser	Asp	Ser	Ala	His	Ala	Leu	Gly	Ser	Thr	Tyr
		115					120					125			
Lys	Gly	Gln	Pro	Ser	Gly	Ser	Ile	Ala	Asp	Phe	Thr	Ser	Phe	Ser	Phe
	130					135					140				
His	Ala	Val	Lys	Asn	Phe	Thr	Thr	Ala	Glu	Gly	Gly	Ser	Ala	Thr	Trp
145					150					155				160	
Lys	Ala	Asn	Pro	Val	Ile	Asp	Asp	Glu	Glu	Met	Tyr	Lys	Glu	Phe	Gln
				165					170					175	
Ile	Leu	Ser	Leu	His	Gly	Gln	Thr	Lys	Asp	Ala	Leu	Ala	Lys	Met	Gln
			180					185					190		
Leu	Gly	Ser	Trp	Glu	Tyr	Asp	Ile	Val	Thr	Pro	Ala	Tyr	Lys	Cys	Asn
	195					200						205			
Met	Thr	Asp	Ile	Met	Ala	Ser	Leu	Gly	Leu	Val	Gln	Leu	Asp	Arg	Tyr
	210					215					220				
Pro	Ser	Leu	Leu	Gln	Arg	Arg	Lys	Asp	Ile	Val	Asp	Arg	Tyr	Asp	Ser
225					230					235				240	
Gly	Phe	Ala	Gly	Ser	Arg	Ile	His	Pro	Leu	Ala	His	Lys	Thr	Glu	Thr
				245					250					255	
Val	Glu	Ser	Ser	Arg	His	Leu	Tyr	Ile	Thr	Arg	Val	Glu	Gly	Ala	Ser
			260					265					270		
Leu	Glu	Glu	Arg	Ser	Leu	Ile	Ile	Gln	Glu	Leu	Ala	Lys	Ala	Gly	Ile
		275					280					285			
Ala	Ser	Asn	Val	His	Tyr	Lys	Pro	Leu	Pro	Leu	Leu	Thr	Ala	Tyr	Lys
	290					295					300				
Asn	Leu	Gly	Phe	Asp	Met	Thr	Asn	Tyr	Pro	Lys	Ala	Tyr	Ala	Phe	Phe
305					310					315				320	
Glu	Asn	Glu	Ile	Thr	Leu	Pro	Leu	His	Thr	Lys	Leu	Ser	Asp	Glu	Glu
				325					330					335	
Val	Asp	Tyr	Ile	Ile	Glu	Thr	Phe	Lys	Thr	Val	Ser	Glu	Lys	Val	Leu
			340					345					350		
Thr	Leu	Ser	Lys	Lys											

(2) INFORMATION FOR SEQ ID NO:2702:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...169

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2702:

```

Asn Pro Leu Ser Val Gln Met Val His Asn Ile Ala Gly Thr Ser Phe
1      5      10      15
Trp Leu Cys Lys Lys Glu Val Leu Glu Leu Ile Asn Gly Phe Glu Lys
      20      25      30
Ile Asp Ser His Gln Asp Gly Val Val Leu Leu Lys Leu Leu Ala Gln
      35      40      45
Gly Tyr Gln Ile Asp Ile Val Arg Glu Phe Leu Val Asn Tyr Tyr Ala
      50      55      60
His Ser Lys Glu Asn Gly Ile Thr Gly Val Thr Gln Lys Thr Ile Asn
65      70      75      80
Ala Asp Glu Glu Tyr Tyr Asn Tyr Cys Arg Lys Tyr Phe Asn Leu Leu
      85      90      95
Ser Phe Asn Glu Arg Ile Leu Val Thr Lys Lys Tyr Tyr Ser Leu Asn
      100     105     110
Ile Lys Arg Leu Leu Leu Ile Gly Asp Lys Cys Lys Ala Leu Lys Val
      115     120     125
Ile Lys Lys Ala Arg Glu Glu Lys Ile Phe Asn Glu Phe Leu Phe Leu
      130     135     140
Lys Tyr Met Leu Leu Tyr Asn Leu Gly Phe Phe Tyr Cys Ile Tyr Asp
145     150     155     160
Asn Tyr Val Gln Leu Lys Phe Arg Lys
      165

```

(2) INFORMATION FOR SEQ ID NO:2703:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...132

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2703:

```
Tyr Ile Leu Ser Thr His Phe Val Leu Gln Glu Leu Lys Lys Thr Arg
1           5           10           15
Ile Arg Lys Cys Leu Met Lys Ser Leu Ala Arg Leu Leu Asn Ile His
20           25           30
Val Phe Ile Ser Ile Phe Leu Phe Phe Ala Leu Ile Ser Gly Ala Val
35           40           45
Ser His Thr Val Leu Leu Leu Leu Leu Leu Phe Leu Pro Ala Leu Asn
50           55           60
Lys Gly Leu Glu Lys Ile Gln Ser Lys Arg Ile Pro Val Leu Asn Ala
65           70           75           80
Ala Leu Phe Phe Leu Leu Ile Ser Phe Pro Gln Leu Leu Thr Asn Pro
85           90           95
Val Gln Trp Lys Phe Ser Ile Phe Leu Val Val Thr Ile Ile Ser Ser
100          105          110
Leu Ala Tyr Phe Tyr Asn Phe Tyr Gln Val Val Lys Glu Val Asp Gln
115          120          125
Lys Gln Leu Ile
130
```

(2) INFORMATION FOR SEQ ID NO:2704:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 172 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...172

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2704:

```
Arg Leu Leu Ser Leu Ser Arg Trp Thr Arg Ile Gly Met Arg Ser Met
1           5           10           15
Thr Ser Cys Ala Ser Glu Leu Pro Lys Lys Asn Leu Phe Ala Leu Ser
20           25           30
Asp Leu Glu Thr Gly Met Val Tyr Leu Thr Ala Ala Ala Lys Gln Asn
35           40           45
Arg Ile Leu Leu Glu His Ile Gln Gly His Ala Leu Tyr Arg Ser Phe
50           55           60
Asp Glu Ile Glu Arg Glu Gln Phe Asp Asp Ala Met Ile Glu Ala His
65           70           75           80
```

Gln	Leu	Val	Ser	Met	Thr	Asp	Leu	Ile	Ser	Gln	Ile	Leu	Gln	Gln	Leu
				85					90					95	
Ser	Ala	Ser	Tyr	Asn	Asn	Ile	Leu	Asn	Asn	Asn	Leu	Asn	Asp	Asn	Leu
			100					105					110		
Thr	Thr	Leu	Thr	Ile	Ile	Ser	Val	Leu	Leu	Ala	Val	Leu	Ala	Val	Val
		115					120						125		
Thr	Gly	Phe	Phe	Gly	Met	Asn	Val	Pro	Leu	Pro	Leu	Thr	Asp	Glu	Pro
	130					135					140				
His	Ala	Trp	Leu	Tyr	Ile	Ser	Leu	Ala	Ser	Ala	Gly	Leu	Trp	Ile	Val
145					150					155					160
Leu	Ser	Leu	Leu	Leu	Arg	Lys	Ile	Ala	Lys	Lys	Ser				
				165					170						

(2) INFORMATION FOR SEQ ID NO:2705:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...272

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2705:

Ala	Trp	Leu	Ser	Cys	Gln	Gln	Gln	His	Ala	Thr	Ser	Glu	Gly	Thr	Asn
1				5					10					15	
Gln	Arg	Gln	Ser	Ser	Ser	Ala	Lys	Val	Pro	Trp	Lys	Ala	Ser	Tyr	Thr
		20					25						30		
Asn	Leu	Asn	Asn	Gln	Val	Ser	Thr	Glu	Glu	Val	Lys	Ser	Leu	Leu	Ser
		35				40						45			
Ala	His	Leu	Asp	Pro	Asn	Ser	Val	Asp	Ala	Phe	Phe	Asn	Leu	Val	Asn
	50					55				60					
Asp	Tyr	Asn	Thr	Ile	Val	Gly	Ser	Thr	Gly	Leu	Ser	Gly	Asp	Phe	Thr
65				70					75					80	
Ser	Phe	Thr	His	Thr	Glu	Tyr	Asp	Val	Glu	Lys	Ile	Ser	His	Leu	Trp
			85						90					95	
Asn	Gln	Lys	Lys	Gly	Asp	Phe	Val	Gly	Thr	Asn	Cys	Arg	Ile	Asn	Ser
		100						105					110		
Tyr	Cys	Leu	Leu	Lys	Asn	Ser	Val	Thr	Ile	Pro	Lys	Leu	Glu	Lys	Asn
	115						120					125			
Asp	Gln	Leu	Leu	Phe	Leu	Asp	Asn	Asp	Ala	Ile	Asp	Lys	Gly	Lys	Val
	130					135					140				
Phe	Asp	Ser	Gln	Asp	Lys	Glu	Glu	Phe	Asp	Ile	Leu	Phe	Ser	Arg	Val
145					150					155					160
Pro	Thr	Glu	Ala	Thr	Thr	Asp	Val	Lys	Val	His	Ala	Glu	Lys	Met	Glu
				165					170					175	
Thr	Phe	Phe	Ser	Gln	Phe	Gln	Phe	Asn	Glu	Lys	Ala	Arg	Met	Leu	Ser
			180					185					190		

Val	Val	Leu	His	Asp	Asn	Leu	Asp	Gly	Glu	Tyr	Leu	Phe	Val	Gly	His
		195					200					205			
Val	Gly	Val	Leu	Val	Pro	Ala	Asp	Asp	Gly	Phe	Leu	Phe	Val	Glu	Lys
	210					215					220				
Leu	Thr	Phe	Glu	Glu	Pro	Tyr	Gln	Ala	Ile	Lys	Phe	Ala	Ser	Lys	Glu
225					230					235					240
Asp	Cys	Tyr	Lys	Tyr	Leu	Gly	Thr	Lys	Tyr	Ala	Asp	Tyr	Thr	Gly	Glu
			245						250					255	
Gly	Leu	Ala	Lys	Pro	Phe	Ile	Met	Asp	Asn	Asp	Lys	Trp	Val	Lys	Leu
			260					265					270		

(2) INFORMATION FOR SEQ ID NO:2706:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...157

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2706:

Gln	Ser	Met	Ser	Asp	Lys	Ile	Gly	Leu	Phe	Thr	Gly	Ser	Phe	Asp	Pro
1				5					10					15	
Met	Thr	Asn	Gly	His	Leu	Asp	Ile	Ile	Glu	Arg	Ala	Ser	Arg	Leu	Phe
		20						25					30		
Asp	Lys	Leu	Tyr	Val	Gly	Ile	Phe	Phe	Asn	Pro	His	Lys	Gln	Gly	Phe
	35					40						45			
Leu	Pro	Ile	Glu	Asn	Arg	Lys	Arg	Gly	Leu	Glu	Lys	Ala	Leu	Gly	His
	50					55					60				
Leu	Glu	Asn	Val	Glu	Val	Val	Ala	Ser	His	Asp	Glu	Leu	Val	Val	Asp
65				70					75						80
Val	Ala	Lys	Arg	Leu	Gly	Ala	Thr	Cys	Leu	Val	Arg	Gly	Leu	Arg	Asn
			85						90					95	
Ala	Ser	Asp	Leu	Gln	Tyr	Glu	Ala	Ser	Phe	Asp	Tyr	Tyr	Asn	His	Gln
		100						105					110		
Leu	Ser	Ser	Asp	Ile	Glu	Thr	Ile	Tyr	Leu	His	Ser	Arg	Pro	Glu	His
		115					120					125			
Leu	Tyr	Ile	Ser	Ser	Ser	Gly	Val	Arg	Glu	Leu	Leu	Lys	Phe	Gly	Gln
	130					135					140				
Asp	Ile	Ala	Cys	Tyr	Val	Pro	Glu	Ser	Ile	Trp	Arg	Lys			
145					150				155						

(2) INFORMATION FOR SEQ ID NO:2707:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...97
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2707:

Glu	Asn	Met	Ser	Asp	Asn	Lys	Thr	Ser	Lys	Ile	Pro	Thr	Asn	Pro	Ala
1				5					10					15	
Asn	Ile	Gly	Leu	Leu	Phe	Leu	Pro	Ile	Phe	Lys	Ala	Ile	Gly	Pro	Ala
			20					25					30		
Lys	Lys	Asp	Ile	Gln	Ala	Ile	Gly	Pro	Val	Ile	Glu	Val	Glu	Lys	Ala
		35					40					45			
Val	Lys	Asp	Thr	Ala	Gln	Lys	Ile	Lys	Thr	Ser	Leu	Glu	Ser	Ser	Gly
	50					55					60				
Phe	Ala	Pro	Ser	Pro	Ile	Ala	Ile	Ser	Ser	Pro	Ser	Ser	Ile	Ile	Ser
65					70					75					80
Ser	Leu	Leu	Leu	Lys	Asn	Lys	Thr	Asn	Ile	Val	Ala	Ile	Ile	Leu	Thr
				85				90						95	

Asn

(2) INFORMATION FOR SEQ ID NO:2708:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 427 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...427
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2708:

Gly	Ser	Met	Ser	Cys	Ser	Ile	Asp	Leu	Leu	Lys	His	Arg	Tyr	Leu	Lys
1				5					10					15	
Asn	Ile	Lys	Glu	Asn	Pro	Glu	Leu	Phe	Val	Gly	Ile	Glu	Leu	Glu	Tyr
			20					25					30		
Pro	Val	Ala	Ser	Leu	Glu	Gly	Asp	Ala	Thr	Asp	Val	Glu	Val	Met	Lys
		35					40					45			
Asp	Leu	Phe	His	Tyr	Leu	Val	Ser	Thr	Leu	Asp	Leu	Thr	Val	Ala	Lys

50		55		60																																																																																																																																																																																																																																																																															
Val	Asp	Asp	Phe	Gly	Asn	65	70	75	80	85	90	Asp	Ala	Ile	Leu	Phe	Glu	95	100	105	110	115	120	Gly	Lys	Ala	Glu	Thr	Ile	125	130	135	140	145	150	Met	Asn	Val	Ile	Gln	Arg	155	160	165	170	175	180	Gly	Cys	Gly	Ile	His	Pro	185	190	195	200	205	210	Ala	Tyr	Pro	Arg	Tyr	Gln	215	220	225	230	235	240	Asn	Ile	Ile	Lys	Ser	Asp	245	250	255	260	265	270	Ile	Cys	Gly	Ser	Gln	Val	275	280	285	290	295	300	Arg	Val	Ile	Asn	Ala	Phe	305	310	315	320	325	330	Phe	Ala	Asn	Ser	Glu	Phe	335	340	345	350	355	360	Arg	Asp	Ile	Phe	Trp	Glu	365	370	375	380	385	390	Val	Gly	Val	Asn	Ala	Arg	395	400	405	410	415	420	Tyr	Leu	Asn	His	Ser	Ala	425	430	435	440	445	450	Tyr	Tyr	Phe	Tyr	Pro	Ile	455	460	465	470	475	480	Ile	Gln	Ala	Phe	Ala	Leu	485	490	495	500	505	510	Glu	Lys	Asp	Phe	Glu	Thr	515	520	525	530	535	540	Thr	Arg	Gly	Thr	Val	Glu	545	550	555	560	565	570	Arg	Thr	Phe	Ala	Ser	Ala	575	580	585	590	595	600	Asp	Lys	Leu	Glu	Ala	Tyr	605	610	615	620	625	630	Gly	Tyr	Asp	Tyr	Lys	Ser	635	640	645	650	655	660	Thr	Asp	Glu	Glu	Glu	Thr	665	670	675	680	685	690	Leu	Leu	Ala	Glu	Glu	Gly	695	700	705	710	715	720	Tyr	Leu	Gln	Pro	Leu	Arg	725	730	735	740	745	750
65	70	75	80	85	90																																																																																																																																																																																																																																																																														
Asp	Ala	Ile	Leu	Phe	Glu	95	100	105	110	115	120	Gly	Lys	Ala	Glu	Thr	Ile	125	130	135	140	145	150	Met	Asn	Val	Ile	Gln	Arg	155	160	165	170	175	180	Gly	Cys	Gly	Ile	His	Pro	185	190	195	200	205	210	Ala	Tyr	Pro	Arg	Tyr	Gln	215	220	225	230	235	240	Asn	Ile	Ile	Lys	Ser	Asp	245	250	255	260	265	270	Ile	Cys	Gly	Ser	Gln	Val	275	280	285	290	295	300	Arg	Val	Ile	Asn	Ala	Phe	305	310	315	320	325	330	Phe	Ala	Asn	Ser	Glu	Phe	335	340	345	350	355	360	Arg	Asp	Ile	Phe	Trp	Glu	365	370	375	380	385	390	Val	Gly	Val	Asn	Ala	Arg	395	400	405	410	415	420	Tyr	Leu	Asn	His	Ser	Ala	425	430	435	440	445	450	Tyr	Tyr	Phe	Tyr	Pro	Ile	455	460	465	470	475	480	Ile	Gln	Ala	Phe	Ala	Leu	485	490	495	500	505	510	Glu	Lys	Asp	Phe	Glu	Thr	515	520	525	530	535	540	Thr	Arg	Gly	Thr	Val	Glu	545	550	555	560	565	570	Arg	Thr	Phe	Ala	Ser	Ala	575	580	585	590	595	600	Asp	Lys	Leu	Glu	Ala	Tyr	605	610	615	620	625	630	Gly	Tyr	Asp	Tyr	Lys	Ser	635	640	645	650	655	660	Thr	Asp	Glu	Glu	Glu	Thr	665	670	675	680	685	690	Leu	Leu	Ala	Glu	Glu	Gly	695	700	705	710	715	720	Tyr	Leu	Gln	Pro	Leu	Arg	725	730	735	740	745	750												
95	100	105	110	115	120																																																																																																																																																																																																																																																																														
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Leu	Leu	Ala	Glu	Glu	Gly	695	700	705	710	715	720	Tyr	Leu	Gln	Pro	Leu	Arg	725	730	735	740	745	750																																																																																																																																																																																																																																																												
695	700	705	710	715	720																																																																																																																																																																																																																																																																														
Tyr	Leu	Gln	Pro	Leu	Arg	725	730	735	740	745	750																																																																																																																																																																																																																																																																								
725	730	735	740	745	750																																																																																																																																																																																																																																																																														

(2) INFORMATION FOR SEQ ID NO:2709:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...238

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2709:

Ser	Leu	Met	Ser	Met	Leu	Lys	Val	Glu	Asn	Leu	Ser	Val	His	Tyr	Gly
1				5					10					15	
Met	Ile	Gln	Ala	Val	Arg	Asp	Val	Ser	Phe	Glu	Val	Asn	Glu	Gly	Glu
			20					25					30		
Val	Val	Ser	Leu	Ile	Gly	Ala	Asn	Gly	Ala	Gly	Lys	Thr	Thr	Ile	Leu
			35				40						45		
Arg	Thr	Leu	Ser	Gly	Leu	Val	Arg	Pro	Ser	Ser	Gly	Lys	Ile	Glu	Phe
			50				55					60			
Leu	Gly	Gln	Glu	Ile	Gln	Lys	Met	Pro	Ala	Gln	Lys	Ile	Val	Ala	Gly
65					70					75					80
Gly	Leu	Ser	Gln	Val	Pro	Glu	Gly	Arg	His	Val	Phe	Pro	Gly	Leu	Thr
				85					90					95	
Val	Met	Glu	Asn	Leu	Glu	Met	Gly	Ala	Phe	Leu	Lys	Lys	Asn	Arg	Glu
			100					105					110		
Glu	Asn	Gln	Ala	Asn	Leu	Lys	Lys	Val	Phe	Ser	Arg	Phe	Pro	Arg	Leu
			115				120					125			
Glu	Glu	Arg	Lys	Asn	Gln	Asp	Ala	Ala	Thr	Leu	Ser	Gly	Gly	Glu	Gln
			130				135					140			
Gln	Met	Leu	Ala	Met	Gly	Arg	Ala	Leu	Met	Ser	Thr	Pro	Lys	Leu	Leu
145					150					155					160
Leu	Leu	Asp	Glu	Pro	Ser	Met	Gly	Leu	Ala	Pro	Ile	Phe	Ile	Gln	Glu
				165					170					175	
Ile	Phe	Asp	Ile	Ile	Gln	Asp	Ile	Gln	Lys	Gln	Gly	Thr	Thr	Val	Leu
			180					185					190		
Leu	Ile	Glu	Gln	Asn	Ala	Asn	Lys	Ala	Leu	Ala	Ile	Ser	Asp	Arg	Gly
			195				200					205			
Tyr	Val	Leu	Glu	Thr	Gly	Lys	Ile	Val	Leu	Ser	Gly	Ser	Gly	Lys	Glu
			210				215					220			
Leu	Ala	Ser	Ser	Glu	Glu	Val	Arg	Lys	Ala	Tyr	Leu	Gly	Gly		
225					230					235					

(2) INFORMATION FOR SEQ ID NO:2710:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 249 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...249

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2710:

Ser	Ile	Met	Ser	Gln	Lys	Asn	Asn	Lys	Lys	Lys	Asn	Lys	Arg	Lys	Asn	
1				5					10					15		
Leu	Leu	Thr	Asn	Ile	Leu	Ala	Gly	Phe	Leu	Ile	Leu	Leu	Ser	Leu	Ala	
			20					25					30			
Leu	Ile	Phe	Asn	Thr	Gln	Ile	Arg	Asn	Ile	Phe	Ile	Val	Trp	Asn	Thr	
		35					40					45				
Asn	Lys	Tyr	Gln	Val	Ser	Gln	Val	Ser	Lys	Glu	Lys	Leu	Glu	Glu	Asn	
	50					55					60					
Gln	Asp	Thr	Glu	Gly	Asn	Phe	Asp	Phe	Asp	Ser	Val	Lys	Ala	Ile	Ser	
65					70					75					80	
Ser	Glu	Ala	Val	Leu	Thr	Ser	Gln	Trp	Asn	Ala	Gln	Lys	Leu	Pro	Val	
			85					90					95			
Ile	Gly	Gly	Ile	Ala	Ile	Pro	Glu	Leu	Glu	Met	Asn	Leu	Pro	Ile	Phe	
			100					105					110			
Lys	Gly	Leu	Asp	Asn	Val	Asn	Leu	Phe	Tyr	Gly	Ala	Gly	Thr	Met	Lys	
	115					120						125				
Arg	Glu	Gln	Val	Met	Gly	Glu	Gly	Asn	Tyr	Ser	Leu	Ala	Ser	His	His	
	130					135					140					
Ile	Phe	Gly	Val	Asp	Asn	Ala	Asn	Lys	Met	Leu	Phe	Ser	Pro	Leu	Asp	
145					150					155					160	
Asn	Ala	Lys	Asn	Gly	Met	Lys	Ile	Tyr	Leu	Thr	Asp	Lys	Asn	Lys	Val	
			165						170					175		
Tyr	Thr	Tyr	Glu	Ile	Arg	Glu	Val	Lys	Arg	Val	Thr	Pro	Asp	Arg	Val	
			180					185					190			
Asp	Glu	Val	Asp	Asp	Arg	Asp	Gly	Val	Asn	Glu	Ile	Thr	Leu	Val	Thr	
	195						200					205				
Cys	Glu	Asp	Leu	Ala	Ala	Thr	Glu	Arg	Ile	Ile	Val	Lys	Gly	Asp	Leu	
	210					215					220					
Lys	Glu	Thr	Lys	Asp	Tyr	Ser	Gln	Thr	Ser	Asp	Glu	Ile	Leu	Thr	Ala	
225					230					235					240	
Phe	Asn	Gln	Pro	Tyr	Lys	Gln	Phe	Tyr								
			245													

(2) INFORMATION FOR SEQ ID NO:2711:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 124 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2711:

Lys	Lys	Met	Ser	Lys	Asn	Ile	Val	Gln	Leu	Asn	Asn	Ser	Phe	Ile	Gln
1				5					10					15	
Asn	Glu	Tyr	Gln	Arg	Arg	Arg	Tyr	Leu	Met	Lys	Glu	Arg	Gln	Lys	Arg
			20					25					30		
Asn	Arg	Phe	Met	Gly	Gly	Val	Leu	Ile	Leu	Ile	Met	Leu	Leu	Phe	Ile
		35					40					45			
Leu	Pro	Thr	Phe	Asn	Leu	Ala	Gln	Ser	Tyr	Gln	Gln	Leu	Leu	Gln	Arg
	50					55					60				
Arg	Gln	Gln	Leu	Ala	Asp	Leu	Gln	Thr	Gln	Tyr	Gln	Thr	Leu	Ser	Asp
65					70					75					80
Glu	Lys	Asp	Lys	Glu	Thr	Ala	Phe	Ala	Thr	Lys	Leu	Lys	Asp	Glu	Asp
			85						90					95	
Tyr	Ala	Ala	Lys	Tyr	Thr	Arg	Ala	Lys	Tyr	Tyr	Tyr	Ser	Lys	Ser	Arg
			100					105					110		
Glu	Lys	Val	Tyr	Thr	Ile	Pro	Asp	Leu	Leu	Gln	Arg				
		115					120								

(2) INFORMATION FOR SEQ ID NO:2712:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...169

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2712:

Thr	Gly	Met	Ser	Phe	Lys	Asn	Asn	Trp	Ile	Asp	Lys	Glu	Gly	Arg	Val
1				5					10					15	
Phe	Ile	Tyr	Phe	Thr	Val	Glu	Glu	Ile	Met	Lys	Arg	Arg	Asn	Ile	Ser
			20					25					30		
Lys	Pro	Thr	Ala	Ile	Lys	Thr	Leu	Asp	Glu	Leu	Asp	Ile	Lys	Lys	Gly
		35					40					45			
Ile	Gly	Leu	Ile	Glu	Arg	Val	Arg	Leu	Gly	Leu	Gly	Lys	Pro	Asn	Ile
	50					55					60				
Ile	Tyr	Val	Lys	Asp	Phe	Met	Ser	Ile	Phe	Gln	Val	Lys	Glu	Asn	Asp
65				70						75					80
Leu	Gln	Lys	Ser	Lys	Asn	Leu	Thr	Ser	Glu	Val	Lys	Asp	Phe	Asn	Leu
			85						90					95	
Arg	Ser	Lys	Glu	Asn	Glu	Leu	Gln	Glu	Val	Lys	Asn	Leu	Asp	Ser	Asn
			100					105					110		
Tyr	Ile	Glu	Asn	Asn	Lys	Ser	Lys	Tyr	Ser	Lys	Arg	Glu	Tyr	Ser	Phe
		115					120					125			
Gly	Glu	Asn	Gly	Leu	Gly	Thr	Phe	Gln	Asn	Val	Phe	Leu	Ala	Ala	Glu
	130					135					140				
Asp	Ile	Ser	Asp	Leu	Gln	Ile	Ile	Met	Asn	Ser	Gln	Leu	Glu	Asn	Tyr

(A) NAME/KEY: misc_feature
(B) LOCATION 1...347

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2714:

Trp	Pro	Val	Ser	Thr	Phe	Phe	Val	Phe	Asn	Val	Asn	Tyr	Thr	Arg	Glu
1				5					10					15	
Val	Val	Arg	Ile	Gln	Glu	Met	Gly	Lys	Thr	Val	Asn	Ser	Leu	Asp	Leu
			20					25					30		
Tyr	Leu	Lys	Asp	Ile	Asn	Glu	Pro	Ala	Ala	Ser	Val	Leu	Arg	Phe	Phe
		35					40					45			
Glu	Asp	Val	Ser	Lys	Asp	Tyr	Lys	Val	Ser	Ile	Ile	Lys	Thr	Asp	Ser
	50					55					60				
Gly	Asp	Glu	Val	Val	Lys	Ser	Gly	Val	Phe	Asp	Lys	Asp	Thr	Phe	Pro
65					70					75					80
Tyr	Gln	Glu	Phe	Gly	Ile	Ser	Ser	Leu	Asp	Phe	Thr	Thr	Asp	Gly	Glu
				85					90					95	
Gly	Val	Tyr	Ser	Asn	Lys	Glu	Ile	Ser	Asn	Lys	Leu	Gly	Thr	Ile	Pro
			100					105					110		
Thr	Phe	Leu	Lys	Ala	Lys	Pro	Ile	Gln	Leu	Met	Thr	Phe	Gln	Thr	Tyr
		115				120						125			
Ile	Lys	Asp	Thr	Ser	Arg	Ser	Leu	Asn	Gly	Arg	Tyr	Thr	Ile	Thr	Ser
	130					135					140				
Thr	Gln	Glu	Met	Asp	Lys	Asp	Arg	Ile	Val	Gln	Lys	Trp	Ser	Asp	Phe
145					150					155					160
Phe	Lys	Ile	Asp	Gln	Ala	Thr	Leu	Leu	Glu	Pro	Thr	Tyr	Lys	Ser	Ala
				165					170					175	
Val	Glu	Val	Ile	Asn	Arg	Asp	Leu	Leu	Leu	Ser	Ala	Ile	Val	Phe	Val
			180				185						190		
Leu	Ala	Ile	Leu	Leu	Leu	Val	Leu	Val	Thr	Val	Tyr	Gln	Pro	Met	Met
		195				200						205			
Glu	Met	Lys	Arg	Val	Gly	Val	Gln	Lys	Leu	Leu	Gly	Phe	Gln	Asp	Arg
	210					215					220				
Ala	Val	Leu	Ala	Asp	Val	Val	Lys	Gly	Asn	Leu	Tyr	Leu	Leu	Leu	Gly
225					230					235					240
Gly	Ala	Leu	Val	Ile	Asn	Leu	Gly	Val	Phe	Phe	Leu	Leu	Asp	Tyr	Lys
				245					250					255	
Pro	Lys	Arg	Phe	Val	Ser	Tyr	Thr	Val	Val	Val	Ser	Phe	Phe	Ala	Val
			260				265						270		
Ala	Ala	Leu	Ser	Leu	Tyr	Gln	Leu	Val	Asp	Leu	Pro	Leu	Asn	Pro	Lys
		275				280						285			
Asn	Asp	Asn	Gln	Leu	Ser	Ala	Glu	Arg	Phe	Phe	Ile	Phe	Gln	Ile	Trp
	290					295					300				
Ser	Tyr	Leu	Gln	Leu	Cys	Asp	Glu	Asn	Arg	Asp	Asn	Tyr	Phe	Thr	Asp
305					310					315					320
Gly	Leu	Thr	Asp	Trp	Gly	Gly	Gln	Lys	Phe	Arg	Thr	Arg	Lys	Gln	Arg
				325					330					335	
Thr	Cys	Leu	Ser	Ala	Thr	Val	Gly	Lys	Ser	Arg					
			340					345							

(2) INFORMATION FOR SEQ ID NO:2715:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

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(ix) FEATURE:
      (A) NAME/KEY: misc_feature
      (B) LOCATION 1...376
```

1	Pro	Val	Ser	Phe	Trp	Arg	Lys	Ile	Met	Lys	Ala	Ser	Pro	His	Arg
			5						10					15	
Pro	Thr	Lys	Val	Leu	Ile	His	Leu	Gly	Ala	Ile	Arg	Gln	Asn	Ile	Gln
			20					25					30		
Gln	Met	Gly	Ala	His	Ile	Pro	Gln	Gly	Thr	Leu	Lys	Trp	Ala	Val	Val
		35				40						45			
Lys	Ala	Asn	Ala	Tyr	Gly	His	Gly	Ala	Val	Ala	Val	Ala	Lys	Ala	Ile
	50					55					60				
Gln	Asp	Asp	Val	Asp	Gly	Phe	Cys	Val	Ser	Asn	Ile	Asp	Glu	Ala	Ile
65					70					75					80
Glu	Leu	Arg	Gln	Ala	Gly	Leu	Ser	Lys	Pro	Ile	Leu	Ile	Leu	Gly	Val
			85						90					95	
Ser	Glu	Ile	Glu	Ala	Val	Ala	Leu	Ala	Lys	Glu	Tyr	Asp	Phe	Thr	Leu
			100					105					110		
Thr	Val	Ala	Gly	Leu	Glu	Trp	Ile	Gln	Ala	Leu	Leu	Asp	Lys	Glu	Val
		115					120					125			
Asp	Leu	Thr	Gly	Leu	Thr	Val	His	Leu	Lys	Ile	Asp	Ser	Gly	Met	Gly
	130					135					140				
Arg	Ile	Gly	Phe	Arg	Glu	Ala	Ser	Glu	Val	Glu	Gln	Ala	Gln	Asp	Leu
145					150					155					160
Leu	Gln	Gln	His	Gly	Val	Arg	Val	Glu	Gly	Ile	Phe	Thr	His	Phe	Ala
			165						170					175	
Thr	Ala	Asp	Glu	Glu	Ser	Asp	Asp	Tyr	Phe	Asn	Ala	Gln	Leu	Glu	Arg
			180					185					190		
Phe	Lys	Thr	Ile	Leu	Ala	Ser	Met	Lys	Glu	Val	Pro	Glu	Leu	Val	His
		195					200					205			
Ala	Ser	Asn	Ser	Ala	Thr	Thr	Leu	Trp	His	Val	Glu	Thr	Ile	Phe	Asn
						215					220				
Ala	Val	Arg	Met	Gly	Asp	Ala	Met	Tyr	Gly	Leu	Asn	Pro	Ser	Gly	Ala
225				230					235						240
Val	Leu	Asp	Leu	Pro	Tyr	Asp	Leu	Ile	Pro	Ala	Leu	Thr	Leu	Glu	Ser
			245						250					255	
Ala	Leu	Val	His	Val	Lys	Thr	Val	Pro	Ala	Gly	Ala	Cys	Met	Gly	Tyr
			260					265					270		
Gly	Ala	Thr	Tyr	Gln	Ala	Asp	Ser	Glu	Gln	Val	Ile	Ala	Thr	Val	Pro
		275					280					285			
Ile	Gly	Tyr	Ala	Asp	Gly	Trp	Thr	Arg	Asp	Met	Gln	Asn	Phe	Ser	Val
	290					295					300				
Leu	Val	Asp	Gly	Gln	Ala	Cys	Pro	Ile	Val	Gly	Arg	Val	Ser	Met	Asp
305				310						315					320
Gln	Ile	Thr	Ile	Arg	Leu	Pro	Lys	Leu	Tyr	Pro	Leu	Gly	Thr	Lys	Val
			325						330					335	
Thr	Leu	Ile	Gly	Ser	Asn	Gly	Asp	Lys	Glu	Ile	Thr	Ala	Thr	Gln	Val

	340		345		350										
Ala	Thr	Tyr	Arg	Val	Thr	Ile	Asn	Tyr	Glu	Val	Val	Cys	Leu	Leu	Ser
	355		360		365										
Asp	Arg	Ile	Pro	Arg	Glu	Tyr	Tyr								
	370		375												

(2) INFORMATION FOR SEQ ID NO:2716:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 124 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...124
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2716:

Ile	Lys	Val	Ser	Ile	Met	Ile	Lys	Val	Ile	Ala	Lys	Thr	Asn	Asp	Asn
1			5				10						15		
Gly	Ala	Ser	Ala	Val	Pro	Ile	Thr	Ile	Pro	Ile	Gly	Ala	Gly	Val	Val
			20				25						30		
Gln	Gly	Lys	Ile	Ile	Leu	Lys	Leu	Phe	Ile	Cys	Arg	Thr	Ser	Thr	Lys
			35				40						45		
Asn	Phe	Ile	Ile	Gln	Thr	Leu	Ile	Ile	Gly	Ala	Val	Thr	Asn	Gly	Ile
			50				55						60		
Lys	Lys	Ile	Gly	Phe	Lys	Thr	Ile	Gly	Ala	Pro	Asn	Arg	Ile	Gly	Ser
			65				70						75		80
Phe	Thr	Pro	Lys	Lys	Val	Gly	Thr	Thr	Asp	Ala	Arg	Pro	Thr	Ile	Leu
			85				90						95		
Phe	Leu	Phe	Asp	Leu	His	Asn	His	Ile	Asn	Ile	Asn	Gly	Thr	Thr	Ser
			100				105						110		
Val	Ala	Pro	Val	Pro	Pro	Ile	Val	Thr	Thr	Lys	Val				
			115				120								

(2) INFORMATION FOR SEQ ID NO:2717:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 80 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...80

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2717:

Trp	Lys	Val	Ser	Gln	Ala	Arg	Gln	Leu	His	Met	Gln	Ala	Cys	Lys	Asn
1				5				10						15	
Leu	Ile	Ser	Trp	Leu	Phe	Phe	Met	Ile	Gln	Met	Ile	Ser	Thr	Trp	Met
			20					25					30		
Val	Arg	Gln	Arg	Ile	Pro	Leu	Gln	Lys	Val	Phe	Val	Thr	Val	Thr	Met
			35					40					45		
Pro	Thr	Val	Gly	Ile	Leu	Pro	Trp	Leu	Lys	Met	Glu	Gln	Thr	Trp	Lys
			50					55				60			
Pro	Ser	Met	Leu	Leu	Ser	Lys	Gln	Gln	Lys	Leu	Gln	Ala	Ser	His	Leu
65						70				75					80

(2) INFORMATION FOR SEQ ID NO:2718:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 331 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...331

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2718:

Leu	Pro	Ser	Ser	Gly	Lys	Trp	Arg	Cys	Leu	Pro	Arg	Trp	Arg	Phe	Asp
1				5					10					15	
Cys	Gly	Arg	Val	Asp	Ala	His	Tyr	Thr	Gly	Glu	Lys	Met	Ser	Phe	Thr
			20						25					30	
Val	Ala	Val	Lys	Glu	Glu	Ile	Leu	Gly	Gln	His	His	Leu	Ser	Trp	His
			35						40					45	
Glu	Leu	Ser	Ala	Ile	Ile	Lys	Met	Ser	Gly	Ser	Ile	Gly	Leu	Ser	Thr
			50				55					60			
Ser	Gly	Leu	Thr	Leu	Ser	Val	Val	Thr	Glu	Asn	Ala	Lys	Leu	Ala	Arg
65						70				75					80
His	Leu	Tyr	Glu	Ser	Phe	Leu	His	Phe	Tyr	Glu	Ile	Lys	Ser	Glu	Ile
				85					90					95	
Arg	His	His	Gln	Arg	Ser	Asn	Leu	Arg	Lys	Asn	Arg	Val	Tyr	Thr	Val
			100						105					110	
Phe	Thr	Asp	Glu	Lys	Val	Gln	Asp	Leu	Leu	Ser	Asp	Leu	His	Leu	Ala
			115				120					125			
Asp	Ser	Phe	Phe	Gly	Leu	Glu	Thr	Gly	Ile	Asp	Glu	Ala	Ile	Leu	Ser
			130				135					140			

Asp	Glu	Glu	Ala	Gly	Arg	Ala	Tyr	Leu	Cys	Gly	Ala	Phe	Leu	Ala	Asn
145					150					155					160
Gly	Ser	Ile	Arg	Asp	Pro	Glu	Ser	Gly	Lys	Tyr	Gln	Leu	Glu	Ile	Ser
			165						170						175
Ser	Val	Tyr	Leu	Asp	His	Ala	Gln	Gly	Ile	Ala	Ser	Leu	Leu	Gln	Gln
			180					185						190	
Phe	Leu	Leu	Asp	Ala	Lys	Val	Leu	Glu	Arg	Lys	Lys	Gly	Ala	Val	Thr
		195					200					205			
Tyr	Leu	Gln	Arg	Ala	Glu	Asp	Ile	Met	Asp	Phe	Leu	Ile	Val	Ile	Gly
	210					215					220				
Ala	Met	Gln	Ala	Arg	Asp	Asp	Phe	Glu	Arg	Val	Lys	Ile	Leu	Arg	Glu
225					230					235					240
Thr	Arg	Asn	Asp	Leu	Asn	Arg	Ala	Asn	Asn	Ala	Glu	Thr	Ala	Asn	Ile
			245						250						255
Ala	Arg	Thr	Val	Ser	Ala	Ser	Met	Lys	Thr	Ile	Asn	Asn	Ile	Ser	Lys
			260					265					270		
Ile	Lys	Asp	Ile	Met	Gly	Leu	Glu	Asn	Leu	Pro	Val	Asp	Leu	Gln	Glu
		275					280					285			
Val	Ala	Gln	Leu	Arg	Ile	Gln	His	Pro	Asp	Tyr	Ser	Ile	Gln	Gln	Leu
	290					295					300				
Ala	Asp	Ser	Leu	Ser	Thr	Pro	Leu	Thr	Lys	Ser	Gly	Val	Asn	His	Arg
305					310					315					320
Leu	Arg	Lys	Ile	Asn	Lys	Ile	Ala	Asp	Glu	Leu					
				325					330						

(2) INFORMATION FOR SEQ ID NO:2719:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 539 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...539

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2719:

Leu	Thr	Ser	Ser	Val	Leu	Ser	Thr	Thr	Ser	Lys	Gln	Cys	Phe	Glu	Gln
1				5					10					15	
Pro	Ala	Ala	Ser	Phe	Leu	Val	Cys	Ser	Leu	Ile	Phe	Ile	Glu	Tyr	Lys
			20					25					30		
Ile	Ile	Thr	Leu	Phe	Ile	Ser	Leu	Lys	Ile	Lys	Lys	Gly	Val	Phe	Ile
		35					40					45			
Met	Lys	Asn	Trp	Lys	Lys	Tyr	Ala	Phe	Ala	Ser	Ala	Ser	Val	Val	Ala
	50					55				60					
Leu	Ala	Ala	Gly	Leu	Ala	Ala	Cys	Gly	Asn	Leu	Thr	Gly	Asn	Ser	Lys
65					70				75					80	
Lys	Ala	Ala	Asp	Ser	Gly	Asp	Lys	Pro	Val	Ile	Lys	Met	Tyr	Gln	Ile
			85					90						95	

Gly	Asp	Lys	Pro	Asp	Asn	Leu	Asp	Glu	Leu	Leu	Ala	Asn	Ala	Asn	Lys	100	105	110
Ile	Ile	Glu	Glu	Lys	Val	Gly	Ala	Lys	Leu	Asp	Ile	Gln	Tyr	Leu	Gly	115	120	125
Trp	Gly	Asp	Tyr	Gly	Lys	Lys	Met	Ser	Val	Ile	Thr	Ser	Ser	Gly	Glu	130	135	140
Asn	Tyr	Asp	Ile	Ala	Phe	Ala	Asp	Asn	Tyr	Ile	Val	Asn	Ala	Gln	Lys	145	150	155
Gly	Ala	Tyr	Ala	Asp	Leu	Thr	Glu	Leu	Tyr	Lys	Lys	Glu	Gly	Lys	Asp	165	170	175
Leu	Tyr	Lys	Ala	Leu	Asp	Pro	Ala	Tyr	Ile	Lys	Gly	Asn	Thr	Val	Asn	180	185	190
Gly	Lys	Ile	Tyr	Ala	Val	Pro	Val	Ala	Ala	Asn	Val	Ala	Ser	Ser	Gln	195	200	205
Asn	Phe	Ala	Phe	Asn	Gly	Thr	Leu	Leu	Ala	Lys	Tyr	Gly	Ile	Asp	Ile	210	215	220
Ser	Gly	Val	Thr	Ser	Tyr	Glu	Thr	Leu	Glu	Pro	Val	Leu	Lys	Gln	Ile	225	230	235
Lys	Glu	Lys	Ala	Pro	Asp	Val	Val	Pro	Phe	Ala	Ile	Gly	Lys	Val	Phe	245	250	255
Ile	Pro	Ser	Asp	Asn	Phe	Asp	Tyr	Pro	Val	Ala	Asn	Gly	Leu	Pro	Phe	260	265	270
Val	Ile	Asp	Leu	Glu	Gly	Asp	Thr	Thr	Lys	Val	Val	Asn	Arg	Tyr	Glu	275	280	285
Val	Pro	Arg	Phe	Lys	Glu	His	Leu	Lys	Thr	Leu	His	Lys	Phe	Tyr	Glu	290	295	300
Ala	Gly	Tyr	Ile	Pro	Lys	Asp	Val	Ala	Thr	Ser	Asp	Thr	Ser	Phe	Asp	305	310	315
Leu	Gln	Gln	Asp	Thr	Trp	Phe	Val	Arg	Glu	Glu	Thr	Val	Gly	Pro	Ala	325	330	335
Asp	Tyr	Gly	Asn	Ser	Leu	Leu	Ser	Arg	Val	Ala	Asn	Lys	Asp	Ile	Gln	340	345	350
Ile	Lys	Pro	Ile	Thr	Asn	Phe	Ile	Lys	Lys	Asn	Gln	Thr	Thr	Gln	Val	355	360	365
Ala	Asn	Phe	Val	Ile	Ser	Asn	Asn	Ser	Lys	Asn	Lys	Glu	Lys	Ser	Met	370	375	380
Glu	Ile	Leu	Asn	Leu	Leu	Asn	Thr	Asn	Pro	Glu	Leu	Leu	Asn	Gly	Leu	385	390	395
Val	Tyr	Gly	Pro	Glu	Gly	Lys	Asn	Trp	Glu	Lys	Ile	Glu	Gly	Lys	Glu	405	410	415
Asn	Arg	Val	Arg	Val	Leu	Asp	Gly	Tyr	Lys	Gly	Asn	Thr	His	Met	Gly	420	425	430
Gly	Trp	Asn	Thr	Gly	Asn	Asn	Trp	Ile	Leu	Tyr	Ile	Asn	Glu	Asn	Val	435	440	445
Thr	Asp	Gln	Gln	Ile	Glu	Asn	Ser	Lys	Lys	Glu	Leu	Ala	Glu	Ala	Lys	450	455	460
Glu	Ser	Pro	Ala	Leu	Gly	Phe	Ile	Phe	Asn	Thr	Asp	Asn	Val	Lys	Ser	465	470	475
Glu	Ile	Ser	Ala	Ile	Ala	Asn	Thr	Met	Gln	Gln	Phe	Asp	Thr	Ala	Ile	485	490	495
Asn	Thr	Gly	Thr	Val	Asp	Pro	Asp	Lys	Ala	Ile	Pro	Glu	Leu	Met	Glu	500	505	510
Lys	Leu	Lys	Ser	Glu	Gly	Ala	Tyr	Glu	Lys	Val	Leu	Asn	Glu	Met	Gln	515	520	525
Lys	Gln	Tyr	Asp	Glu	Phe	Leu	Lys	Asn	Lys	Lys						530	535	

(2) INFORMATION FOR SEQ ID NO:2720:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...80

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2720:

Pro	Ser	Ser	Ser	Ser	Phe	Phe	Thr	Tyr	Ser	Cys	Glu	Gln	Ala	Ala	Arg
1				5					10					15	
Leu	Lys	Ala	Ser	Lys	Ala	Ala	Gln	Asp	Lys	Val	Ser	Phe	Phe	His	Phe
			20					25					30		
Tyr	Ser	Phe	Ile	Ser	Asn	Ser	Leu	Ser	Thr	Ser	Asp	Asp	Lys	His	Ser
		35					40					45			
Thr	Asn	Leu	Leu	Ile	Ser	Ser	Arg	Phe	Tyr	Leu	Ala	Ser	Phe	Cys	Cys
	50					55					60				
His	Phe	Phe	Lys	Gly	Thr	His	Gln	Thr	Gly	Pro	Arg	Pro	Leu	Arg	Pro
65					70					75					80

(2) INFORMATION FOR SEQ ID NO:2721:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...66

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2721:

Glu	Gly	Ser	Ser	Val	Lys	Leu	Glu	Asn	Ile	Asp	Lys	Ser	Ile	Gln	Lys
1				5					10					15	
Gln	Asp	Ile	Leu	Gln	Gly	Ile	Ser	Leu	Glu	Val	Ser	Pro	Gln	Lys	Leu
			20					25					30		
Thr	Ala	Phe	Ile	Gly	Pro	Asn	Gly	Ala	Gly	Lys	Ser	Thr	Leu	Pro	Leu
		35					40						45		

His His Glu Gln Thr Asn Gln Glu Arg Ser Gly Ser Ser Gln Tyr Gln
 50 55 60
 Arg Thr
 65

(2) INFORMATION FOR SEQ ID NO:2722:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...78

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2722:

Arg Met Pro Ser Leu Ile Lys Ser Thr Arg Leu Ala Leu Leu Ala Ala
 1 5 10 15
 Ala Val Glu Trp Val Thr Met Arg Met Val Trp Pro Arg Ser Leu Ile
 20 25 30
 Ser Ser Lys Thr Ser Ser Lys Ala Ala Asp Asp Leu Glu Ser Arg Ala
 35 40 45
 Pro Val Gly Ser Ser Ala Arg Arg Ile Ser Gly Ser Val Met Met Ala
 50 55 60
 Arg Ala Thr Ala Thr Arg Cys Phe Trp Pro Pro Glu Ile Ser
 65 70 75

(2) INFORMATION FOR SEQ ID NO:2723:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...96

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2723:

Ile Leu Thr Ser Arg Arg Lys Leu Ser Leu Ser Leu Glu Glu Cys Gln

1				5					10					15			
Leu	Met	Leu	Glu	Glu	Gly	Thr	Lys	Asp	Gln	Leu	Ala	Glu	Leu	Thr	Tyr		
			20					25					30				
Pro	Phe	Gly	Arg	Gly	Val	Asn	Leu	Ser	Phe	Gly	Ile	Lys	Asp	Val	Pro		
		35					40					45					
Lys	Leu	Tyr	Gln	Lys	Val	Met	Glu	Ala	Asn	Tyr	Pro	Ile	Tyr	Arg	Leu		
	50					55					60						
Leu	Thr	Lys	Arg	Lys	Phe	Arg	Val	Ser	Asp	Pro	Tyr	Ile	Tyr	Pro	His		
65					70					75					80		
Lys	Phe	Ala	Val	Leu	Asp	Pro	Asp	Gly	Tyr	Phe	Leu	Arg	Phe	Ser	Glu		
				85				90						95			

(2) INFORMATION FOR SEQ ID NO:2724:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 72 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...72
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2724:

Lys	Glu	Thr	Ser	Asn	Ala	His	Glu	Thr	Thr	Asn	Thr	Gly	Ile	Lys	Thr
1				5					10				15		
Met	Thr	Lys	Gln	Ile	Pro	Lys	Phe	Thr	Lys	Asp	Thr	Ala	Gln	Leu	Tyr
		20						25				30			
Thr	Cys	Lys	Trp	Leu	Leu	Tyr	Asn	Lys	Val	Thr	Lys	Met	Tyr	Asp	His
	35					40					45				
Thr	Val	Val	Asn	His	Ser	Val	Arg	Glu	Tyr	Ile	Thr	Asp	Ser	Ile	Ser
	50				55						60				
Thr	Asn	Thr	Ser	Lys	Glu	Ser	Gly								
65				70											

(2) INFORMATION FOR SEQ ID NO:2725:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 279 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...279

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2725:

Ser	Val	Ala	Ser	Glu	Ser	Leu	Ser	Arg	His	Gly	Ser	Leu	Lys	Thr	Lys
1				5					10					15	
Gly	Glu	Met	Met	His	Thr	Tyr	Leu	Gln	Lys	Lys	Ile	Glu	Asn	Ile	Lys
			20					25					30		
Thr	Thr	Leu	Gly	Glu	Met	Ser	Gly	Gly	Tyr	Arg	Arg	Met	Val	Ala	Ala
		35					40					45			
Met	Ala	Asp	Leu	Gly	Phe	Ser	Gly	Thr	Met	Lys	Ala	Ile	Trp	Asp	Asp
	50					55				60					
Leu	Phe	Ala	His	Arg	Ser	Phe	Ala	Gln	Trp	Ile	Tyr	Leu	Leu	Val	Leu
65				70					75					80	
Gly	Ser	Phe	Pro	Leu	Trp	Leu	Glu	Leu	Val	Tyr	Glu	His	Arg	Ile	Val
			85						90				95		
Asp	Trp	Ile	Gly	Met	Ile	Cys	Ser	Leu	Thr	Gly	Ile	Ile	Cys	Val	Ile
		100						105					110		
Phe	Val	Ser	Glu	Gly	Arg	Ala	Ser	Asn	Tyr	Leu	Phe	Gly	Leu	Ile	Asn
	115					120					125				
Ser	Val	Ile	Tyr	Leu	Ile	Leu	Ala	Leu	Gln	Lys	Gly	Phe	Tyr	Gly	Glu
	130					135					140				
Val	Leu	Thr	Thr	Leu	Tyr	Phe	Thr	Val	Met	Gln	Pro	Ile	Gly	Leu	Leu
145				150					155					160	
Val	Trp	Ile	Tyr	Gln	Ala	Gln	Phe	Lys	Lys	Glu	Lys	Gln	Glu	Phe	Val
			165						170					175	
Ala	Arg	Lys	Leu	Asp	Gly	Lys	Gly	Trp	Thr	Lys	Tyr	Leu	Ser	Ile	Ser
		180					185						190		
Val	Leu	Trp	Trp	Leu	Ala	Phe	Gly	Phe	Ile	Tyr	Gln	Ser	Ile	Gly	Ala
	195					200						205			
Asn	Arg	Pro	Tyr	Arg	Asp	Ser	Ile	Thr	Asp	Ala	Thr	Asn	Gly	Val	Gly
	210					215					220				
Gln	Ile	Leu	Met	Thr	Ala	Val	Tyr	Arg	Glu	Gln	Trp	Ile	Phe	Trp	Ala
225				230					235					240	
Ala	Thr	Asn	Val	Phe	Ser	Ile	Tyr	Leu	Trp	Trp	Gly	Lys	Ser	Leu	Gln
			245						250					255	
Ile	Gln	Gly	Lys	Tyr	Leu	Ile	Tyr	Leu	Ile	Asn	Ser	Leu	Ile	Trp	Leu
		260						265					270		
Val	Ser	Met	Glu	Gln	Gly	His									
		275													

(2) INFORMATION FOR SEQ ID NO:2726:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 78 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...78

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2726:

```
Arg Ser Ala Ser Ser Val Lys Gly Ala Ser Lys Ser Met Val Ser Pro
1          5          10          15
Lys Thr Leu Lys Thr Arg Pro Lys Val Ser Leu Pro Thr Gly Thr Glu
          20          25          30
Ile Gly Arg Pro Val Ser Asn Thr Ser Ile Pro Arg Val Asn Pro Ser
          35          40          45
Val Asp Ser Met Ala Ile Val Arg Thr Ile Pro Ser Pro Asn Ser Lys
          50          55          60

Ala Thr Ser Arg Thr Ile Phe Val Phe Leu Ser Ser Phe Leu
65          70          75
```

(2) INFORMATION FOR SEQ ID NO:2727:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...233

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2727:

```
Asn Leu Ala Ser Glu Thr Asn His Glu Ile Asp Ser Asn Phe Ala Gly
1          5          10          15
Arg Leu Asn Ile Leu Arg Ala Gly Val Leu Gly Ala Asn Asp Gly Ile
          20          25          30
Ile Ser Ile Ala Gly Val Val Ile Gly Val Ala Ser Ala Thr Thr Asn
          35          40          45
Ile Trp Ile Ile Phe Leu Ser Gly Phe Ala Ala Ile Leu Ala Gly Ala
          50          55          60
Phe Ser Met Ala Gly Gly Glu Tyr Val Ser Val Ser Thr Pro Lys Asp
65          70          75          80
Thr Glu Glu Ala Ala Val Ser Arg Glu Lys Leu Leu Leu Asp Gln Asp
          85          90          95
Arg Glu Leu Ala Lys Lys Ser Leu Tyr Ala Ala Tyr Ile Gln Asn Gly
          100          105          110
Glu Cys Lys Thr Ser Ala Gln Leu Leu Thr Asn Lys Ile Phe Leu Lys
          115          120          125
Asn Pro Leu Lys Ala Leu Val Glu Glu Lys Tyr Gly Ile Glu Tyr Glu
          130          135          140
```

Glu	Phe	Thr	Asn	Pro	Trp	His	Ala	Ala	Ile	Ser	Ser	Phe	Val	Ala	Phe
145					150					155					160
Phe	Leu	Arg	Ser	Leu	Pro	Pro	Met	Leu	Ser	Val	Thr	Ile	Phe	Pro	Ser
				165						170					175
Glu	Tyr	Arg	Ile	Pro	Ala	Thr	Val	Leu	Ile	Val	Gly	Val	Ala	Leu	Leu
			180						185					190	
Leu	Thr	Gly	Tyr	Thr	Ser	Ala	Arg	Leu	Gly	Lys	Asp	Pro	Thr	Arg	Thr
		195					200					205			
Ala	Met	Ile	Arg	Asn	Leu	Ala	Ile	Gly	Leu	Leu	Thr	Arg	Gly	Val	Thr
	210						215					220			
Phe	Leu	Leu	Glu	Gln	Leu	Phe	Ser	Ile							
225							230								

(2) INFORMATION FOR SEQ ID NO:2728:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...79

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2728:

Lys	Met	Ala	Ser	Cys	Tyr	Ala	Lys	Ser	Ser	Met	Leu	Leu	Met	Lys	Leu
1				5					10					15	
Ile	Ser	Ile	Ala	Leu	Lys	Ile	Val	Ile	Arg	Leu	Met	Ile	Phe	Thr	Lys
			20						25					30	
Lys	Phe	Leu	Lys	Ile	Phe	Lys	Met	Leu	Gly	Thr	Gln	Glu	Asn	Phe	Ile
		35					40					45			
Arg	His	Val	Gln	Arg	Leu	Ile	Leu	Leu	Pro	Lys	Phe	Leu	Thr	Gln	Asn
	50					55					60				
Leu	Glu	Asn	Gln	Trp	Gln	Thr	Leu	Leu	Ala	Glu	Gln	Glu	Ala	Ser	
65					70					75					

(2) INFORMATION FOR SEQ ID NO:2729:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...100

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2729:

```
Met Asn Thr Leu Gly Asp Lys Leu Met Glu Leu Ser Ala Ile Tyr His
1          5          10          15
Arg Thr Glu Ser Glu Tyr Ala Tyr Leu Tyr Lys Asp Lys Lys Leu His
          20          25          30
Ile Arg Ile Arg Thr Lys Lys Gly Asp Ile Glu Ser Ile Asn Leu His
          35          40          45
Tyr Gly Asp Pro Phe Ile Phe Met Glu Glu Phe Tyr Gln Asp Thr Lys
          50          55          60
Glu Met Val Lys Ile Thr Ser Gly Thr Leu Phe Asp His Trp Gln Val
65          70          75          80
Glu Val Ser Val Asp Phe Ala Arg Ile Gln Tyr Leu Phe Glu Leu Arg
          85          90          95
Asp Thr Glu Gly
          100
```

(2) INFORMATION FOR SEQ ID NO:2730:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 82 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...82

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2730:

```
Leu Arg Gln Ser Tyr Pro Ala Thr Ser Lys Gln Cys Phe Glu Gln Pro
1          5          10          15
Ala Ala Ser Phe Leu Gln Ile Leu Val Gly Thr Arg Phe Asn Ser Cys
          20          25          30
Asp Asn Val Lys Ile Val Arg Ala Phe Tyr Ile Glu Tyr Thr Trp Glu
          35          40          45
Trp Ser Leu Leu Pro Phe Pro Tyr Leu Ile Glu Lys Glu Glu Leu Asn
          50          55          60
Ala Thr Leu Tyr Lys Arg Arg Leu Ala Arg Ile Gly Cys Arg Asn His
65          70          75          80
Tyr Ala
```

(2) INFORMATION FOR SEQ ID NO:2731:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 91 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...91
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2731:

Gln	Ser	Gln	Ser	His	Ile	Tyr	Gly	Lys	Ala	Thr	Leu	Ala	Arg	Phe	Glu
1				5					10					15	
Glu	Ile	Phe	Glu	Glu	Tyr	Lys	Asn	Pro	Gln	Asp	Thr	Phe	Phe	Tyr	Pro
		20						25					30		
Leu	Val	Tyr	Lys	Glu	Asn	Thr	Tyr	Glu	Lys	Thr	Ala	Ile	Ser	Ile	Phe
		35					40					45			
Ala	Leu	Leu	Met	Leu	Gly	Val	Cys	Cys	Leu	Phe	Leu	Phe	Ser	Gln	Gln
	50					55					60				
Ser	Tyr	Lys	Lys	Leu	Val	Gln	Tyr	Tyr	Ala	Asn	Asp	Gln	Asn	Leu	Pro
65				70						75					80
Ser	Arg	Ile	Thr	Tyr	Ser	Glu	Tyr	Ser	Asp	Lys					
			85						90						

(2) INFORMATION FOR SEQ ID NO:2732:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 308 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...308
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2732:

Arg	Cys	Gln	Ser	Gln	Ile	Val	Trp	Phe	Val	Glu	Asp	Thr	Tyr	Met	Ile
1				5					10					15	
Gln	Ala	Arg	Asn	Lys	Leu	Ser	Gln	Glu	Glu	Leu	Ser	Glu	Ala	Lys	Lys
		20						25					30		
Val	Ile	Asn	Cys	Cys	Gln	Asn	Tyr	Asp	Gly	Thr	Tyr	Arg	Asp	Pro	Tyr
		35					40					45			

```

Leu Ser Asn Met Leu Asn Phe Asp Pro Asn Met Pro Ala Phe Phe Leu
 50          55          60
Tyr Tyr Glu Lys Gly Glu Leu Val Gly Leu Leu Thr Val Tyr Ala Asp
65          70          75          80
Asp Gln Asp Val Glu Val Thr Ile Leu Val His Pro Gly His Arg Arg
          85          90          95
Gln Gly Ile Ala Arg Ala Leu Phe Thr Ser Phe Glu Arg Glu Thr Ala
          100          105          110
Ser Phe Pro Ile Arg Ser Val Thr Phe Gln Thr Glu Arg Ile Phe Leu
          115          120          125
Glu Asn His Pro Asp Phe Ala Ser Asn Trp Gly Leu Ile Glu Asp Glu
          130          135          140
Glu Thr Glu Thr Trp Leu Gly Lys Asp Arg Arg Pro Tyr Gln Leu Ala
145          150          155          160
Lys Leu Ser Asn Leu Glu Val Leu Leu Ala Asp Ser Ser Tyr Gln Glu
          165          170          175
Gln Ile Ser Gln Leu Lys Phe Gln Ala Phe Ser Gly Glu His Glu Ser
          180          185          190
Arg Glu Val Val Asp Arg Tyr Val Ala Glu Ala Leu Lys Asp Pro Glu
          195          200          205
Ser Arg Leu Tyr Ile Leu Leu Lys Asp Gly Gln Val Ile Gly Thr Cys
          210          215          220
Thr Val Asp Leu Ser Ser Asp Thr Asn Tyr Phe Tyr Gly Leu Ala Ile
225          230          235          240
Ser Glu Pro Glu Arg Gly Lys Gly Tyr Gly Ser Tyr Leu Ala Lys Ser
          245          250          255
Leu Val Asn Gln Leu Ile Glu Gln Asn Asp Lys Glu Phe Gln Ile Ala
          260          265          270
Val Glu Asp Ser Asn Val Gly Ala Lys Arg Leu Tyr Glu Lys Ile Gly
          275          280          285
Phe Val Lys Gln Thr Gln Val Val Tyr Leu Asn Glu Lys Gly Ala Arg
          290          295          300
Asp Ser Glu Val
305

```

(2) INFORMATION FOR SEQ ID NO:2733:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 228 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...228
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2733:

```

Ile Cys Thr Leu Phe Gln Leu Pro Ser Val Cys Phe Trp Glu Ser Ala
1           5           10           15

```

```

Tyr Phe Pro Thr Arg Leu Asn Asp Leu Leu Glu Asn Tyr Gln Val Phe
    20          25          30
Val Leu Trp Ser Phe Ala Gly Ala Ile Ile Gly Thr Val Pro Ser Leu
    35          40          45
Leu Lys Glu Ser Thr Arg Glu Ser Asp Arg Asp Lys Ile Asp Leu Ala
    50          55          60
Trp Leu Trp Thr Thr Phe Ile Ile Ser Gly Leu Gly Leu Tyr Ala Leu
    65          70          75          80
Asn Phe Val Val Gly Thr Leu Ser Ala Ser Phe Leu Asn Phe Val Leu
    85          90          95
Ala Gly Ala Leu Leu Ala Leu Gly Val Leu Val Pro Gly Leu Ser Pro
    100         105         110
Ser Asn Leu Leu Leu Ile Leu Gly Leu Tyr Ala Pro Met Leu Thr Gly
    115         120         125
Phe Lys Thr Phe Asp Leu Leu Gly Thr Phe Phe Pro Ile Gly Ile Gly
    130         135         140
Ala Gly Ala Thr Leu Ile Val Phe Ser Lys Leu Met Asp Tyr Ala Leu
    145         150         155         160
Asn Asn Tyr His Ser Arg Val Tyr His Phe Ile Ile Gly Ile Val Leu
    165         170         175
Ser Ser Thr Leu Leu Ile Leu Ile Pro Asn Ala Gly Asn Ala Glu Ser
    180         185         190
Ile Gln Tyr Thr Gly Leu Ser Leu Val Gly Tyr Val Ile Ile Ala Phe
    195         200         205
Phe Phe Ala Leu Gly Ile Trp Leu Gly Ile Trp Met Ser Gln Leu Glu
    210         215         220
Asp Lys Tyr Lys
225

```

(2) INFORMATION FOR SEQ ID NO:2734:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...79

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2734:

```

Cys Arg Lys Ser Phe Gly Thr Gly Cys Leu Leu Gly Ala Val Val Ala
1      5      10      15
Ser Phe Ile Gly Leu Glu Lys Gly Gln Glu Leu Lys Ser Leu Glu Thr
    20      25      30
Ala Met Leu Val Tyr Asn Ile Ala Gly Glu Met Ala Glu Lys Arg Pro
    35      40      45
Asn Gly His Leu Pro Gly Thr Phe Lys Val Glu Phe Ile Asn Ala Leu
    50      55      60

```

Tyr Glu Ile Thr Asp Glu Asp Val Lys Glu Phe Lys Arg Val Lys
65 70 75

(2) INFORMATION FOR SEQ ID NO:2735:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...65

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2735:

Ala Leu Trp Ser Lys Arg Arg Asp Arg Ile Arg Thr Arg Asn Leu Pro
1 5 10 15
Glu Asn Trp Leu Ile Ser Phe Thr Thr Pro Cys Ala Ile Val Ala Ile
20 25 30
Asn His Ile Asp Leu Thr Lys Thr Val Phe Glu Lys Asp Lys Thr Ala
35 40 45
Ala Val Asn Tyr Gln His Lys His Asn Leu Glu Gly Phe Leu Lys Gly
50 55 60
Lys
65

(2) INFORMATION FOR SEQ ID NO:2736:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...224

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2736:

Gly Gly Trp Ser Met Lys Cys Leu Leu Cys Gly Gln Thr Met Lys Thr
1 5 10 15
Val Leu Thr Phe Ser Ser Leu Leu Leu Leu Arg Asn Asn Asp Ser Cys

			85					90					95				
Gln	Ile	Gln	Lys	Ala	Leu	Arg	Asp	Asp	Thr	Ile	Leu	Val	Ser	Thr	Met		
			100					105					110				
Phe	Ala	Asn	Asn	Glu	Thr	Gly	Asn	Leu	Leu	Pro	Ile	Ala	Glu	Ile	Gly		
		115					120					125					
Gln	Ile	Leu	Lys	Gln	His	Pro	Ala	Ala	Tyr	His	Val	Asp	Ala	Val	Gln		
	130					135					140						
Ala	Ile	Gly	Lys	Ile	Pro	Ile	His	Ser	Glu	Glu	Leu	Gly	Ile	Asp	Phe		
145					150					155					160		
Leu	Thr	Ala	Ser	Ala	His	Lys	Phe	His	Gly	Pro	Lys	Gly	Ile	Gly	Phe		
			165						170					175			
Leu	Tyr	Ala	Ser	Ser	Met	Asp	Phe	Asp	Ser	Tyr	Leu	His	Gly	Gly	Asp		
		180						185					190				
Gln	Glu	Gln	Lys	Lys	Arg	Ala	Gly	Thr	Glu	Asn	Leu	Pro	Ala	Ile	Val		
	195						200					205					
Gly	Met	Val	Ala	Ala	Leu	Lys	Glu	Asp	Leu	Glu	Lys	Gln	Glu	Glu	His		
	210					215					220						
Phe	Gln	His	Val	Gln	Asn	Leu	Glu	Thr	Ala	Phe	Leu	Ala	Glu	Leu	Glu		
225					230				235						240		
Gly	Ile	Gln	Tyr	Tyr	Leu	Asn	Arg	Gly	Lys	His	His	Leu	Pro	Tyr	Val		
		245						250						255			
Leu	Asn	Ile	Gly	Phe	Pro	Gly	Gln	Lys	Asn	Asp	Leu	Leu	Leu	Leu	Arg		
		260						265						270			
Leu	Asp	Leu	Ala	Gly	Ile	Ser	Ile	Ser	Thr	Gly	Ser	Ala	Cys	Thr	Ala		
	275						280					285					
Gly	Val	Val	Gln	Ser	Ser	His	Val	Leu	Glu	Ala	Met	Tyr	Gly	Ala	Asn		
	290					295					300						
Ser	Glu	Arg	Leu	Lys	Glu	Ser	Leu	Arg	Ile	Ser	Leu	Ser	Pro	Gln	Asn		
305				310					315						320		
Thr	Val	Glu	Asp	Leu	Gln	Thr	Leu	Ala	Lys	Thr	Leu	Lys	Glu	Ile	Ile		
			325					330						335			
Gly	Gly																

(2) INFORMATION FOR SEQ ID NO:2738:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...257

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2738:

Ile	Arg	Trp	Ser	Leu	Ile	Cys	Thr	Met	Ile	Tyr	Phe	Gln	Asn	Val	Ser
1				5				10					15		
Lys	Leu	Tyr	Gly	Asp	Lys	Asp	Ala	Leu	Ser	Asn	Leu	Asn	Leu	Gln	Ile


```

          35          40          45
Leu Phe Lys Pro Arg Gln Leu Tyr Leu Gln Pro Gln Asn Ser Val Leu
   50          55          60
Ser Asn Leu Trp Leu Ala Ser
65          70

```

(2) INFORMATION FOR SEQ ID NO:2740:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 102 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...102
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2740:

```

Ser Thr Thr Leu Gly Asn Ser Glu Asn Cys Pro Val Leu Phe Tyr Phe
1          5          10          15
Glu Lys Ile Trp Ser Leu Ser Leu Lys Leu Leu Asp Cys Ile Leu Asp
   20          25          30
Tyr Gln Glu Arg Phe Asn Gly Lys Thr Cys Gln Val Ser Thr Asn Tyr
   35          40          45
Lys Tyr Leu Glu Ile Phe Lys Val Asn Phe Cys Leu Thr Asp Leu His
   50          55          60
His Leu Phe Asp Leu Tyr Lys Ile Thr Arg Asp Tyr Ala Ser Gln Thr
65          70          75          80
Lys Pro Ala Ile Gln Ala Gly Val Phe Ile Leu Glu Asp Phe Arg Asn
   85          90          95
Ile Leu Cys Thr Met Met
   100

```

(2) INFORMATION FOR SEQ ID NO:2741:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 503 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature

(B) LOCATION 1...503

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2741:

Leu	Leu	Phe	Pro	Phe	Pro	His	Tyr	Lys	Arg	Val	Asn	Ser	Tyr	Asn	Leu
1				5					10					15	
Pro	Phe	His	Ala	Leu	Pro	His	His	Lys	Ala	Gly	Gln	Ser	Leu	Pro	Thr
			20					25					30		
Ala	His	Gln	Thr	Glu	Ser	Tyr	Phe	Ala	Ser	Glu	Ser	Ser	His	Gln	Val
		35					40					45			
Leu	Phe	Leu	Val	Ser	Cys	Pro	Thr	Ile	Leu	Pro	Lys	Arg	Ala	Gly	Phe
	50				55						60				
Cys	Tyr	Asn	Gly	His	Met	Asn	Glu	Lys	Val	Phe	Arg	Asp	Pro	Val	His
65				70					75					80	
Asn	Tyr	Ile	His	Val	Asn	Asn	Gln	Ile	Ile	Tyr	Asp	Leu	Ile	Asn	Thr
			85					90						95	
Lys	Glu	Phe	Gln	Arg	Leu	Arg	Arg	Ile	Lys	Gln	Leu	Gly	Thr	Ser	Ser
		100						105					110		
Tyr	Thr	Phe	His	Gly	Gly	Glu	His	Ser	Arg	Phe	Ser	His	Cys	Leu	Gly
	115					120					125				
Val	Tyr	Glu	Ile	Ala	Arg	Arg	Ile	Thr	Glu	Ile	Phe	Glu	Glu	Lys	Tyr
	130					135					140				
Pro	Glu	Glu	Trp	Asn	Pro	Ala	Glu	Ser	Leu	Leu	Thr	Met	Thr	Ala	Ala
145				150					155						160
Leu	Leu	His	Asp	Leu	Gly	His	Gly	Ala	Tyr	Ser	His	Thr	Phe	Glu	His
			165					170						175	
Leu	Phe	Asp	Thr	Asp	His	Glu	Ala	Ile	Thr	Gln	Glu	Ile	Ile	Gln	Asn
		180						185					190		
Pro	Glu	Thr	Glu	Ile	His	Gln	Val	Leu	Leu	Gln	Val	Ala	Pro	Asp	Phe
	195					200						205			
Pro	Glu	Lys	Val	Ala	Ser	Val	Ile	Asp	His	Thr	Tyr	Pro	Asn	Lys	Gln
	210					215					220				
Val	Val	Gln	Leu	Ile	Ser	Ser	Gln	Ile	Asp	Ala	Asp	Arg	Met	Asp	Tyr
225				230					235					240	
Leu	Leu	Arg	Asp	Ser	Tyr	Phe	Thr	Gly	Ala	Ser	Tyr	Gly	Glu	Phe	Asp
			245					250						255	
Leu	Thr	Arg	Ile	Leu	Arg	Val	Ile	Arg	Pro	Val	Glu	Asn	Gly	Ile	Ala
		260						265					270		
Phe	Gln	Arg	Asn	Gly	Met	His	Ala	Ile	Glu	Asp	Tyr	Val	Leu	Ser	Arg
	275					280						285			
Tyr	Gln	Met	Tyr	Met	Gln	Val	Tyr	Phe	His	Pro	Ala	Thr	Arg	Ala	Met
290				295							300				
Glu	Val	Leu	Leu	Gln	Asn	Leu	Leu	Lys	Arg	Ala	Lys	Glu	Leu	Tyr	Pro
305				310					315					320	
Glu	Asp	Lys	Asn	Phe	Phe	Ala	Arg	Thr	Ser	Pro	His	Leu	Leu	Pro	Phe
			325					330						335	
Phe	Glu	Lys	Asn	Val	Thr	Leu	Thr	Asp	Tyr	Leu	Ala	Leu	Asp	Asp	Gly
		340						345				350			
Val	Met	Asn	Thr	Tyr	Phe	Gln	Leu	Trp	Met	Thr	Ser	Pro	Asp	Lys	Ile
	355					360						365			
Leu	Ala	Asp	Leu	Ser	Gln	Arg	Phe	Val	Asn	Arg	Lys	Val	Phe	Lys	Ser
	370					375					380				
Ile	Thr	Phe	Ser	Gln	Glu	Asp	Gln	Asp	Gln	Leu	Thr	Ser	Met	Arg	Lys
385				390					395					400	
Leu	Val	Glu	Asp	Ile	Gly	Phe	Asp	Pro	Asp	Tyr	Tyr	Thr	Ala	Ile	His
			405					410					415		
Lys	Asn	Phe	Asp	Leu	Pro	Tyr	Asp	Ile	Tyr	Arg	Pro	Glu	Ser	Gln	Asn

			420					425				430			
Pro	Arg	Thr	Gln	Ile	Glu	Ile	Leu	Gln	Lys	Asn	Gly	Glu	Leu	Ala	Glu
			435					440				445			
Leu	Ser	Ser	Leu	Ser	Pro	Ile	Val	Gln	Ser	Leu	Ala	Gly	Ser	Arg	His
			450					455				460			
Gly	Asp	Asn	Arg	Phe	Tyr	Phe	Pro	Lys	Glu	Met	Leu	Asp	Gln	Asn	Ser
465					470					475					480
Ile	Phe	Ala	Ser	Ile	Thr	Gln	Gln	Phe	Leu	His	Leu	Ile	Glu	Asn	Asp
				485					490					495	
His	Phe	Thr	Pro	Asn	Lys	Asn									
				500											

(2) INFORMATION FOR SEQ ID NO:2742:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...169

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2742:

His	Ala	Phe	Pro	Asp	Gly	Val	Thr	Ile	Asp	Ala	Gln	Phe	Ser	Thr	Leu
1				5					10					15	
Asn	Gly	Arg	Pro	Leu	Thr	Glu	Ala	Thr	Val	Gly	Asp	Asp	Leu	Tyr	Ala
			20					25					30		
Thr	Glu	Thr	Glu	Ser	Pro	Thr	Gln	Thr	Ile	Lys	Val	Gly	Lys	Gln	Gln
			35				40					45			
Met	Asn	Gly	Ser	Thr	Leu	Leu	Asn	Tyr	Ala	Arg	Phe	Arg	Asp	Asp	Asp
	50				55					60					
Glu	Ala	Asp	Tyr	Gly	Arg	Thr	Lys	Arg	Gln	Gln	Gln	Val	Leu	Thr	Ala
65				70					75					80	
Ile	Leu	Glu	Gln	Ile	Lys	Asp	Pro	Thr	Lys	Leu	Phe	Thr	Gly	Ser	Glu
			85					90					95		
Ala	Leu	Gly	Lys	Val	Phe	Ala	Met	Thr	Ser	Thr	Asn	Val	Pro	Tyr	Thr
			100				105						110		
Phe	Leu	Leu	Thr	Asn	Gly	Leu	Ser	Val	Leu	Asp	Gly	Ala	Lys	Asn	Gly
			115				120					125			
Ile	Glu	Lys	Leu	Thr	Ile	Pro	Glu	Leu	Gly	Asp	Trp	Val	Asp	Ala	Tyr
	130				135					140					
Asp	Val	Tyr	Gly	Gly	Leu	Gly	Leu	Leu	Val	Asp	Gln	Asn	Lys	Tyr	Gln
145				150					155						160
Thr	Lys	Leu	Ala	Gln	Met	Gly	Leu	Arg							
				165											

(2) INFORMATION FOR SEQ ID NO:2743:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 327 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...327
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2743:

Gly	Ala	Phe	Pro	Ser	Arg	Glu	Ala	Ile	Ser	Leu	Phe	Asp	Phe	Pro	Ser	1	5	10	15
Phe	Phe	Pro	Ser	Ser	Asn	Leu	Asn	Ile	Trp	Leu	Ser	Thr	Gln	Pro	Ile	20	25	30	
Leu	Ala	Gln	Ile	Tyr	Ala	Phe	Pro	Leu	Ala	Thr	Ala	Thr	Met	Ala	Ala	35	40	45	
Ile	Leu	Ser	Phe	Leu	Phe	Phe	Leu	Ser	Phe	Tyr	Lys	Lys	Asn	Lys		50	55	60	
Gln	Ile	Arg	Phe	Tyr	Ser	Gly	Ile	Leu	Leu	Leu	Ser	Leu	Ile	Leu		65	70	75	80
Leu	Leu	Phe	Gly	Thr	Asp	Lys	Thr	Leu	Ser	Ser	Ala	Ser	Asn	Lys	Thr	85	90	95	
Lys	Thr	Leu	Lys	Leu	Val	Thr	Trp	Asn	Val	Ala	Asn	Gln	Ile	Glu	Ala	100	105	110	
Gln	His	Ile	Glu	Arg	Ile	Phe	Ser	His	Phe	Asp	Ala	Asp	Met	Ala	Ile	115	120	125	
Phe	Pro	Glu	Leu	Ala	Thr	Asn	Ile	Arg	Gly	Glu	Gln	Glu	Asn	Gln	Arg	130	135	140	
Ile	Lys	Leu	Leu	Phe	His	Gln	Val	Gly	Leu	Ser	Met	Ala	Asn	Tyr	Asp	145	150	155	160
Ile	Phe	Thr	Ser	Pro	Pro	Thr	Asn	Ser	Gly	Ile	Ala	Pro	Val	Thr	Val	165	170	175	
Ile	Val	Lys	Lys	Ser	Tyr	Gly	Phe	Tyr	Thr	Glu	Ala	Lys	Thr	Phe	His	180	185	190	
Thr	Thr	Arg	Phe	Gly	Thr	Ile	Val	Leu	His	Ser	Arg	Lys	Gln	Asn	Ile	195	200	205	
Pro	Asp	Ile	Ile	Ala	Leu	His	Thr	Ala	Pro	Pro	Leu	Pro	Gly	Leu	Met	210	215	220	
Glu	Ile	Trp	Lys	Gln	Asp	Leu	Asn	Ile	Ile	His	Asn	Gln	Leu	Ala	Ser	225	230	235	240
Lys	Tyr	Pro	Lys	Ala	Ile	Ile	Ala	Gly	Asp	Phe	Asn	Ala	Thr	Met	Arg	245	250	255	
His	Gly	Ala	Leu	Ala	Lys	Ile	Ser	Ser	His	Arg	Asp	Ala	Leu	Asn	Ala	260	265	270	
Leu	Pro	Pro	Phe	Glu	Arg	Gly	Thr	Trp	Asn	Ser	Gln	Ser	Pro	Lys	Leu	275	280	285	
Phe	Asn	Ala	Thr	Ile	Asp	His	Ile	Leu	Leu	Pro	Lys	Asn	His	Tyr	Tyr	290	295	300	
Val	Lys	Asp	Leu	Asp	Ile	Val	Ser	Phe	Gln	Asn	Ser	Asp	His	Arg	Cys				

305 310 315 320
Ile Phe Thr Glu Ile Thr Phe
 325

(2) INFORMATION FOR SEQ ID NO:2744:

- ```
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 71 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...71

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2744:
```

[illegible]

(2) INFORMATION FOR SEQ ID NO:2745:

- ```
(i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 435 amino acids
      (B) TYPE: amino acid
      (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
      (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:
      (A) NAME/KEY: misc_feature
      (B) LOCATION 1...435

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2745:
```

Met Gln Phe Pro Glu Gly Phe Val Glu Lys Tyr Lys Glu Ile Leu Gly
1 5 10 15

Asp	Glu	Ala	Arg	Asp	Phe	Leu	Ala	Ser	Phe	Glu	Glu	Glu	Ala	Val	Ser			
			20					25					30					
Ala	Phe	Arg	Val	Asn	Pro	Leu	Xaa	Glu	Glu	Gln	Leu	Ser	Phe	Ser	Asp			
		35					40					45						
Ala	Ile	Thr	Gln	Thr	Pro	Trp	Gly	His	Tyr	Gly	Lys	Val	Ser	Gly	Xaa			
	50					55					60							
Ser	Pro	Xaa	His	Ala	Thr	Gly	Leu	Val	Tyr	Xaa	Gln	Glu	Thr	Ala	Ala			
65					70					75					80			
Gln	Met	Val	Ala	Gln	Val	Ala	Gln	Pro	Ser	Pro	Gly	Met	Lys	Val	Leu			
				85					90					95				
Lys	Leu	Ala	Ala	Ala	Pro	Gly	Gly	Lys	Ser	Thr	Gln	Leu	Ala	Ala	Tyr			
			100					105					110					
Leu	Ala	Gly	Glu	Gly	Leu	Leu	Val	Ser	Asn	Glu	Ile	Ser	Ser	Lys	Arg			
		115					120					125						
Ala	Lys	Ile	Leu	Val	Glu	Asn	Met	Glu	Arg	Phe	Gly	Ala	Thr	Asn	Val			
	130					135					140							
Val	Val	Thr	Asn	Glu	Ser	Ala	Asp	Arg	Leu	Val	Lys	Val	Phe	Lys	Gly			
145					150					155					160			
Tyr	Phe	Asp	Leu	Ile	Val	Leu	Asp	Ala	Pro	Cys	Ser	Gly	Glu	Gly	Met			
			165					170						175				
Phe	Arg	Lys	Gln	Pro	Asp	Ala	Met	Asp	Tyr	Trp	Ser	Leu	Asp	Tyr	Pro			
		180					185						190					
Ser	Gln	Cys	Ala	Ser	Leu	Gln	Arg	Glu	Ile	Leu	Trp	Glu	Asp	Ala	Val			
	195					200					205							
Thr	Met	Leu	Ala	Glu	Gly	Gly	His	Leu	Val	Tyr	Ser	Thr	Cys	Thr	Trp			
	210					215					220							
Ala	Pro	Glu	Glu	Asn	Glu	Glu	Ile	Val	Asn	Trp	Leu	Leu	Glu	Glu	Tyr			
225					230					235					240			
Asp	Phe	Asp	Leu	Leu	Pro	Val	Glu	His	Ile	Asn	Gly	Met	Val	Ala	Gly			
			245						250					255				
Ile	Asp	Leu	Pro	Glu	Thr	Ala	Arg	Met	Tyr	Pro	His	Gln	Phe	Lys	Gly			
		260					265						270					
Glu	Gly	Gln	Phe	Val	Ala	His	Leu	Gln	Phe	Lys	Gly	Asn	Asn	Pro	Ala			
	275					280						285						
Pro	Lys	Phe	Lys	Ala	Ser	Lys	Ser	Asn	Leu	Ser	Arg	Glu	Gln	Val	Ala			
	290					295					300							
Leu	Trp	Gln	Glu	Phe	Ala	Gln	Asn	His	Leu	Lys	Val	Asn	Leu	Pro	Gly			
305					310					315					320			
Ile	Leu	Gln	Thr	Phe	Gly	Asp	Gln	Leu	Tyr	Leu	Leu	Pro	Glu	Leu	Leu			
			325						330					335				
Pro	Asp	Leu	Gly	Lys	Leu	Lys	Ile	Ala	Arg	Asn	Gly	Leu	His	Leu	Gly			
		340						345					350					
Thr	Phe	Lys	Lys	Arg	Phe	Glu	Pro	Ser	Phe	Ala	Leu	Gly	Leu	Ala				
	355					360					365							
Leu	Lys	Pro	Ser	Gln	Val	Glu	Gln	Ser	Val	Glu	Ile	Gly	Gln	Glu	Ala			
	370					375					380							
Phe	Val	Lys	Tyr	Ala	Ala	Gly	Glu	Ile	Val	Gln	Leu	Ala	Glu	Ser	Leu			
385					390					395					400			
Pro	Asn	Gly	Trp	Tyr	Gln	Val	Leu	Val	Lys	Gly	Asn	Gly	Leu	Gly	Phe			
			405						410					415				
Ala	Lys	Val	Thr	Gly	Asn	Val	Leu	Lys	Asn	Tyr	Phe	Pro	Lys	Gly	Leu			
		420						425					430					
Arg	Phe	Lys																
		435																

(2) INFORMATION FOR SEQ ID NO:2746:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 119 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...119
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2746:

```

Leu Ser Phe Pro Ile Val Ile Pro Arg Tyr Gln Ala Gly Tyr Leu Arg
1          5          10          15
Val Thr His Pro Phe Ala Thr His Pro Glu Lys Gln Ala Pro Pro Ser
          20          25          30
Ala Phe Tyr Leu His Val Leu Gly Thr Pro Pro Ala Phe Val Leu Ser
          35          40          45
Gln Asp Gln Thr Leu Ile Lys Ser Leu Ser Ser His Ser Phe Leu Ser
          50          55          60
Leu Thr Asp Leu Leu Phe Phe Ser Leu Phe Ser Thr Thr Thr Tyr Val
65          70          75          80
Val Ala Pro Cys Thr Leu Val Arg Leu Val Gln Phe Ser Lys Val Phe
          85          90          95
Val Thr Cys Phe Ser Gln Ala Thr Thr Ile Leu Val Tyr His Ser His
          100         105         110
Phe His Leu Ser Thr Leu Phe
          115

```

(2) INFORMATION FOR SEQ ID NO:2747:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...60
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2747:

```

Ala His Leu Phe Arg Thr Ser Leu Ile Phe Phe Arg Lys Asp Ile Lys
1          5          10          15

```

Val	Ser	Gly	Gly	Lys	Thr	Ser	Leu	Lys	Ser	Gly	Met	Phe	Val	Leu	Ile
		20						25					30		
Lys	Leu	Thr	Lys	Ser	Arg	Ala	Ile	Ser	Phe	Trp	Ser	Glu	Leu	Gly	Arg
		35					40					45			
Phe	Ser	Ile	Ile	Val	Arg	Lys	Ser	Pro	Asn	Ser	Arg				
	50					55					60				

(2) INFORMATION FOR SEQ ID NO:2748:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 255 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2748:

Lys	Glu	Leu	Pro	Ser	Met	Gly	Thr	Phe	Ser	Val	Arg	His	Leu	Asp	Leu
1				5					10					15	
Phe	Tyr	Gly	Asp	Phe	Gln	Ala	Leu	Lys	Asn	Ile	Ser	Ile	Gln	Leu	Pro
		20						25					30		
Glu	Arg	Gln	Ile	Thr	Ala	Leu	Ile	Gly	Pro	Ser	Gly	Cys	Gly	Lys	Ser
		35					40					45			
Thr	Phe	Leu	Lys	Thr	Leu	Asn	Arg	Met	Asn	Asp	Leu	Val	Pro	Ser	Cys
		50				55					60				
His	Ile	Glu	Gly	Gln	Val	Leu	Leu	Asp	Glu	Gln	Asp	Ile	Tyr	Ser	Ser
65					70				75					80	
Lys	Phe	Asn	Leu	Asn	Gln	Leu	Arg	Lys	Arg	Val	Gly	Met	Val	Phe	Gln
		85						90						95	
Gln	Pro	Asn	Pro	Phe	Ala	Met	Ser	Ile	Tyr	Asp	Asn	Val	Ala	Tyr	Gly
		100						105					110		
Pro	Arg	Thr	His	Gly	Ile	Arg	Asp	Lys	Lys	Gln	Leu	Asp	Ala	Leu	Val
		115				120					125				
Glu	Lys	Ser	Leu	Lys	Gly	Ala	Ala	Ile	Trp	Glu	Glu	Val	Lys	Asp	Asp
		130				135					140				
Leu	Lys	Lys	Ser	Ala	Met	Ser	Leu	Ser	Gly	Gly	Gln	Gln	Gln	Arg	Leu
145				150					155					160	
Cys	Ile	Ala	Arg	Ala	Leu	Ala	Val	Glu	Pro	Asp	Ile	Leu	Leu	Met	Asp
		165						170						175	
Glu	Pro	Thr	Ser	Ala	Leu	Asp	Pro	Ile	Ser	Thr	Leu	Lys	Ile	Glu	Asp
		180						185					190		
Leu	Ile	Gln	Gln	Leu	Lys	Lys	Asp	Tyr	Thr	Ile	Ile	Ile	Val	Thr	His
		195				200					205				
Asn	Met	Gln	Gln	Ala	Ser	Arg	Ile	Ser	Asp	Lys	Thr	Ala	Phe	Phe	Leu
	210					215					220				
Thr	Gly	Glu	Ile	Cys	Glu	Phe	Gly	Asp	Thr	Val	Asp	Val	Phe	Thr	Asn

(2) INFORMATION FOR SEQ ID NO:2749:

(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: YES

(A) ORGANISM: *Streptococcus pneumoniae*

(B) LOCATION 1...68

[illegible]

(2) INFORMATION FOR SEQ ID NO:2750:

(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: YES

(A) ORGANISM: *Streptococcus pneumoniae*

(B) LOCATION 1...295

1793

Ile	Phe	Cys	Phe	Thr	Phe	Arg	Phe	Ile	Pro	Leu	Ser	Tyr	His	Ile	Leu
			20					25					30		
Ser	Tyr	Asn	Arg	Ala	Met	Lys	Ile	Thr	Lys	Leu	Glu	Lys	Lys	Lys	Arg
		35					40					45			
Leu	Tyr	Leu	Met	Glu	Leu	Asp	Asn	Gly	Asp	Lys	Cys	Tyr	Ile	Thr	Glu
	50					55					60				
Asp	Thr	Ile	Val	Arg	Phe	Met	Leu	Ser	Arg	Asp	Lys	Val	Ile	Ser	Glu
65					70					75					80
Glu	Glu	Leu	Lys	Glu	Ile	Gln	Asp	Phe	Ala	Gln	Phe	Ser	Tyr	Gly	Lys
				85					90					95	
Asn	Leu	Ala	Leu	Tyr	His	Leu	Ser	Phe	Lys	Ala	Arg	Thr	Glu	Lys	Glu
			100					105					110		
Val	Arg	Glu	Tyr	Leu	Lys	Lys	Tyr	Asp	Ile	Asp	Lys	Asn	Ile	Val	Ser
		115					120					125			
Gln	Val	Ile	Ala	Asn	Leu	Lys	Glu	Asp	Lys	Trp	Ile	Asn	Asp	Gly	Gln
	130					135					140				
Tyr	Ala	Tyr	Ala	Ile	Ile	Asn	Thr	Asn	Gln	Leu	Ser	Gly	Asp	Lys	Gly
145					150					155					160
Pro	Tyr	Val	Leu	Thr	Gln	Lys	Leu	Ala	Gln	Lys	Gly	Ile	Ser	Lys	Ser
				165					170					175	
Thr	Ile	Glu	Glu	Asn	Leu	Lys	Glu	Phe	Asp	Phe	Ser	Glu	Val	Ala	Gln
		180						185					190		
Arg	Val	Ala	Asn	Lys	Leu	Leu	Lys	Lys	Tyr	Glu	Gly	Lys	Leu	Pro	Ala
		195					200					205			
Arg	Ala	Leu	Gln	Asp	Lys	Ile	Ile	Gln	Asn	Leu	Thr	Asn	Lys	Gly	Phe
	210					215					220				
Ser	Tyr	Ser	Asp	Ala	Lys	Ile	Ala	Phe	Asp	Asp	Leu	Asp	Ser	Gln	Val
225					230					235					240
Asp	Gln	Glu	Thr	Thr	Gln	Glu	Leu	Ile	Phe	Lys	Glu	Leu	Asp	Lys	Gln
				245					250					255	
Tyr	Thr	Lys	Tyr	Ala	Arg	Lys	Tyr	Glu	Gly	Tyr	Glu	Leu	Lys	Gln	Arg
			260					265					270		
Leu	Thr	Gln	Val	Leu	Ala	Arg	Lys	Gly	Tyr	Asp	Phe	Ser	Asp	Ile	Ala
		275					280					285			
Ser	Ala	Leu	Arg	Glu	Tyr	Leu									
	290					295									

(2) INFORMATION FOR SEQ ID NO:2751:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...61

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2751:

Ala	Ile	Val	Pro	Arg	Lys	Ala	Arg	Lys	Arg	Arg	Lys	Gly	Trp	Leu	Ala
1				5				10						15	
Lys	Ser	Thr	Ala	Lys	Arg	Leu	Ser	Val	Trp	Phe	Thr	Val	Cys	Arg	Phe
				20				25						30	
Ile	Leu	Val	Leu	Leu	Ser	Met	Leu	Gly	Cys	Ile	Asp	Phe	Thr	Ile	Asp
		35					40					45			
Leu	Ala	Gly	Phe	His	Gln	Val	Ile	Val	Leu	Ala	Asn	Ser			
	50					55					60				

(2) INFORMATION FOR SEQ ID NO:2752:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...359

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2752:

Pro	Gly	Ser	Pro	Ile	Phe	Lys	Lys	Tyr	Arg	Arg	Ile	Lys	Met	Ala	Glu
1				5				10						15	
Ile	Thr	Ala	Lys	Leu	Val	Lys	Glu	Leu	Arg	Glu	Lys	Ser	Gly	Ala	Gly
			20					25					30		
Val	Met	Asp	Ala	Lys	Lys	Ala	Leu	Val	Glu	Thr	Asp	Gly	Asp	Ile	Glu
		35					40					45			
Lys	Ala	Ile	Glu	Leu	Leu	Arg	Glu	Lys	Gly	Met	Ala	Lys	Ala	Ala	Lys
	50					55				60					
Lys	Ala	Asp	Arg	Val	Ala	Ala	Glu	Gly	Leu	Thr	Gly	Val	Tyr	Val	Asn
65				70					75					80	
Gly	Asn	Val	Ala	Ala	Val	Ile	Glu	Val	Asn	Ala	Glu	Thr	Asp	Phe	Val
			85					90						95	
Ala	Lys	Asn	Ala	Gln	Phe	Val	Glu	Leu	Val	Asn	Thr	Thr	Ala	Lys	Val
		100						105					110		
Ile	Ala	Glu	Gly	Lys	Pro	Ala	Asn	Asn	Glu	Glu	Ala	Leu	Ala	Leu	Ile
		115					120					125			
Met	Pro	Ser	Gly	Glu	Thr	Leu	Glu	Ala	Ala	Tyr	Val	Ser	Ala	Thr	Ala
	130					135					140				
Thr	Ile	Gly	Glu	Lys	Ile	Ser	Phe	Arg	Arg	Phe	Ala	Leu	Ile	Glu	Lys
145				150					155					160	
Thr	Asp	Ala	Gln	His	Phe	Gly	Ala	Tyr	Gln	His	Asn	Gly	Gly	Arg	Ile
			165					170						175	
Gly	Val	Ile	Ser	Val	Val	Glu	Gly	Gly	Asp	Glu	Ala	Leu	Ala	Lys	Gln
		180					185					190			
Leu	Ser	Met	His	Ile	Ala	Ala	Met	Lys	Pro	Thr	Val	Leu	Ser	Tyr	Lys
		195					200					205			

Glu	Leu	Asp	Glu	Gln	Phe	Val	Lys	Asp	Glu	Leu	Ala	Gln	Leu	Asn	His
210						215					220				
Val	Ile	Asp	Gln	Asp	Asn	Glu	Ser	Arg	Ala	Met	Val	Asn	Lys	Pro	Ala
225					230					235					240
Leu	Pro	His	Leu	Lys	Tyr	Gly	Ser	Lys	Ala	Gln	Leu	Thr	Asp	Asp	Val
			245						250					255	
Ile	Ala	Gln	Ala	Glu	Ala	Asp	Ile	Lys	Ala	Glu	Leu	Ala	Ala	Glu	Gly
		260					265						270		
Lys	Pro	Glu	Lys	Ile	Trp	Asp	Lys	Ile	Ile	Pro	Gly	Lys	Met	Asp	Arg
	275					280						285			
Phe	Met	Leu	Asp	Asn	Thr	Lys	Val	Asp	Gln	Ala	Tyr	Thr	Leu	Leu	Ala
290					295						300				
Gln	Val	Tyr	Ile	Met	Asp	Asp	Ser	Lys	Thr	Val	Glu	Ala	Tyr	Leu	Glu
305				310					315						320
Ser	Val	Asn	Ala	Ser	Val	Val	Glu	Phe	Ala	Arg	Phe	Glu	Val	Gly	Glu
			325					330						335	
Gly	Ile	Glu	Lys	Ala	Ala	Asn	Asp	Phe	Glu	Ala	Glu	Val	Ala	Ala	Thr
		340				345						350			
Met	Ala	Ala	Ala	Leu	Asn	Asn									
		355													

(2) INFORMATION FOR SEQ ID NO:2753:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...62

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2753:

Gly	Met	Leu	Phe	Arg	Pro	Thr	Pro	Pro	Val	Thr	Ile	Thr	Glu	Thr	Cys
1			5						10					15	
Gly	Ile	Gly	Ala	Leu	Thr	Ala	Glu	Ile	Tyr	Ala	Gly	Leu	Arg	Val	Leu
		20					25					30			
Pro	Gly	Lys	Ser	Leu	Met	Ile	Ser	Leu	Pro	Ala	Ser	Ser	Ala	Val	Val
	35					40					45				
Ile	Ser	Val	Arg	Val	Ile	Gln	Pro	Gly	Met	Tyr	Gly	Val	Leu		
50					55						60				

(2) INFORMATION FOR SEQ ID NO:2754:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...199
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2754:

```

Ser Cys Thr Pro Pro His Leu Pro Arg Pro His Ser Gly Ala Arg Gly
1      5      10      15
Ala Thr Arg Arg Thr Pro Gln Arg Ser Arg Pro Gln Pro Pro Gln Ile
20      25      30
Arg Gly Asn Gln Thr Glu Gln Gln Ala Thr Thr His Ala Pro Pro Pro
35      40      45
Ala Pro Ala His Ala His Pro Pro Gln Pro Arg Ala Arg His Ala Ala
50      55      60
Gln His Arg Gln Gln Gly Asp Glu Pro Pro Pro Arg Thr Gly Pro
65      70      75      80
Pro Gly Pro Arg Pro Ala Thr Pro Ser Pro Pro Gln Gly Glu Lys Thr
85      90      95
Lys Pro Pro Arg Pro Thr Asn Ala Pro Pro Arg Ser Ser Leu Thr Lys
100     105     110
Glu Ile Pro Thr Lys Ser Ile Lys Phe Arg Arg Lys Gly Ile Lys Glu
115     120     125
Arg Ser Gly Arg Ala Thr Phe Asp Asn Phe Asn Gln Cys Ser Lys Pro
130     135     140
His Pro Leu Pro Ser Ile Arg Asn Ile Ile Arg Asn Ile Asn Phe Leu
145     150     155     160
Ser Thr Ser Ile Ser Lys Leu Pro Ile Met Phe Leu Met Cys Phe Lys
165     170     175
Tyr Ile Lys Arg Arg Lys Asn Thr Pro Ile Asp Asn Gly Val Glu Ile
180     185     190
Gly Leu Leu Leu Met Arg Leu
195

```

(2) INFORMATION FOR SEQ ID NO:2755:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 83 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...83

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2755:

Val	Phe	Thr	Pro	Trp	Leu	Leu	Arg	Ser	Asn	Phe	Asn	Ser	Glu	Arg	Ser
1				5					10					15	
Lys	Ser	Thr	Pro	Arg	Ala	Ala	Gly	Lys	Ser	Met	Thr	Thr	Arg	Pro	Thr
			20					25					30		
Arg	Thr	Gly	Lys	Ile	Leu	Asn	Ser	Ile	Leu	Arg	Lys	Asp	Ala	Ala	Gly
		35					40					45			
Lys	Ser	Gly	Lys	Ser	Lys	Tyr	Ile	Ser	Thr	Asn	Glu	Met	Ala	Asp	Lys
	50					55					60				
Ile	Ala	Met	Val	Glu	Ser	Arg	Arg	Val	Phe	Val	Ile	Thr	Gly	Ser	Ser
65					70					75					80
Asn	Phe	Leu													

(2) INFORMATION FOR SEQ ID NO:2756:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...74

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2756:

Thr	Phe	Thr	Pro	Asn	Lys	Ala	Ala	Glu	Ile	Ile	Leu	Lys	Val	Leu	Asn
1				5					10					15	
Ser	Ala	Val	Ala	Asn	Ala	Glu	Asn	Asn	Phe	Gly	Leu	Asp	Lys	Ala	Asn
			20					25					30		
Leu	Val	Val	Ser	Glu	Ala	Phe	Ala	Asn	Glu	Gly	Pro	Thr	Met	Lys	Arg
		35					40					45			
Phe	Arg	Pro	Arg	Ala	Lys	Gly	Ser	Ala	Ser	Pro	Ile	Asn	Lys	Arg	Thr
	50					55					60				
Ala	His	Ile	Thr	Val	Ala	Val	Ala	Glu	Lys						
65					70										

(2) INFORMATION FOR SEQ ID NO:2757:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2757:

```
Val Ile Thr Pro Cys His Pro Pro Thr Lys Asn Pro Asp Lys Ile Ala
1           5           10           15
Gly Val Leu Gln Gly Asn Val Thr Pro Glu Asn Gly Cys Met Lys Pro
          20           25           30
Val Ala Ile Ala Pro Tyr Thr Ile Thr Ala Ala Ser Thr Gly Thr Arg
          35           40           45
Met Lys Gly Thr Asn Ile Thr Gly Phe Met Thr Ile Gly Asn Pro Asn
          50           55           60
Thr Thr Gly Ser Phe Thr Leu Asn Ile Ala Gly Lys Ala Ala Thr Phe
65           70           75           80
Pro Lys Ala Trp Tyr Cys Phe Asp Phe Ala Ala Lys Ser Met Ala Thr
          85           90           95
Thr Arg Pro Asn Val Ile Pro Glu Pro Asp Arg Ile Lys Asn Glu Ser
          100          105          110
Lys Asn Cys
          115
```

(2) INFORMATION FOR SEQ ID NO:2758:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...154

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2758:

```
Phe Leu Ala Pro Ala Gly Ile Ser Ala Asn Glu Val Lys Gln Asp Val
1           5           10           15
Thr Ser Glu Val Val Ile Gly Val Leu Asp Ser Lys Glu Glu Leu Lys
          20           25           30
Glu Ser Glu Asn Asp Ala Pro Lys Leu Glu Thr Pro Leu Arg Glu Glu
          35           40           45
Pro Arg Leu Ala Pro Gln Thr Leu Pro Glu Ala Ser Glu Val Leu Glu
          50           55           60
Asn Lys Arg Glu Glu Ser Lys Val Glu Ile Thr Glu Pro Ala Gln Ala
65           70           75           80
```

```

Asp Asp Ile Arg Lys Val Val Gly Glu Leu Ala Lys Asp Ile Ser Ile
      85          90          95
Thr Lys Leu Tyr Met Thr Gly His Ser Leu Gly Gly Tyr Leu Ala Gln
      100        105        110
Ile Ala Ala Val Glu Asp Tyr Gln Lys Tyr Pro Asp Phe Tyr Asn His
      115          120        125
Val Leu Arg Lys Val Thr Thr Phe Ser Ala Pro Lys Val Ile Thr Ser
      130          135        140
Arg Thr Val Trp Asp Ala Lys Asn Gly Phe
145          150

```

(2) INFORMATION FOR SEQ ID NO:2759:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...178

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2759:

```

Glu Arg Ala Pro Pro Ala Ala Leu Thr Pro Ile Ser Asp Pro Thr Val
1      5      10      15
Ser Arg Ile Asn Leu Thr Ser Ala Ile Val Ala Pro Pro Val Glu Lys
      20      25      30
Pro Val Asp Val Leu Thr Lys Ser Ala Pro Ala Phe Trp Ala Asn Trp
      35      40      45
Gln Thr Thr Ile Phe Ser Trp Ser Val Arg Arg Gln Ala Ser Ile Met
      50      55      60
Thr Phe Thr Asn Leu Ser Pro Leu Ala Ser Thr Thr Ala Arg Ile Ser
65      70      75      80
Asp Ser Thr Lys Ala Lys Leu Pro Asp Leu Arg Ala Pro Thr Leu Ile
      85      90      95
Thr Ile Ser Ile Ser Ser Ala Pro Phe Trp Ile Ala Ser Phe Val Ser
      100     105     110
Asn Ala Phe Thr Ala Glu Val Val Ala Pro Lys Gly Lys Pro Thr Thr
      115     120     125
Val Gln Thr Leu Thr Ser Val Pro Ser Ser Pro Phe Leu Ala Cys Ser
      130     135     140
Thr Gln Val Gly Leu Thr Gln Thr Leu Ala Lys Ser Tyr Ser Leu Ala
145     150     155     160
Ser Asp Asn Lys Leu Ser Ile Cys Phe Phe Cys Ala Ser Cys Leu Pro
      165     170     175
Ser Val

```

(2) INFORMATION FOR SEQ ID NO:2760:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 65 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...65
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2760:

```

Leu Phe Tyr Pro Ile Ser Ile Ser Phe His Tyr Ile Ile Ala Ile Val
1      5      10      15
Phe Phe Phe Met Ile Leu Ile Leu Leu Tyr Arg Phe Asp Thr Val Asn
      20      25      30
Ser Phe Leu Ala Leu Tyr Phe Ile Ile Ser Asn Leu Ile Ile Val Leu
      35      40      45
Phe Leu Ile Lys Phe Asn Tyr Leu Tyr Val Lys Phe Leu Ile Ser Lys
      50      55      60
Lys
65

```

(2) INFORMATION FOR SEQ ID NO:2761:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 132 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...132
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2761:

```

Leu Ile Tyr Pro Val Leu Ile Ser Phe Tyr Tyr Ser Ser Met Asn Tyr
1      5      10      15
Glu Gly Ser Lys Gln Leu Thr Asp Ala Arg Phe Lys Cys Leu Val Gly
      20      25      30
Val Gln Arg Thr Thr Phe Glu Glu Met Leu Ala Val Leu Lys Thr Ala
      35      40      45
Tyr Gln Leu Lys His Ala Lys Gly Gly Arg Lys Pro Lys Leu Ser Leu

```


50		55		60														
Glu	Asp	Leu	Leu	Met	Ala	Thr	Leu	His	Tyr	Val	Arg	Glu	Tyr	Arg	Thr			
65					70					75					80			
Tyr	Glu	Glu	Ile	Ala	Ala	Asp	Phe	Gly	Ile	His	Glu	Ser	Asn	Leu	Leu			
				85					90					95				
Arg	Arg	Ser	Gln	Trp	Val	Glu	Val	Thr	Leu	Val	Gln	Ser	Gly	Val	Thr			
			100					105					110					
Ile	Ser	Arg	Thr	Pro	Leu	Ser	Ser	Glu	Asp	Thr	Val	Met	Ile	Ile	Asp			
		115				120					125							
Ala	Thr	Glu	Val															
130																		

(2) INFORMATION FOR SEQ ID NO:2762:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 85 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...85
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2762:

Lys	Gly	Tyr	Pro	Met	His	Ile	His	Tyr	Asn	Thr	Asn	Gln	Thr	Thr	Leu			
1				5				10					15					
Pro	Leu	Glu	Ile	Ser	Ser	Phe	Leu	Pro	Gln	Asp	His	Leu	Val	Phe	Thr			
			20				25					30						
Ile	Glu	Lys	Val	Val	Asn	Thr	Leu	Glu	Asp	Cys	His	Phe	His	Ala	Phe			
		35			40				45									
Tyr	His	Ala	Phe	Asp	Arg	Pro	Ser	Tyr	His	Pro	Lys	Met	Leu	Val	Ser			
	50				55				60									
Thr	Leu	Leu	Phe	Ala	Tyr	Ser	Gln	Gly	Ile	Phe	Ser	Gly	Arg	Lys	Ile			
65				70				75					80					
Glu	Lys	Trp	Lys	Ser														
				85														

(2) INFORMATION FOR SEQ ID NO:2763:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 176 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...176

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2763:

```
Lys Gly Tyr Pro Met His Ile His Tyr Asn Thr Asn Gln Thr Thr Leu
1      5      10      15
Pro Leu Glu Ile Asn Ser Phe Leu Pro Gln Asp His Leu Val Phe Thr
      20      25      30
Ile Glu Lys Val Val Asn Thr Asp Glu Lys Glu Val Asn His Leu Ile
      35      40      45
Lys Tyr Ala Met Phe Asp Lys Glu Gln Lys Arg Gly Tyr Lys Gln Ser
      50      55      60
Ala Arg Asn Leu Ala Asn Trp His Tyr Asn Asp Lys Glu Asp Ser Tyr
      65      70      75      80
Thr His Pro Asp Gly Trp Tyr Tyr Arg Phe His His Thr Lys Tyr Gln
      85      90      95
Lys Thr Gln Thr Asp Phe Gln Gln Glu Ile Lys Val Tyr Tyr Ala Asp
      100     105     110
Glu Pro Glu Ser Ala Pro Gln Lys Gly Leu Tyr Met Asn Glu Arg Tyr
      115     120     125
Gln Asn Leu Lys Ala Lys Glu Cys Gln Ala Leu Leu Ser Pro Gln Gly
      130     135     140
Arg Gln Ile Phe Ala Gln Arg Lys Ile Asp Val Glu Pro Val Phe Gly
      145     150     155     160
Gln Ile Lys Ala Ser Leu Gly Tyr Lys Arg Cys Asn Leu Arg Gly Lys
      165     170     175
```

(2) INFORMATION FOR SEQ ID NO:2764:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2764:

```
Leu Leu Thr Leu Ser Val Leu Ser Thr Thr Ser Lys Gln Tyr Phe Glu
1      5      10      15
Leu Ser Ala Pro Ser Phe Leu Val Cys Ser Leu Ile Phe Ile Glu Tyr
      20      25      30
Thr Thr Ile Leu Leu Pro Leu Ala Arg Asp Phe Val Tyr Val Glu Gly
      35      40      45
```

Leu Gly Ser Tyr Val Val Glu Leu Phe Cys Ser Phe
 50 55 60

(2) INFORMATION FOR SEQ ID NO:2765:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...208

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2765:

Leu	Cys	Leu	Phe	Ser	Val	Cys	Leu	Ala	Phe	Pro	Arg	Arg	Leu	Phe	Val
1				5					10					15	
Phe	Ala	Asp	Asp	Ser	Leu	Ser	Ala	Asn	Ser	Lys	Val	Val	Ser	Gly	Glu
		20						25					30		
Ala	Gln	Phe	Glu	Asn	Gly	Ser	Ser	Val	Arg	Phe	Gly	Asp	Thr	Gln	Val
		35					40					45			
Asn	Ile	Leu	Ser	Asp	Glu	Val	Leu	Glu	Val	Val	Asn	Pro	Asp	Gly	Ser
	50					55					60				
Val	Asp	Thr	Ile	Glu	Arg	Arg	Ala	Asp	Gly	Val	Tyr	Ile	Asn	Gly	Ala
65				70					75					80	
Phe	Tyr	Met	Ala	Tyr	Gln	Lys	Asn	Glu	Ile	Asp	Leu	Asn	Ile	Ser	Phe
			85						90					95	
Arg	Ser	Tyr	Asp	Pro	Asn	Val	Trp	Asn	Tyr	Val	Asn	Thr	Ile	His	Gly
			100					105					110		
Asn	Lys	Gln	Ala	Asn	Thr	Phe	Ala	Asn	Phe	Met	Thr	Gly	Ala	Gly	Ile
		115					120					125			
Ser	Tyr	Met	Ile	Gly	Arg	Ile	Gly	Ala	Leu	Leu	Gly	Gly	Pro	Trp	Gly
	130					135					140				
Ala	Ile	Ile	Gly	Gly	Ala	Tyr	Phe	Gly	Ile	Gln	Ala	Tyr	Gln	Ser	Tyr
145					150					155				160	
Leu	Asp	Ser	Gln	Ser	Pro	Tyr	Pro	Tyr	Tyr	Ile	Thr	Ser	Thr	Tyr	Ile
			165						170					175	
His	Val	Ala	Gln	Arg	Lys	Trp	Lys	Phe	Ile	Thr	Glu	Tyr	Tyr	Arg	Asn
			180					185					190		
Ser	Asn	Tyr	Thr	Gly	Tyr	Val	Lys	Thr	Val	Thr	Thr	Tyr	Val	Asn	Phe
		195					200						205		

(2) INFORMATION FOR SEQ ID NO:2766:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...131
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2766:

```

Ala Arg His Pro Leu Val Leu Tyr Ser Ser Pro Pro Pro Pro Ser Pro
1          5          10          15
Leu Trp Arg Glu Gly Arg Asp Pro Pro His Pro Pro Ala Gln Pro Ala
20          25          30
Ala Ala Ser Pro Asp Pro Arg Gln Pro Asn Gly Ala Ala Gly His His
35          40          45
Thr Arg Thr Pro Pro Arg Pro Gly Pro Arg Pro Pro Ala Thr Thr Gln
50          55          60
Ser Ala Pro Arg Ser Pro Ala Gln Thr Ala Arg Arg Arg Ala Thr Pro
65          70          75          80
Ala Pro His Gly Thr Pro Gly Pro Pro Pro Arg Asp Pro Gln Pro Pro
85          90          95
Thr Gly Arg Glu Asn Gln Ala Thr Pro Thr His Gln Arg Thr Thr Glu
100         105         110
Val Gln Pro His Gln Arg Asn Ser Asn Lys Val Asn Lys Val Gln Lys
115         120         125
Glu Gly Asn
130

```

(2) INFORMATION FOR SEQ ID NO:2767:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 368 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...368
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2767:

```

Pro Ile Asn Pro Tyr Leu Gln His Arg Cys Thr Ser Tyr Leu Gly Gly
1          5          10          15
Ser Val Met Asn Lys Lys Gln Trp Leu Gly Leu Gly Leu Val Ala Val
20          25          30

```

Ala	Ala	Val	Gly	Leu	Ala	Ala	Cys	Gly	Asn	Arg	Ser	Ser	Arg	Asn	Ala
	35						40					45			
Ala	Ser	Ser	Ser	Asp	Val	Lys	Thr	Lys	Ala	Ala	Ile	Val	Thr	Asp	Thr
	50					55					60				
Gly	Gly	Val	Asp	Asp	Lys	Ser	Phe	Asn	Gln	Ser	Ala	Trp	Glu	Gly	Leu
65					70				75					80	
Gln	Ala	Trp	Gly	Lys	Glu	His	Asn	Leu	Ser	Lys	Asp	Asn	Gly	Phe	Thr
			85						90				95		
Tyr	Phe	Gln	Ser	Thr	Ser	Glu	Ala	Asp	Tyr	Ala	Asn	Asn	Leu	Gln	Gln
		100						105					110		
Ala	Ala	Gly	Ser	Tyr	Asn	Leu	Ile	Phe	Gly	Val	Gly	Phe	Ala	Leu	His
	115						120					125			
Asn	Ala	Val	Glu	Glu	Ala	Ala	Lys	Glu	His	Thr	Asp	Leu	Asn	Tyr	Val
	130					135					140				
Leu	Ile	Asp	Asp	Val	Ile	Lys	Asp	Gln	Lys	Asn	Val	Ala	Ser	Val	Thr
145					150					155					160
Phe	Ala	Asp	Asn	Glu	Ser	Gly	Tyr	Leu	Ala	Gly	Val	Ala	Ala	Ala	Lys
				165					170					175	
Thr	Thr	Lys	Thr	Lys	Gln	Val	Gly	Phe	Val	Gly	Gly	Ile	Glu	Ser	Glu
		180						185					190		
Val	Ile	Ser	Arg	Phe	Glu	Ala	Gly	Phe	Lys	Ala	Gly	Val	Ala	Ser	Val
	195						200					205			
Asp	Pro	Ser	Ile	Lys	Val	Gln	Val	Asp	Tyr	Ala	Gly	Ser	Phe	Gly	Asp
	210					215					220				
Ala	Ala	Lys	Gly	Lys	Thr	Ile	Ala	Ala	Ala	Gln	Tyr	Ala	Ala	Gly	Ala
225					230					235					240
Asp	Ile	Val	Tyr	Gln	Val	Ala	Gly	Gly	Thr	Gly	Ala	Gly	Val	Phe	Ala
				245					250					255	
Glu	Ala	Lys	Ser	Leu	Asn	Glu	Ser	Arg	Pro	Glu	Asn	Glu	Lys	Val	Trp
		260						265					270		
Val	Ile	Gly	Val	Asp	Arg	Asp	Gln	Glu	Ala	Glu	Gly	Lys	Tyr	Thr	Ser
	275						280					285			
Lys	Asp	Gly	Lys	Glu	Ser	Asn	Phe	Val	Leu	Val	Ser	Thr	Leu	Lys	Gln
	290					295					300				
Val	Gly	Thr	Thr	Val	Lys	Asp	Ile	Ser	Asn	Lys	Ala	Glu	Lys	Gly	Glu
305					310					315					320
Phe	Pro	Gly	Gly	Gln	Val	Ile	Val	Tyr	Ser	Leu	Lys	Asp	Lys	Gly	Val
				325					330					335	
Asp	Leu	Ala	Val	Thr	Asn	Leu	Ser	Glu	Glu	Gly	Lys	Lys	Ala	Val	Glu
		340						345					350		
Asp	Ala	Lys	Ala	Lys	Ile	Leu	Asp	Gly	Ser	Val	Lys	Val	Pro	Glu	Lys
	355						360					365			

(2) INFORMATION FOR SEQ ID NO:2768:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2768:

Gln	Met	Asn	Pro	Ile	Gln	Arg	Ser	Trp	Ala	Tyr	Val	Ser	Arg	Lys	Arg
1				5					10					15	
Leu	Arg	Ser	Phe	Ile	Leu	Phe	Leu	Ile	Leu	Leu	Val	Leu	Leu	Ala	Gly
			20					25					30		
Ile	Ser	Ala	Cys	Leu	Thr	Leu	Met	Lys	Ser	Asn	Lys	Thr	Val	Glu	Ser
		35					40					45			
Asn	Leu	Tyr	Lys	Ser	Leu	Asn	Thr	Ser	Phe	Ser	Ile	Lys	Lys	Ile	Glu
	50					55					60				
Asn	Gly	Gln	Thr	Phe	Lys	Leu	Ser	Asp	Leu	Ala	Ser	Val	Ser	Lys	Ile
65					70					75					80
Lys	Gly	Leu	Glu	Asn	Val	Ser	Pro	Glu	Leu	Glu	Thr	Val	Ala	Lys	Leu
				85					90					95	
Lys	Asp	Lys	Glu	Ala	Val	Thr	Gly	Glu	Gln	Ser	Val	Glu	Arg	Asp	Asp
			100					105					110		
Leu	Ser	Ala	Ala	Asp	Asn	Asn	Leu	Val	Ser	Leu	Thr	Ala	Leu	Glu	Asp
		115					120					125			
Ser	Ser	Lys	Asp	Val	Thr	Phe	Thr	Ser	Ser	Ala	Phe	Asn	Leu	Lys	Glu
	130					135					140				
Gly	Arg	His	Leu	Gln	Lys	Gly	Asp	Ser	Lys	Lys	Ile	Leu	Ile	His	Glu
145					150					155					160
Glu	Leu	Ala	Lys	Lys	Asn	Gly	Leu	Ser	Leu	His	Asp	Lys	Ile	Gly	Leu
				165					170					175	
Asp	Ala	Gly	Gln	Ser	Glu	Ser	Gly	Lys	Gly	Gln	Thr	Val	Glu	Phe	Glu
			180					185					190		
Ile	Ile	Gly	Ile	Phe	Ser	Gly	Lys	Lys	Gln	Glu	Lys	Phe	Thr	Gly	Leu
		195					200					205			
Ser	Ser	Asp	Phe	Ser	Glu	Asn	Gln	Val	Phe	Thr	Asp	Tyr	Glu	Ser	Ser
	210					215					220				
Gln	Thr	Leu	Leu	Gly	Asn	Ser	Glu	Ala	Gln	Val	Ser	Ala	Ala	Arg	Phe
225					230					235					240
Tyr	Val	Glu	Asn	Pro	Lys	Glu	Met	Asp	Gly	Leu	Met	Lys	Gln	Val	Glu
				245					250					255	
Asn	Leu	Ala	Leu	Glu	Asn	Gln	Gly	Tyr	Gln	Val	Glu	Lys	Glu	Asn	Lys
		260						265					270		
Ala	Phe	Glu	Gln	Ile	Lys	Asp	Ser	Val	Ala	Thr	Phe	Gln	Thr	Phe	Leu
		275					280					285			
Thr	Ile	Phe	Leu	Tyr	Gly	Met	Leu	Ile	Ala	Gly	Ala	Gly	Ala	Leu	Ile
	290					295					300				
Leu	Val	Leu	Ser	Leu	Trp	Leu	Arg	Glu	Arg	Val	Tyr	Glu	Val	Gly	Ile
305					310					315					320
Leu	Leu	Ala	Leu	Gly	Lys	Gly	Lys	Ser	Ser	Ile	Phe	Leu	Gln	Phe	Cys
				325					330					335	
Leu	Glu	Val	Val	Leu	Val	Ser	Leu	Gly	Ala	Leu	Leu	Pro	Ala	Phe	Val
			340					345					350		
Ala	Gly	Asn	Gly	Ile	Thr	Thr	Tyr	Leu	Leu	Gln	Thr	Leu	Leu	Ala	Ser
		355					360					365			
Gly	Asp	Gln	Ala	Ser	Leu	Gln	Asp	Thr	Leu	Ala	Lys	Ala	Ser	Ser	Leu
	370					375					380				
Ser	Thr	Ser	Ile	Leu	Ser	Phe	Ala	Glu	Ser	Tyr	Val	Phe	Leu	Val	Leu
385					390					395					400
Leu	Ser	Cys	Leu	Ser	Val	Ala	Leu	Cys	Phe	Leu	Phe	Leu	Phe	Arg	Lys

				405					410					415
Ser	Pro	Lys	Glu	Ile	Leu	Ser	Ser	Ile	Ser					
				420				425						

(2) INFORMATION FOR SEQ ID NO:2769:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...391

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2769:

Leu	Lys	Asp	Pro	Ile	Gln	Leu	Leu	Glu	Leu	Ser	His	Thr	Gln	Gly	Gln
1				5				10						15	
Leu	Thr	Asp	Glu	Gln	Leu	Phe	Trp	Leu	Gln	Cys	Leu	Leu	Asn	Leu	Ser
			20					25					30		
Gln	Thr	Asn	Asn	Leu	Val	Lys	Ile	Lys	Lys	Ile	Glu	Glu	His	Lys	Tyr
			35				40					45			
Asp	Tyr	Lys	Thr	Glu	Cys	Asn	Ser	Val	Leu	Gln	Phe	Leu	Leu	Asp	Lys
			50			55					60				
Thr	Val	Asn	Ser	Glu	Gly	Arg	Ile	Thr	Ser	Ser	Thr	Glu	Phe	Gly	Asn
65					70				75						80
Phe	Val	Ser	Asn	Leu	Ser	Phe	Gln	His	Gly	Ile	Ala	Gly	Leu	Leu	Phe
				85					90					95	
Pro	Leu	Asn	Lys	Leu	Tyr	Pro	Pro	Glu	Leu	Asp	Ser	Lys	Ile	Leu	Ser
			100					105					110		
Ile	Ile	Lys	Lys	Ala	Val	Thr	Ile	Arg	Thr	Thr	His	Thr	Tyr	Glu	Tyr
		115					120				125				
Gln	Tyr	Ser	Leu	Leu	Phe	Gly	Asp	Ala	Gly	Tyr	Leu	Trp	Leu	Leu	Leu
	130					135					140				
His	Leu	Phe	Ser	Ile	Ser	Lys	Asn	Gln	Tyr	Tyr	Leu	Gln	Leu	Ala	Asn
145					150				155						160
Val	Thr	Ala	Lys	Lys	Leu	Ile	Glu	Asn	Tyr	Asp	Thr	Leu	Glu	Glu	Ile
				165					170					175	
Asp	Phe	Ala	Leu	Gly	Lys	Ser	Gly	Val	Leu	Leu	Ser	Leu	Ile	Lys	Tyr
			180					185					190		
Tyr	Gln	Phe	Thr	Asn	Asp	Asn	Thr	Leu	Lys	Ile	Phe	Ile	His	Asn	Ser
		195					200					205			
Ile	Gly	Glu	Ile	Tyr	His	Tyr	Phe	Leu	Gln	Arg	Asp	Thr	Ala	Lys	Glu
	210					215					220				
Ser	Ile	Leu	Asp	Tyr	Ser	Phe	Ala	His	Gly	Tyr	Cys	Gly	Ile	Ala	Tyr
225					230					235					240
Ala	Leu	Phe	Ala	Tyr	Ser	Lys	Val	Leu	Glu	Pro	Ser	Met	Phe	Tyr	Asn
			245						250					255	
Asp	Leu	His	Thr	Phe	His	Thr	Glu	Leu	Lys	Lys	Leu	Leu	Glu	Lys	Val

(2) INFORMATION FOR SEQ ID NO:2771:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...99

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2771:

Val	Arg	Ser	Pro	Arg	Ile	Val	Phe	Ala	Asn	Lys	Met	Asp	Lys	Ile	Gly
1			5						10					15	
Ala	Asp	Phe	Leu	Tyr	Ser	Val	Ser	Thr	Leu	His	Asp	Arg	Leu	Gln	Ala
			20					25					30		
Asn	Ala	His	Pro	Ile	Gln	Leu	Pro	Ile	Gly	Ser	Glu	Asp	Asp	Phe	Arg
		35					40				45				
Gly	Ile	Ile	Asp	Leu	Ile	Lys	Met	Lys	Ala	Glu	Ile	Tyr	Thr	Asn	Asp
	50					55			60						
Leu	Gly	Thr	Asp	Ile	Leu	Glu	Glu	Asp	Ile	Pro	Ala	Glu	Tyr	Leu	Asp
65					70				75					80	
Gln	Ala	Gln	Glu	Tyr	Arg	Glu	Lys	Leu	Ile	Glu	Ala	Val	Ala	Glu	Thr
			85					90						95	
Asp	Glu	Asn													

(2) INFORMATION FOR SEQ ID NO:2772:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...74

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2772:

Gln	Val	Gly	Pro	Glu	Val	Gln	Leu	Val	Phe	Leu	Asp	Pro	Pro	Tyr	Thr
1				5					10					15	
Lys	Glu	Gln	Ile	Val	Ala	Asp	Ile	Glu	Lys	Met	Ala	Glu	Arg	Glu	Leu
			20					25					30		
Phe	Ser	Glu	Asp	Val	Met	Val	Val	Cys	Glu	Thr	Asp	Lys	Ala	Val	Glu
		35					40					45			
Leu	Pro	Glu	Glu	Ile	Ala	Cys	Leu	Gly	Ile	Trp	Lys	Glu	Lys	Ile	Tyr
	50					55					60				
Gly	Ile	Ser	Lys	Val	Thr	Val	Tyr	Val	Arg						
65					70										

(2) INFORMATION FOR SEQ ID NO:2773:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...182

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2773:

Ile	Lys	Thr	Phe	Val	Ser	Ala	Asn	Leu	Leu	Glu	Ile	Phe	Ser	Asn	Thr
1				5					10					15	
Ile	Trp	Val	Ser	Ser	Ile	Ile	Leu	Val	Phe	Val	Thr	Glu	Leu	Leu	Asn
			20					25					30		
Lys	Thr	Glu	Ser	Tyr	Trp	Gly	Tyr	Ser	Asn	Thr	Ala	Tyr	Ser	Ile	Gly
		35					40					45			
Ile	Ile	Ile	Ser	Gly	Leu	Ile	Ala	Phe	Arg	Leu	Ser	Glu	Lys	Phe	Leu
	50				55					60					
Ala	Ala	Lys	Trp	Glu	Ser	Ile	Leu	Phe	Pro	Leu	Val	Ala	Met	Ala	Ile
65					70				75					80	
Val	Thr	Leu	Thr	Ile	Leu	Tyr	Phe	Pro	Asn	Ala	Gln	Met	Phe	Leu	Leu
			85					90					95		
Phe	Ser	Ala	Leu	Val	Gly	Met	Leu	Ser	Gln	Leu	Lys	Glu	Val	Pro	Glu
		100					105						110		
Ser	Val	Phe	Leu	Gln	Glu	Thr	Val	Glu	Glu	Asn	His	Leu	Val	Asn	Val
		115					120					125			
Tyr	Ser	Val	Leu	Glu	Val	Ile	Ser	Thr	Leu	Ala	Phe	Ser	Val	Phe	Val
	130					135				140					
Leu	Leu	Met	Ser	Tyr	Ile	Thr	Glu	Ser	Phe	Gly	Ile	Ser	Ile	Ser	Phe
145					150					155				160	
Trp	Leu	Ser	Ala	Ile	Cys	Leu	Met	Ile	Glu	Ala	Ile	Leu	Ile	Tyr	Ile
			165					170					175		
Arg	Arg	Asp	Tyr	Phe	Lys										
			180												

(2) INFORMATION FOR SEQ ID NO:2774:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 300 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...300
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2774:

```

Val Tyr Met Leu Leu Glu Ile Ser Ile Lys Asn Phe Ala Ile Ile Glu
1      5      10      15
Ala Ile Ser Leu Asn Phe Glu Lys Gly Met Thr Val Leu Thr Gly Glu
20      25      30
Thr Gly Ala Gly Lys Ser Ile Ile Asp Ala Met Asn Met Met Leu
35      40      45
Gly Ala Arg Ala Thr Thr Asp Val Ile Arg His Gly Ala Pro Lys Ala
50      55      60
Glu Ile Glu Gly Leu Phe Ser Val Glu Asn Ser Arg Leu Leu Gln Glu
65      70      75      80
Ile Phe Asp Glu Gln Gly Leu Glu Leu Gly Asp Glu Ile Ile Ile Arg
85      90      95
Arg Glu Ile Leu Gln Asn Gly Arg Ser Ile Ser Arg Val Asn Gly Gln
100     105     110
Met Val Asn Leu Ser Val Leu Arg Ala Ile Gly Gln His Leu Val Asp
115     120     125
Ile His Gly Gln His Asp His Glu Glu Leu Met Arg Pro Gln Leu His
130     135     140
Ile Gln Met Leu Asp Glu Phe Gly Asp Ala Ala Phe Trp Asp Leu Lys
145     150     155     160
Glu Thr Tyr Gln Thr Ser Phe Asp Ala Tyr Arg Lys Met Arg Lys Gln
165     170     175
Val Leu Glu Val Lys Lys Asn Gln Gln Glu His Lys Ala Arg Ile Glu
180     185     190
Met Leu Glu Phe Gln Met Ala Glu Ile Glu Ala Ala Asn Leu Gln Ala
195     200     205
Gly Glu Asp Leu Asp Leu Asn Gln Glu Arg Asp Lys Leu Leu Asn His
210     215     220
Lys Asn Ile Ala Asp Thr Leu Thr Asn Ala Tyr Ser Met Leu Asp Asn
225     230     235     240
Glu Asp Phe Ser Ser Leu Ala Asn Val Arg Ser Ala Met Asn Asp Met
245     250     255
Glu Ser Val Glu Glu Tyr Asp Pro Glu Tyr Arg Glu Ile Ser Ser Ser
260     265     270
Leu Ser Glu Thr Tyr Tyr Val Leu Glu Asp Ile Ser Lys Arg Leu Glu
275     280     285
Ala Ile Ile Glu Asp Leu Asp Phe Asp Gly Asn Arg

```

(2) INFORMATION FOR SEQ ID NO:2775:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 664 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...664

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2775:

```

Ile Ser Met Phe Arg Leu Thr Asn Lys Leu Ala Val Ser Asn Leu Ile
1      5      10      15
Lys Asn Arg Lys Leu Tyr Tyr Pro Phe Ala Leu Ala Val Leu Leu Ala
20      25      30
Val Thr Leu Thr Tyr Leu Phe Tyr Ser Leu Thr Phe Asn Pro Lys Ile
35      40      45
Ala Glu Ile Arg Gly Gly Thr Thr Ile Gln Ala Thr Leu Gly Phe Gly
50      55      60
Met Phe Val Val Thr Leu Ala Ser Ala Ile Ile Val Leu Tyr Ala Asn
65      70      75      80
Ser Phe Val Met Lys Lys Arg Ser Lys Glu Leu Gly Ile Tyr Gly Met
85      90      95
Leu Gly Leu Glu Lys Arg His Leu Ile Ser Met Thr Phe Lys Glu Leu
100     105     110
Val Val Phe Gly Ile Leu Thr Val Gly Ala Gly Ile Gly Ile Gly Ala
115     120     125
Leu Phe Asp Lys Leu Ile Phe Ala Phe Leu Leu Lys Leu Met Lys Leu
130     135     140
Lys Val Glu Leu Val Ala Thr Phe Gln Thr Lys Val Val Ile Thr Val
145     150     155     160
Leu Val Val Phe Gly Leu Ile Phe Leu Gly Leu Met Phe Leu Asn Ala
165     170     175
Leu Arg Ile Ala Arg Met Asn Ala Leu Gln Leu Ser Arg Glu Lys Ala
180     185     190
Ser Gly Glu Lys Lys Gly Arg Phe Leu Pro Leu Gln Thr Ile Leu Gly
195     200     205
Ser Ile Ser Leu Gly Ile Gly Tyr Tyr Leu Ala Leu Thr Val Lys Asp
210     215     220
Pro Leu Thr Ala Leu Thr Thr Phe Phe Ile Ala Val Leu Leu Val Ile
225     230     235     240
Phe Gly Thr Tyr Leu Leu Phe Asn Ala Gly Ile Thr Val Phe Leu Gln
245     250     255
Ile Leu Lys Lys Asn Lys Lys Tyr Tyr Tyr Gln Pro Asn Asn Leu Ile
260     265     270
Ser Val Ser Asn Leu Ile Phe Arg Met Lys Lys Asn Ala Val Gly Leu

```


- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...63
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2776:

Thr	Phe	Met	Phe	Leu	Ser	Val	Phe	Ser	Phe	Ser	Leu	Pro	Leu	Phe	Gln
1				5					10					15	
Glu	Leu	Phe	Leu	Ile	Gln	Phe	Tyr	Tyr	Ser	Tyr	Ser	Ser	Phe	Phe	Leu
			20					25					30		
Arg	Ser	Ile	Lys	Asp	Leu	Arg	Lys	Tyr	Asn	Gln	Asn	Gly	Tyr	Leu	Ser
		35					40					45			
Ser	Thr	Gln	Pro	Ser	Ser	Phe	Ser	Ser	Tyr	Pro	Phe	His	Asn	Phe	
	50					55					60				

(2) INFORMATION FOR SEQ ID NO:2777:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 70 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...70
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2777:

Ile	Ser	Met	Phe	Ser	Leu	Val	Leu	Ile	Leu	Thr	Ile	Gln	Glu	Ile	Ser
1				5					10					15	
Arg	Thr	Leu	Tyr	Asn	Phe	Gln	Ser	Asn	Lys	Leu	His	Ser	Phe	Ser	Gln
			20					25					30		
Ala	Gly	Ile	Leu	Val	Trp	Ile	Asn	Lys	Lys	Phe	Arg	Lys	Phe	Lys	Asn
		35					40					45			
Arg	Lys	Glu	Asn	Lys	Ser	Tyr	Gly	Lys	Arg	Tyr	Ser	Cys	Leu	Thr	Leu
	50					55					60				
Leu	Pro	Leu	Tyr	Ser	Asn										
65					70										

(2) INFORMATION FOR SEQ ID NO:2778:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 115 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2778:

```
Ser Leu Met Leu Glu Gln Ala Phe Lys Glu Lys His Tyr Glu Asn Thr
1          5          10          15
Ile Leu His Ser Asp Gln Gly Trp Gln Tyr Gln His Asp Ser Tyr His
20          25          30
Arg Phe Leu Glu Ser Lys Gly Ile Gln Ala Ser Met Ser Arg Lys Gly
35          40          45
Asn Ser Gln Asp Asn Gly Arg Met Glu Ser Phe Phe Gly Ile Leu Lys
50          55          60
Ser Glu Met Phe Tyr Gly Tyr Glu Gln Thr Phe Lys Ser Leu Asn Gln
65          70          75          80
Leu Glu Gln Ala Ile Ile Asp Tyr Ile Asp Tyr Tyr Asn Asn Lys Arg
85          90          95
Ile Lys Ile Lys Leu Lys Gly Leu Ser Ser Val Gln Tyr Arg Thr Lys
100          105          110
Ser Phe Gly
115
```

(2) INFORMATION FOR SEQ ID NO:2779:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 262 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...262

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2779:

```
Pro Cys Phe Pro Lys Ile Arg Arg Ser Glu Gly Ser Gly Thr Phe Tyr
1          5          10          15
Arg Gln Ser Ser Lys Asn Cys Asn Gly Ser Thr Asn Leu Gly Glu Met
```

		20					25				30				
Met	Lys	Glu	Gln	Asn	Thr	Ile	Glu	Ile	Asp	Val	Phe	Gln	Val	Leu	Lys
		35					40					45			
Thr	Leu	Trp	Lys	His	Lys	Leu	Ile	Ile	Leu	Leu	Val	Ala	Leu	Val	Thr
		50				55					60				
Gly	Ala	Gly	Ala	Phe	Ala	Tyr	Ser	Thr	Phe	Ile	Val	Lys	Pro	Glu	Tyr
65					70					75				80	
Thr	Ser	Thr	Thr	Arg	Ile	Tyr	Val	Val	Asn	Arg	Asn	Gln	Glu	Gly	Lys
				85					90				95		
Ser	Gly	Leu	Thr	Asn	Gln	Asp	Leu	Gln	Ala	Gly	Thr	Tyr	Leu	Val	Lys
			100					105					110		
Asp	Tyr	Arg	Glu	Ile	Ile	Leu	Ser	Gln	Asp	Val	Leu	Glu	Lys	Val	Ala
		115					120					125			
Thr	Asn	Leu	Lys	Leu	Asp	Met	Pro	Ala	Lys	Ala	Leu	Thr	Ser	Lys	Val
		130				135					140				
Gln	Val	Thr	Val	Pro	Thr	Asp	Thr	Arg	Ile	Val	Ser	Ile	Ser	Val	Lys
145					150					155				160	
Asp	Lys	Glu	Pro	Glu	Glu	Ala	Ser	Arg	Ile	Ala	Asn	Ser	Leu	Arg	Glu
				165					170					175	
Val	Ala	Ala	Gly	Lys	Ile	Val	Ala	Val	Thr	Arg	Val	Ser	Asp	Val	Thr
			180					185					190		
Thr	Leu	Glu	Glu	Ala	Arg	Pro	Ala	Thr	Thr	Pro	Ser	Ser	Pro	Asn	Val
		195					200					205			
Arg	Arg	Asn	Thr	Leu	Val	Gly	Phe	Leu	Gly	Gly	Ala	Val	Val	Thr	Val
		210				215					220				
Ile	Thr	Val	Leu	Leu	Ile	Glu	Leu	Leu	Asp	Thr	Arg	Val	Lys	Arg	Pro
225					230					235				240	
Glu	Glu	Val	Glu	Glu	Val	Leu	Gln	Val	Pro	Leu	Leu	Gly	Val	Val	Pro
				245					250					255	
Asp	Leu	Asp	Lys	Met	Lys										
				260											

(2) INFORMATION FOR SEQ ID NO:2780:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2780:

Lys	Ile	Phe	Pro	Gly	Leu	Asp	Xaa	Tyr	Asp	Phe	Asp	Ala	Ala	Lys	Leu
1				5				10						15	
Asn	Lys	Lys	Ile	Gly	Phe	Trp	Gly	Ser	Lys	Phe	Phe	Ile	Gly	Phe	Ile
			20					25					30		

Leu Gly Ile Val Ile Gly Ile Met Gly Thr Pro His Pro Ile Ala Gly
 35 40 45
 Val Ala Asp Ala Asp Lys Trp Arg Leu Val Ile Lys Gly Trp Leu Ser
 50 55 60
 Leu Gly Leu Thr Ala Gly Val Ser Leu Glu Leu Phe Ser Leu Ile Gly
 65 70 75 80
 Ser Trp Phe Ile Ala Ala Val Glu Pro Leu Ser Gln Gly Ile Thr Asn
 85 90 95
 Val Ala Thr Lys Arg Leu Gln Gly Arg Lys Phe Asn Ile Gly Leu Asp
 100 105 110
 Trp Pro Phe Ile Ala Gly Arg Ala Glu Ile Trp Ala Cys Ala Asn Val
 115 120 125
 Leu Ala Pro Ile Met Leu Ile Glu Ala Val Leu Leu Ser Lys Val Gly
 130 135 140
 Asn Gly Ile Leu Pro Leu Ala Gly Ile Ile Ala Arg Gly Val Thr Pro
 145 150 155 160
 Ala Leu Leu Val Val Thr Arg Gly Lys Leu Leu Arg Met Ile Ile Phe
 165 170 175
 Gly Thr Leu Leu Leu Pro Leu Phe Leu Leu Ser Gly Thr Leu Ile Ala
 180 185 190
 Pro Phe Ala Thr Glu Leu Ala Lys Gly Val Gly Ala Phe Pro Glu Gly
 195 200 205
 Val Ser Gln Thr Gln Leu Ile Thr His Ser Thr Leu Glu Gly Pro Ile
 210 215 220
 Glu Lys Leu Leu Gly Trp Thr Ile Gly Asn Thr Thr Thr Gly Asp Ile
 225 230 235 240
 Lys Ala Ile Leu Gly Ala Val Ala Phe Leu Val Phe Tyr Ile Gly Ile
 245 250 255
 Phe Ala Trp Tyr Arg Lys Gln Met Ile Lys Arg Asn Glu Glu Tyr Ala
 260 265 270
 Ala Lys Ala Lys
 275

(2) INFORMATION FOR SEQ ID NO:2781:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...65

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2781:

Thr Ser Leu Pro Ile Thr Ala Gln Cys Tyr Arg Ile Lys His Leu Thr
 1 5 10 15
 Gln Phe Thr Pro His Cys Leu Asp Arg Leu Phe Gln Ser Ser Ala Leu
 20 25 30

Val Ser Leu Leu Arg Pro Ser Ile Thr Thr Tyr Ser Ser Thr Gly Ile
35 40 45
Ser Thr Cys Cys Pro Ser Asp Thr Pro Phe Gly Leu Ser Leu Gly Pro
50 55 60
Asp
65

(2) INFORMATION FOR SEQ ID NO:2782:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 211 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...211

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2782:

Ser Lys Met Phe His Lys Glu Leu Leu Lys Leu Tyr Phe Ile Cys Gly
1 5 10 15
Thr Thr Thr Cys Gln Gly Lys Asn Leu Tyr Thr Val Val Glu Glu Ala
20 25 30
Leu Lys Gly Gly Ile Thr Leu Phe Gln Phe Arg Glu Lys Gly Glu Ser
35 40 45
Ala Leu Glu Gly Leu Glu Lys Leu Glu Leu Ala Ile Gln Ile Lys Glu
50 55 60
Leu Cys Lys Lys Tyr Asn Val Pro Phe Ile Val Asn Asp Asp Ile Asp
65 70 75 80
Leu Ala Met Glu Ile Asp Ala Asp Gly Val His Val Gly Gln Asp Asp
85 90 95
Ile Gly Val Asp Glu Ile Arg Lys Leu Met Pro Asp Lys Ile Ile Gly
100 105 110
Leu Ser Ile Arg Asn Glu Glu Glu Phe Gln Gln Ser Lys Val Glu Tyr
115 120 125
Val Asp Tyr Val Gly Val Gly Pro Val Phe Asp Thr Gln Ser Lys Asp
130 135 140
Asp Ala Gly Gly Ala Ile Gly Tyr Glu Gly Leu Glu Leu Met Arg Lys
145 150 155 160
Leu Leu Pro Gln Met Pro Leu Val Ala Ile Gly Gly Ile Gln Thr Lys
165 170 175
His Ile Lys Asp Ile Ile Lys Thr Asn Val Asp Gly Val Ser Ile Ile
180 185 190
Ser Ala Ile Ser Tyr Ala Lys Asn Ile Glu Lys Thr Val Arg Glu Met
195 200 205
Ser Glu Gln
210

(2) INFORMATION FOR SEQ ID NO:2783:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 443 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...443

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2783:

Arg	Arg	Met	Phe	Leu	Glu	Arg	Trp	Cys	Leu	Gln	Met	Ser	Gln	Thr	Tyr
1			5					10						15	
Gln	Ile	Lys	Gln	Asn	Asp	Ile	Val	Val	Asp	Leu	Pro	Lys	Thr	Val	Gly
			20					25					30		
Ala	Gly	Tyr	Gly	Gln	Phe	Trp	Arg	Ser	Arg	Ser	Leu	Tyr	Arg	Val	Val
		35					40					45			
Lys	Gly	Ser	Arg	Gly	Ser	Lys	Lys	Ser	Lys	Thr	Thr	Ala	Leu	Asn	Tyr
	50					55				60					
Val	Ile	Arg	Leu	Leu	Lys	Tyr	Pro	Trp	Ala	Asn	Leu	Leu	Val	Ile	Arg
65					70					75					80
Arg	Tyr	Ser	Asn	Thr	Asn	Lys	Gln	Ser	Thr	Tyr	Thr	Asp	Phe	Lys	Trp
			85						90					95	
Ala	Cys	Asn	Val	Leu	Gly	Val	Thr	His	Leu	Phe	Lys	Phe	Asn	Glu	Ser
			100					105					110		
Leu	Pro	Glu	Ile	Thr	Ile	Lys	Ala	Thr	Gly	Gln	Lys	Ile	Leu	Phe	Arg
		115					120						125		
Gly	Leu	Asp	Asp	Glu	Leu	Lys	Ile	Thr	Ser	Ile	Thr	Val	Asp	Ile	Gly
	130					135					140				
Ser	Leu	Cys	Trp	Ala	Trp	Phe	Glu	Glu	Ala	Tyr	Gln	Ile	Glu	Thr	Glu
145					150					155					160
Asp	Lys	Phe	Ser	Thr	Val	Val	Glu	Ser	Ile	Arg	Gly	Ser	Leu	Asp	Val
			165						170					175	
Pro	Asp	Phe	Phe	Lys	Gln	Ile	Thr	Val	Thr	Phe	Asn	Pro	Trp	Asn	Glu
		180						185					190		
Arg	His	Trp	Leu	Lys	Arg	Val	Phe	Phe	Asp	Glu	Glu	Thr	Arg	Arg	Ala
	195						200						205		
Asp	Thr	Phe	Ala	Thr	Thr	Thr	Thr	Tyr	Lys	Cys	Asn	Glu	Trp	Leu	Asp
	210					215					220				
Glu	Val	Asp	Ile	Lys	Arg	Tyr	Glu	Asp	Leu	Tyr	His	Thr	Asn	Pro	Arg
225					230					235					240
Arg	Ala	Arg	Ile	Val	Cys	Asp	Gly	Glu	Trp	Gly	Val	Ala	Glu	Gly	Leu
			245						250					255	
Ile	Tyr	Glu	Asn	Val	Thr	Val	Lys	Asp	Phe	Asn	Lys	Asp	Glu	Leu	Leu
		260						265					270		
Gln	Asp	Ser	Ala	Asn	Lys	Leu	Cys	Ile	Gly	Leu	Asp	Phe	Gly	Phe	Thr
	275						280					285			
His	Asp	Pro	Thr	Ala	Leu	Cys	Cys	Ser	Leu	Ile	Asn	Asp	Thr	Thr	Lys

290		295		300
Glu Ile Tyr Val Phe Asp	Glu Ala Tyr Lys Val Gly Leu Ile Thr Lys			
305	310	315		320
Glu Val Ala Lys Met Ile Lys Asp Lys Gly Tyr His Arg Ser Gln Ile				
	325	330		335
Ile Ala Asp Ser Ala Glu Ser Arg Leu Ile Glu Glu Leu Arg Ser Glu				
	340	345		350
His Gly Ile Ser Arg Ile Lys Glu Ser Arg Lys Gly Lys Asp Ser Ile				
	355	360		365
Met Ala Gly Val Ser Lys Leu Gln Gly Tyr Ala Ile Tyr Val His Pro				
	370	375		380
Asp Cys Lys Asn Ile Met Asp Glu Phe Tyr Ser Tyr Cys Tyr Gln Arg				
385	390	395		400
Asp Lys Glu Gly Asn Trp Leu Asn Lys Pro Glu Asp Lys Asn Asn His				
	405	410		415
Leu Met Asp Ala Leu Arg Tyr Ser Leu Gln Cys Ile Glu Gly Gly Lys				
	420	425		430
Ala Thr Val Arg Arg Arg Ser Asp Tyr Gly Leu				
	435	440		

(2) INFORMATION FOR SEQ ID NO:2784:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2784:

Lys	Gln	Ile	Pro	Ile	Phe	Arg	Gly	Gly	Gly	Cys	Met	Lys	Lys	Val	Lys
1			5					10						15	
Leu	Gly	Gln	Val	Ala	Thr	Phe	Ile	Asn	Gly	Tyr	Ala	Phe	Lys	Pro	Gln
		20					25					30			
Asp	Trp	Ser	Ser	Glu	Gly	Lys	Glu	Ile	Ile	Arg	Ile	Gln	Asn	Leu	Thr
		35				40						45			
Lys	Thr	Ser	Lys	Gly	Ile	Asn	Tyr	Tyr	Ser	Gly	Thr	Ile	Asp	Lys	Lys
	50				55			60							
Tyr	Ile	Val	Glu	Ala	Gly	Asp	Ile	Leu	Ile	Ser	Trp	Ser	Gly	Thr	Leu
65			70				75							80	
Gly	Val	Phe	Gln	Trp	Cys	Gly	Arg	Ser	Ala	Val	Leu	Asn	Gln	His	Ile
		85				90							95		
Phe	Lys	Val	Val	Phe	Asp	Lys	Ile	Asp	Ile	Asp	Lys	Ser	Tyr	Phe	Lys
		100				105						110			
Tyr	Val	Val	Glu	Lys	Gly	Leu	Gln	Asp	Ala	Val	Lys	His	Thr	His	Gly
		115				120						125			
Gln	Gln														

130

(2) INFORMATION FOR SEQ ID NO:2785:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 521 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...521

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2785:

Arg	Arg	Ile	Pro	Ile	Val	Ser	Asn	Lys	Pro	Ile	Ala	Asp	Met	Ile	Glu
1			5						10					15	
Thr	Ile	Glu	His	Phe	Ala	Gln	Thr	Gln	Pro	Ser	Tyr	Pro	Val	Tyr	Asn
			20					25					30		
Val	Leu	Gly	Gln	Glu	His	Thr	Tyr	Gly	Asp	Leu	Lys	Ala	Asp	Ser	Asp
		35					40					45			
Ser	Leu	Ala	Ala	Val	Ile	Asp	Gln	Leu	Gly	Leu	Pro	Glu	Lys	Ser	Pro
	50					55					60				
Val	Val	Val	Phe	Gly	Gly	Gln	Glu	Tyr	Glu	Met	Leu	Ala	Thr	Phe	Val
65				70					75					80	
Ala	Leu	Thr	Lys	Ser	Gly	His	Ala	Tyr	Ile	Pro	Ile	Asp	Ser	His	Ser
			85					90					95		
Ala	Leu	Glu	Arg	Val	Ser	Ala	Ile	Leu	Glu	Val	Ala	Glu	Pro	Ser	Leu
			100					105					110		
Ile	Ile	Ala	Ile	Ser	Ala	Phe	Pro	Leu	Glu	Gln	Val	Ser	Thr	Pro	Met
		115				120						125			
Ile	Asn	Leu	Ala	Gln	Val	Gln	Glu	Ala	Phe	Ala	Gln	Gly	Asn	Asn	Tyr
	130					135					140				
Glu	Ile	Thr	His	Pro	Val	Lys	Gly	Asp	Asp	Asn	Tyr	Tyr	Ile	Ile	Phe
145				150					155					160	
Thr	Ser	Gly	Thr	Thr	Gly	Lys	Pro	Lys	Gly	Val	Gln	Ile	Ser	His	Asp
			165					170					175		
Asn	Leu	Leu	Ser	Phe	Thr	Asn	Trp	Met	Ile	Thr	Asp	Lys	Glu	Phe	Ala
			180					185					190		
Thr	Pro	Ser	Arg	Pro	Gln	Met	Leu	Ala	Gln	Pro	Pro	Tyr	Ser	Phe	Asp
		195				200						205			
Leu	Ser	Val	Met	Tyr	Trp	Ala	Pro	Thr	Leu	Ala	Leu	Gly	Gly	Thr	Leu
	210					215					220				
Phe	Thr	Leu	Pro	Ser	Val	Ile	Thr	Gln	Asp	Phe	Lys	Gln	Leu	Phe	Ala
225				230					235					240	
Ala	Ile	Phe	Ser	Leu	Pro	Ile	Ala	Ile	Trp	Thr	Ser	Thr	Pro	Ser	Phe
			245					250					255		
Ala	Asp	Met	Ala	Met	Leu	Ser	Glu	Tyr	Phe	Asn	Ser	Glu	Lys	Met	Pro
		260					265					270			
Gly	Ile	Thr	His	Phe	Tyr	Phe	Asp	Gly	Glu	Glu	Leu	Thr	Val	Lys	Thr

Leu	Lys	Pro	Tyr	Thr	Val	Ile	Gln	Leu	His	Pro	Asp	Asp	Leu	Pro	Lys
			500					505					510		
Arg	Asp	Gly	Ala	Ala	Arg	Asp	Phe	Tyr	Glu	His	Met	Leu	Glu	Glu	Ala
		515					520					525			
Ala	Lys	Tyr	Val	Asn	Pro	Lys	Thr	Gly	Lys	Asn	Glu	Pro	Ile	Pro	Val
	530					535					540				
Ile	Leu	Thr	Val	Tyr	Thr	Ala	Gly	Asn	Met	Pro	Tyr	Tyr	Thr	Ser	Ala
545					550					555					560
His	Trp	Leu	Ser	Thr	Ser	Trp	Ile	Asp	Lys	Met	Tyr	Gln	Lys	Tyr	Pro
				565					570					575	
Asn	Leu	His	Gly	Ile	Phe	Ser	Thr	Glu	Asn	Tyr	Trp	Ile	Trp	Ala	Asn
			580					585					590		
Asp	Ile	Glu	Asn	Lys	Ala	Ala	Asp	Tyr	Leu	Lys	Val	Ser	Ala	Lys	Asn
		595					600					605			
Gly	Gly	Tyr	Phe	Ile	Trp	Ala	Glu	Gln	Asn	Asn	Gly	Ser	Ala	Ile	Glu
	610					615					620				
Lys	Ala	Phe	Gly	Lys	Asn	Gly	Lys	Ile	Ala	Phe	Gln	Lys	Ser	Val	Asp
625					630					635					640
Lys	Tyr	Trp	Lys	Asn	Leu	Ile	Phe	Met	Phe	Lys	Asn	Thr	Pro	Ala	Ala
				645					650					655	
Glu	Gly	Asn	Asp	Ser	Thr	Thr	Glu	Ser	Tyr	Met	Lys	Gly	Leu	Trp	Leu
		660						665					670		
Ser	Asn	His	Thr	Tyr	Gln	Trp	Gly	Gly	Leu	Met	Asp	Thr	Trp	Lys	Trp
	675						680					685			
Tyr	Glu	Thr	Gly	Lys	Trp	Lys	Leu	Phe	Ala	Ser	Gly	Asn	Ile	Gly	Lys
	690					695					700				
Ser	Gln	Gly	Asp	Arg	Gln	Trp	Leu	Thr	Glu	Pro	Glu	Ser	Met	Leu	Gly
705					710					715					720
Glu	Glu	Ala	Leu	Gly	Val	Tyr	Leu	Asn	Gly	Gly	Val	Val	Tyr	Asn	Phe
				725					730					735	
Glu	His	Pro	Ala	Tyr	Thr	Tyr	Gly	Val	Asn	Asn	Lys	Glu	Ser	Leu	Leu
			740				745						750		
Phe	Ser	Glu	Val	Ile	Lys	Glu	Phe	Phe	Arg	Tyr	Val	Ile	Ala	His	Pro
	755						760					765			
Ala	Pro	Ser	Lys	Glu	Lys	Val	Leu	Glu	Asp	Thr	Lys	Val	Phe	Ile	His
	770					775					780				
Gly	Asp	Tyr	Ser	Asn	Lys	Gly	Asn	Gly	Lys	Phe	Phe	Val	Asn	Val	Asn
785					790					795					800
Thr	Asp	Arg	Glu	Gln	Thr	Pro	Leu	Tyr	Met	Thr	Gly	Arg	Tyr	Asn	Val
				805					810					815	
Ile	Pro	Ala	Ile	Pro	Gly	Val	Leu	Lys	Thr	Asp	Lys	Leu	Lys	Glu	Ser
			820					825					830		
Val	Ser	Gly	Ser	Arg	Ile	Gln	Ile	Lys	Glu	Ile	Thr	Ser	Pro	Glu	Phe
	835						840					845			
Ser	Ser	Thr	Gln	Ala	Arg	Lys	Glu	Tyr	Leu	Asn	Lys	Leu	Tyr	Pro	Met
	850					855					860				
Asn	Tyr	Glu	Gly	Asp	Ile	Phe	Ala	Gln	Lys	Leu	Asp	Asn	Arg	Trp	Phe
865					870					875					880
Val	Tyr	Asn	Tyr	Lys	Val	Asn	Glu	Asn	Val	Lys	Gln	Thr	Gly	Lys	Leu
				885					890					895	
Lys	Phe	Asn	Ser	Leu	Glu	Met	Asp	Val	Glu	Phe	Glu	Pro	His	Thr	Tyr
		900						905					910		
Gly	Ile	Phe	Glu	Arg	Ile	Ser	Asn	Gly	Leu	Lys	Val	Asn	Leu	Asn	Asn
		915					920					925			
Phe	Arg	Thr	Asn	Lys	Asp	Ser	Leu	Trp	Ser	Asn	Ala	Gln	Asp	Ala	Asn
	930					935					940				
Gln	Ala	Lys	Lys	Leu	Pro	Gln	Leu	Thr	Lys	Lys	Gly	Ala	Ile	Lys	Trp

945		950		955		960									
Ile	Glu	Glu	His	Tyr	Ile	Lys	Asp	Thr	Gln	Phe	Gly	Glu	Lys	Arg	Val
				965					970					975	
Thr	Lys	Ile	Val	Leu	Arg	Gly	Ile	Asp	Lys	Leu	Pro	Thr	Ile	His	Ser
			980					985					990		
Leu	Ser	Gly	Thr	Asn	Asn	Ser	Tyr	Asp	Gln	Pro	Ser	Leu	Asn	Phe	Asp
		995					1000					1005			
Gln	Lys	Asn	His	Met	Val	Thr	Ile	Thr	Ile	Asn	Ser	Asn	Gly	Asn	Leu
	1010					1015					1020				
Glu	Phe	Glu	Leu	His	Phe										
1025					1030										

(2) INFORMATION FOR SEQ ID NO:2787:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 93 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...93
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2787:

Pro	Pro	Pro	Pro	Pro	Pro	Thr	Pro	Pro	Pro	Pro	Pro	Thr	Pro	Pro	Pro
1				5					10					15	
Pro	Gln	Pro	Thr	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	His	Pro	Pro	Pro
			20					25				30			
Pro	Pro	Pro	Pro	Asn	Thr	Pro	His	Pro	Lys	Asn	Pro	Gln	Lys	Lys	Lys
		35				40					45				
Thr	Lys	Lys	Lys	Asn	Phe	Phe	Glu	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys
	50				55				60						
Lys	Lys	Lys	Asn	Leu	Gly	Leu	Leu	Gly	Arg	Lys	Thr	Leu	Ala	Asn	Ile
65				70					75					80	
Trp	Ser	Ile	Arg	Pro	Pro	Lys	Ala	Pro	Lys	Ile	Val	Thr			
			85					90							

(2) INFORMATION FOR SEQ ID NO:2788:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 69 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...69

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2788:

```
Thr Pro Pro Pro Pro His Pro Pro His Pro Pro Pro Pro Pro Pro Pro
1          5          10          15
Pro Pro Asn Pro Pro Pro Pro Pro Pro Pro Pro Pro Pro Thr Pro Pro
          20          25          30
Pro Pro Pro Pro Pro Thr Pro His Thr Pro Lys Thr His Lys Lys Lys
          35          40          45
Lys Gln Lys Lys Lys Ile Phe Leu Lys Lys Lys Lys Lys Lys Lys Lys
          50          55          60
Lys Lys Lys Lys Thr
65
```

(2) INFORMATION FOR SEQ ID NO:2789:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 207 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2789:

```
Ile Val Tyr Pro Phe Phe Cys Val Ser Glu Val Thr Met Lys Arg Ile
1          5          10          15
Ile Pro Val Tyr Ile Phe Gln Gln Val Asn Val Leu Leu Val Ser Leu
          20          25          30
Tyr Leu Leu Lys Phe Leu Cys Ile Gly Glu Leu Thr Ile Leu Gln Ile
          35          40          45
Leu Tyr Gly Ser Ser Leu Ile Ser Phe Leu Trp Met Tyr Gly Gln Arg
          50          55          60
Lys Gln Ala His Lys Val Asn Met Lys Ser Arg Met Lys Trp Leu Gly
65          70          75          80
Ile Gly Phe Val Ser Leu Leu Ile Ile Ser Leu Cys Phe Ser Leu Ile
          85          90          95
His Ala Gln Glu Ser Thr Asn Gln Ala Asn Leu Ile Gly Leu Gln His
          100          105          110
Gln Val Pro Trp Phe Ser Phe Leu Leu Phe Leu Ile Asn Ala Ser Met
          115          120          125
Val Glu Glu Phe Leu Tyr Arg Glu Ile Leu Trp Asn Leu Val Arg Lys
          130          135          140
```

Leu	Asp	Ile	Arg	Val	Ala	Leu	Thr	Ser	Val	Leu	Phe	Ala	Leu	Ala	His
145					150					155					160
His	Pro	Gly	Thr	Ile	Ile	Ala	Trp	Cys	Leu	Tyr	Val	Ser	Leu	Gly	Met
				165					170						175
Phe	Leu	Gly	Leu	Val	Arg	Tyr	Lys	Leu	Asp	Leu	Trp	Gly	Ser	Met	Gly
			180					185					190		
Leu	His	Leu	Val	Trp	Ser	Leu	Leu	Val	Tyr	Ser	Leu	Leu	Leu	Phe	
	195						200					205			

(2) INFORMATION FOR SEQ ID NO:2790:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 369 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...369

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2790:

Ile	Gln	Tyr	Pro	Trp	Trp	Lys	Met	Ser	Asn	Val	Ile	Cys	Ser	Asp	Ser
1				5					10					15	
Ser	Tyr	Ser	Phe	His	Asn	Lys	Asn	Phe	Met	Ile	Phe	Ile	Arg	Arg	Lys
			20					25					30		
Ser	Leu	Met	Val	Val	Lys	Val	Gly	Ile	Asn	Gly	Phe	Gly	Arg	Ile	Gly
		35					40					45			
Arg	Leu	Ala	Phe	Arg	Arg	Ile	Gln	Asn	Val	Lys	Gly	Val	Glu	Val	Thr
		50				55					60				
Arg	Ile	Asn	Asp	Leu	Thr	Asp	Pro	Val	Met	Leu	Ala	His	Leu	Leu	Lys
65					70				75						80
Tyr	Asp	Thr	Thr	Gln	Gly	Arg	Phe	Asp	Gly	Thr	Val	Glu	Val	Lys	Glu
			85					90						95	
Gly	Gly	Phe	Glu	Val	Asn	Gly	Lys	Phe	Val	Lys	Val	Ser	Ala	Glu	Arg
		100						105					110		
Asp	Pro	Glu	Gln	Ile	Asp	Trp	Ala	Thr	Asp	Gly	Val	Lys	Ile	Val	Leu
		115					120					125			
Glu	Ala	Thr	Gly	Phe	Phe	Ala	Lys	Lys	Glu	Ala	Ala	Glu	Lys	His	Leu
	130					135					140				
Lys	Gly	Gly	Ala	Lys	Lys	Val	Val	Ile	Thr	Ala	Pro	Gly	Gly	Asn	Asp
145				150					155						160
Val	Lys	Thr	Val	Val	Phe	Asn	Thr	Asn	His	Asp	Val	Leu	Asp	Gly	Thr
			165					170						175	
Glu	Thr	Val	Ile	Ser	Gly	Ala	Ser	Cys	Thr	Thr	Asn	Cys	Leu	Ala	Pro
		180					185						190		
Met	Ala	Lys	Ala	Leu	Gln	Asp	Asn	Phe	Gly	Val	Val	Glu	Gly	Leu	Met
	195					200						205			
Thr	Thr	Ile	His	Ala	Tyr	Thr	Gly	Asp	Gln	Met	Ile	Leu	Asp	Gly	Pro
	210					215					220				

```

His Arg Gly Gly Asp Leu Arg Arg Ala Arg Ala Gly Ala Ala Asn Ile
225                230                235                240
Val Pro Asn Ser Thr Gly Ala Ala Lys Ala Ile Gly Leu Val Ile Pro
                245                250                255
Glu Leu Asn Gly Lys Leu Asp Gly Ser Ala Gln Arg Val Pro Thr Pro
                260                265                270
Thr Gly Ser Val Thr Glu Leu Val Ala Val Leu Glu Lys Asn Val Thr
                275                280                285
Val Asp Glu Val Asn Ala Ala Met Lys Ala Ala Ser Asn Glu Ser Tyr
                290                295                300
Gly Tyr Thr Glu Asp Pro Ile Val Ser Ser Asp Ile Val Gly Met Ser
305                310                315                320
Tyr Gly Ser Leu Phe Asp Ala Thr Gln Thr Lys Val Leu Asp Val Asp
                325                330                335
Gly Lys Gln Leu Val Lys Val Val Ser Trp Tyr Asp Asn Glu Met Ser
                340                345                350
Tyr Thr Ala Gln Leu Val Arg Thr Leu Glu Tyr Phe Ala Lys Ile Ala
                355                360                365
Lys

```

(2) INFORMATION FOR SEQ ID NO:2791:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 320 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...320

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2791:

```

Thr Ala His Pro Pro Arg Leu Ser Ala Ile Gly Val Arg Arg Ala Ala
1                5                10                15
Thr Leu Asp Gly Ala Cys Arg Ala Ile Arg Ala Gly Leu Asp His Arg
                20                25                30
Ala Leu His Arg Ala Gly Gly Arg Arg Arg His Glu Arg Ala Gly Gly
                35                40                45
Arg Arg Asp Pro Leu Asp Ser Arg Arg Ala His Arg Ala Val Ala Gln
50                55                60
Ala Gly Arg Arg Gln Pro Leu Ser Gly His Arg Arg Ala Ala Leu Gly
65                70                75                80
Glu Pro Gly His Glu Pro Asp Arg Arg Arg Arg Ser Ala Pro Cys Gly
                85                90                95
Arg Thr Leu Ala Arg Met Ala Gly Glu Val Arg Gly Ser Arg Val Ala
                100                105                110
Ala Glu Asp Arg Arg Ile Pro Glu Arg Pro Gly Gln Arg Ser Arg Pro
                115                120                125

```

Gly	His	Arg	Glu	Asp	Arg	Gly	Asp	Pro	Pro	Val	Ala	Ala	Pro	Gly	Tyr
130						135					140				
Pro	Arg	Asn	Gln	Arg	Leu	Arg	Thr	Gly	Leu	Arg	Ala	Val	Ala	Glu	Pro
145					150					155					160
Leu	Arg	Met	Ser	Leu	Ala	Leu	Leu	Leu	Arg	Val	Arg	Arg	Leu	Arg	Leu
				165					170					175	
Asp	Arg	Ala	Glu	Arg	Ala	Gln	Gly	Arg	Gln	Leu	Leu	Arg	Val	Arg	Ala
			180					185					190		
Ala	Ala	Gln	Glu	His	Thr	Glu	Arg	Gln	Ala	Ala	Gln	Arg	Asp	Tyr	Arg
		195					200					205			
Asp	Trp	Arg	Leu	Ala	Glu	Glu	Gln	Arg	Leu	Phe	Leu	Ala	Cys	Gln	Ala
	210					215					220				
Ala	Met	Leu	Asp	Arg	Arg	Arg	Leu	Glu	Ala	Trp	Gln	Gln	Gln	Val	Gly
225					230				235						240
Leu	Leu	Arg	Glu	Lys	Glu	Ala	Gly	Leu	Glu	Gln	Asp	Cys	Ala	Glu	Thr
				245					250					255	
Ala	Gln	Arg	Leu	Glu	Gly	Glu	Arg	Glu	Arg	Leu	Arg	Gln	Cys	Arg	Arg
			260					265					270		
Glu	Leu	Leu	Glu	Arg	Gln	Arg	Gln	Leu	Glu	Lys	Phe	Ala	Glu	Leu	Glu
		275					280					285			
Arg	His	Val	Asp	Ala	Glu	Arg	Gln	Gly	Leu	Arg	Glu	Arg	Ser	Glu	Glu
	290					295					300				
Gly	Glu	Leu	Glu	Glu	Phe	Thr	Arg	His	Glu	Thr	Trp	Pro	Cys	Ser	Ser
305					310					315					320

(2) INFORMATION FOR SEQ ID NO:2792:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...67

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2792:

Ala	Phe	Asn	Pro	Ile	Asn	Asn	Val	Ala	Phe	Gln	Pro	Arg	Phe	Gly	Ile
1				5				10						15	
Gln	Pro	Cys	Leu	Ser	Val	Gly	Ile	Phe	Tyr	Ser	Gly	Leu	Tyr	Leu	Leu
			20					25					30		
Glu	Asn	Ile	Ile	Ser	Phe	Ser	Lys	Leu	Tyr	Tyr	Tyr	Ile	Met	Phe	Leu
		35					40					45			
Arg	Thr	Cys	Lys	Val	Phe	Phe	Asp	Lys	Lys	Gln	Lys	Tyr	Asn	Arg	Leu
	50					55					60				
Lys	Leu	Glu													
65															

(2) INFORMATION FOR SEQ ID NO:2793:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 152 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...152
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2793:

```

Pro Asn Asn Pro Phe Val Phe Cys Leu Glu Ala Asp Asn Gln Glu Gln
1      5      10      15
Leu Phe Asp Gln Val Ala Ser Leu Leu Glu Glu Arg Glu Ile Val Thr
20      25      30
Pro Thr Tyr Arg Glu Ala Leu Ile Thr Arg Glu Lys Ser Phe Pro Thr
35      40      45
Gly Leu Asp Met Glu Phe Leu Gly Lys Asp Leu Pro Asn Val Ala Ile
50      55      60
Pro His Thr Asp Ile Val His Asn Leu Ala Glu Lys Val Val Val Val
65      70      75      80
Arg Leu Glu Lys Pro Val Thr Phe His Asn Met Ile Ala Pro Gly Lys
85      90      95
Glu Val Glu Val Ser Leu Leu Phe Phe Ile Ile Asn Asn Ser Ser Ser
100     105     110
Ser Gln Thr Asn Ile Leu Ala Gln Leu Met Asp Phe Phe Thr Gly Asn
115     120     125
Gly His Leu Glu Asp Leu Ser Lys Ile Ser Glu Pro Glu Lys Leu Tyr
130     135     140
Ala Tyr Ile Ala Glu Ala Thr Ala
145     150

```

(2) INFORMATION FOR SEQ ID NO:2794:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 248 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...248

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2794:

Thr	Pro	Asn	Pro	Pro	Leu	Leu	His	Ala	Lys	Arg	Gly	Leu	Glu	Ser	Glu
1				5					10					15	
Asn	His	Phe	Met	Lys	Lys	Pro	Val	Ile	Gly	Ile	Thr	Gly	Asn	Glu	Lys
			20					25					30		
Thr	His	Pro	Asp	Asp	Asp	Ile	Met	Met	Ser	Tyr	Ala	Ala	Lys	Gly	Phe
		35					40					45			
Val	Glu	Gly	Val	Lys	Asp	Ala	Gly	Gly	Ile	Pro	Ile	Ile	Leu	Pro	Ile
	50					55					60				
Gly	Asp	Gln	Glu	Met	Ala	Cys	His	Tyr	Ile	Ser	Leu	Ile	Asp	Lys	Leu
65					70				75						80
Ile	Leu	Thr	Gly	Gly	Gln	Asn	Val	Asp	Pro	Lys	Phe	Tyr	Gly	Glu	Pro
			85					90					95		
Lys	Thr	Ile	Asp	Ser	Asp	Asp	Tyr	His	Leu	Gln	Arg	Asp	Ile	Phe	Glu
			100				105						110		
Leu	Ala	Leu	Ile	Lys	Glu	Ala	Ile	Lys	Gln	Lys	Lys	Pro	Ile	Phe	Ser
		115					120					125			
Val	Cys	Arg	Gly	Thr	Gln	Leu	Phe	Asn	Val	Ala	Met	Gly	Gly	Thr	Leu
	130					135					140				
Tyr	Gln	Asp	Ile	Glu	Asp	His	Trp	Gln	Asp	Ser	Ser	Val	Glu	Tyr	Thr
145				150					155						160
Thr	Gln	Arg	Leu	Val	Thr	Glu	Pro	Asp	Thr	Val	Leu	Gln	Glu	Ile	Tyr
			165					170						175	
Gly	Glu	Ile	Ser	His	Ile	Asn	Ser	Phe	His	His	Gln	Ser	Ile	Lys	Asp
			180				185						190		
Leu	Ala	Pro	Asn	Leu	Lys	Val	Val	Ala	His	Asp	Pro	Lys	Asp	Gly	Ile
		195					200					205			
Ile	Glu	Ala	Val	Met	Ser	Thr	Asp	Asp	Val	Ala	Phe	Leu	Gly	Val	Gln
	210					215				220					
Trp	His	Pro	Glu	Leu	Leu	Phe	Glu	Asn	Arg	Pro	Lys	Asp	Lys	Lys	Leu
225				230					235						240
Phe	Asp	Tyr	Val	Val	Asn	Glu	Leu								
			245												

(2) INFORMATION FOR SEQ ID NO:2795:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...331

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2795:

Val Met Ser Pro Ile Cys Glu Pro His Phe Ser Asp Thr Ser Tyr Gly

1				5					10					15			
Phe	Arg	Pro	Asn	Arg	Ser	Cys	Glu	Lys	Ala	Ile	Met	Lys	Leu	Leu	Glu		
			20					25					30				
Tyr	Leu	Asn	Asp	Gly	Tyr	Glu	Trp	Ile	Val	Asp	Ile	Asp	Leu	Glu	Lys		
		35					40					45					
Phe	Phe	Asp	Thr	Val	Pro	Gln	Asp	Arg	Leu	Met	Ser	Leu	Val	His	Asn		
	50					55					60						
Ile	Ile	Glu	Asp	Gly	Asp	Thr	Glu	Ser	Leu	Ile	Arg	Lys	Tyr	Leu	His		
65					70					75					80		
Ser	Gly	Val	Ile	Ile	Asn	Gly	Gln	Arg	Tyr	Lys	Thr	Leu	Val	Gly	Thr		
				85					90					95			
Pro	Gln	Gly	Gly	Asn	Leu	Ser	Pro	Leu	Leu	Ser	Asn	Ile	Met	Leu	Asn		
			100					105					110				
Glu	Leu	Asp	Lys	Glu	Leu	Glu	Lys	Arg	Gly	Leu	Arg	Phe	Val	Arg	Tyr		
		115					120					125					
Ala	Asp	Asp	Cys	Val	Ile	Thr	Val	Val	Ser	Glu	Ala	Ala	Ala	Lys	Arg		
	130					135					140						
Met	Met	Tyr	Ser	Val	Ser	Arg	Phe	Ile	Glu	Lys	Arg	Leu	Gly	Leu	Lys		
145					150					155					160		
Val	Asn	Met	Thr	Lys	Thr	Lys	Ile	Thr	Arg	Pro	Arg	Glu	Leu	Lys	Tyr		
				165					170					175			
Leu	Gly	Phe	Gly	Phe	Trp	Lys	Ser	Ser	Asp	Gly	Trp	Lys	Ser	Arg	Pro		
		180					185						190				
His	Gln	Asp	Ser	Val	Arg	Arg	Phe	Lys	Leu	Lys	Leu	Lys	Lys	Leu	Thr		
	195						200					205					
Gln	Arg	Lys	Trp	Ser	Ile	Asp	Leu	Thr	Arg	Arg	Ile	Glu	Gln	Leu	Asn		
	210				215						220						
Leu	Ser	Ile	Arg	Gly	Trp	Ile	Asn	Tyr	Phe	Ser	Leu	Gly	Asn	Met	Lys		
225					230				235						240		
Ser	Ile	Val	Ala	Ser	Ile	Asp	Glu	Arg	Leu	Arg	Thr	Arg	Leu	Arg	Val		
			245					250						255			
Ile	Ile	Trp	Lys	Gln	Trp	Lys	Lys	Lys	Ser	Arg	Arg	Leu	Trp	Gly	Leu		
		260					265						270				
Leu	Lys	Leu	Gly	Val	Pro	Lys	Trp	Ile	Ala	Asp	Lys	Val	Ser	Gly	Trp		
	275					280					285						
Gly	Asp	His	Tyr	Gln	Leu	Val	Ala	Gln	Lys	Ser	Val	Leu	Lys	Arg	Ala		
	290				295					300							
Ile	Ser	Lys	Pro	Val	Leu	Glu	Lys	Arg	Gly	Leu	Val	Ser	Cys	Leu	Asp		
305					310					315					320		
Tyr	Tyr	Leu	Glu	Arg	His	Ala	Leu	Lys	Val	Ser							
				325					330								

(2) INFORMATION FOR SEQ ID NO:2796:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...221

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2796:

Trp	Phe	Leu	Pro	Arg	Leu	Arg	Tyr	Asp	Ile	Glu	Leu	Gly	Asn	Gln	Leu
1			5					10					15		
Ala	Gln	Asp	Leu	Gly	Val	Lys	Val	Lys	Tyr	Ile	Ser	Val	Asp	Ala	Ala
		20						25					30		
Asn	Arg	Ala	Glu	Tyr	Leu	Ile	Ser	Asn	Lys	Val	Asp	Ile	Thr	Leu	Ala
		35					40					45			
Asn	Phe	Thr	Val	Thr	Asp	Glu	Arg	Lys	Lys	Gln	Val	Asp	Phe	Ala	Leu
	50					55				60					
Pro	Tyr	Met	Lys	Val	Ser	Leu	Gly	Val	Val	Ser	Pro	Lys	Thr	Gly	Leu
65				70						75					80
Ile	Thr	Asp	Val	Lys	Gln	Leu	Glu	Gly	Lys	Thr	Leu	Ile	Val	Thr	Lys
			85						90					95	
Gly	Thr	Thr	Ala	Glu	Thr	Tyr	Phe	Glu	Lys	Asn	His	Pro	Glu	Ile	Lys
			100					105					110		
Leu	Gln	Lys	Tyr	Asp	Gln	Tyr	Ser	Asp	Ser	Tyr	Gln	Ala	Leu	Leu	Asp
	115						120					125			
Gly	Arg	Gly	Asp	Ala	Phe	Ser	Thr	Asp	Asn	Thr	Glu	Val	Leu	Ala	Trp
	130					135					140				
Ala	Leu	Glu	Asn	Lys	Gly	Phe	Glu	Val	Gly	Ile	Thr	Ser	Leu	Gly	Asp
145				150						155					160
Pro	Asp	Thr	Ile	Ala	Ala	Val	Gln	Lys	Gly	Asn	Gln	Glu	Leu	Leu	
			165					170					175		
Asp	Phe	Ile	Asn	Lys	Asp	Ile	Glu	Lys	Leu	Gly	Lys	Glu	Asn	Phe	Phe
		180						185					190		
His	Lys	Ala	Tyr	Glu	Lys	Thr	Leu	His	Pro	Thr	Tyr	Gly	Asp	Ala	Ala
	195						200					205			
Lys	Ala	Asp	Asp	Leu	Val	Val	Glu	Gly	Gly	Lys	Val	Asp			
	210					215					220				

(2) INFORMATION FOR SEQ ID NO:2797:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 392 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...392

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2797:

Lys	Glu	Leu	Pro	Met	Asn	Tyr	Leu	Val	Ile	Ser	Pro	Tyr	Tyr	Pro	Gln
1			5					10						15	

Asn	Phe	Gln	Gln	Phe	Thr	Ile	Glu	Leu	Ala	Asn	Lys	Gly	Ile	Thr	Ala		
		20						25					30				
Leu	Gly	Ile	Gly	Gln	Glu	Ser	Tyr	Glu	Gln	Leu	Asp	Glu	Pro	Leu	Arg		
	35					40					45						
Asn	Ser	Leu	Thr	Glu	Tyr	Phe	Arg	Val	Asp	Asn	Leu	Glu	Asn	Ile	Asp		
	50				55					60							
Glu	Val	Lys	Arg	Ala	Val	Ala	Phe	Leu	Phe	Tyr	Lys	His	Gly	Pro	Ile		
65					70					75					80		
Asp	Arg	Ile	Glu	Ser	His	Asn	Glu	Tyr	Trp	Leu	Glu	Leu	Asp	Ala	Thr		
			85						90					95			
Leu	Arg	Glu	Gln	Phe	Asn	Val	Phe	Gly	Ala	Lys	Pro	Glu	Asp	Leu	Lys		
		100						105					110				
Lys	Thr	Lys	Tyr	Lys	Ser	Glu	Met	Lys	Lys	Leu	Phe	Lys	Lys	Ala	Gly		
	115					120						125					
Val	Pro	Val	Val	Pro	Gly	Ala	Val	Ile	Lys	Thr	Glu	Ala	Asp	Val	Asp		
	130				135						140						
Gln	Ala	Val	Lys	Glu	Ile	Gly	Leu	Pro	Met	Ile	Ala	Lys	Pro	Asp	Asn		
145					150					155					160		
Gly	Val	Arg	Ala	Ala	Ala	Thr	Phe	Lys	Leu	Glu	Thr	Glu	Asp	Asp	Ile		
			165					170						175			
Asn	His	Phe	Lys	Gln	Glu	Trp	Asp	His	Ser	Thr	Leu	Tyr	Phe	Phe	Glu		
	180						185						190				
Lys	Phe	Val	Thr	Ser	Ser	Glu	Ile	Cys	Thr	Phe	Asp	Gly	Leu	Val	Asp		
	195					200					205						
Lys	Asp	Gly	Lys	Ile	Val	Phe	Ser	Thr	Thr	Phe	Asp	Tyr	Ala	Tyr	Thr		
	210				215						220						
Pro	Leu	Asp	Leu	Met	Ile	Tyr	Lys	Met	Asp	Asn	Ser	Tyr	Tyr	Val	Leu		
225					230				235						240		
Lys	Asp	Met	Asp	Pro	Lys	Leu	Arg	Lys	Tyr	Gly	Glu	Ala	Ile	Val	Lys		
		245						250						255			
Glu	Phe	Gly	Met	Lys	Glu	Arg	Phe	Phe	His	Ile	Glu	Phe	Phe	Arg	Glu		
		260					265						270				
Gly	Asp	Asp	Tyr	Ile	Thr	Ile	Glu	Tyr	Asn	Asn	Arg	Pro	Ala	Gly	Gly		
	275					280					285						
Phe	Thr	Ile	Asp	Val	Tyr	Asn	Phe	Ala	His	Ser	Leu	Asp	Leu	Tyr	Arg		
	290				295					300							
Gly	Tyr	Ala	Ala	Ile	Val	Ala	Gly	Glu	Glu	Phe	Pro	Ala	Ser	Asp	Phe		
305				310					315						320		
Glu	Thr	Gln	Tyr	Cys	Leu	Ala	Thr	Ser	Arg	Arg	Ala	Asn	Ala	His	Tyr		
		325						330						335			
Val	Tyr	Ser	Glu	Glu	Asp	Leu	Leu	Ala	Lys	Tyr	Ser	Gln	Gln	Phe	Lys		
		340						345					350				
Val	Lys	Lys	Val	Met	Pro	Ala	Ala	Phe	Ala	Glu	Leu	Gln	Gly	Asp	Tyr		
	355				360							365					
Leu	Tyr	Met	Leu	Thr	Thr	Pro	Ser	Arg	Gln	Glu	Met	Glu	Gln	Met	Ile		
	370				375						380						
Ala	Asp	Phe	Gly	Gln	Arg	Gln	Glu										
385					390												

(2) INFORMATION FOR SEQ ID NO:2798:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...264

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2798:

```
Pro Pro Leu Pro Thr Val Thr Pro Arg Glu Pro His Phe Ala His His
1      5      10      15
Ser Gly Leu Pro Leu Tyr Ala Ala Leu Thr Arg Gly Ala Cys Ser Asn
      20      25      30
Phe Ser Ser Pro Thr Pro His Thr Pro Thr Leu Pro Leu Gln Gln Ile
      35      40      45
Pro Ser Gln Leu Leu Pro Leu Phe Pro Asn Pro Val Ala Ser Pro Arg
      50      55      60
His Thr Ser Val Gln Pro Ile Ser Pro Cys Arg His Gly Pro Pro His
65      70      75      80
Thr Asn Cys Pro Pro Leu Thr Pro Leu His Pro Ser Pro Asp Arg Pro
      85      90      95
Arg Leu Asn Pro Gly His Pro Thr Ser Leu His Pro Pro Phe Pro Arg
      100     105     110
Met Pro Pro Pro Ser Thr Arg Pro Ile Pro His Arg Ala Arg Ala Thr
      115     120     125
Pro Pro Pro His Pro His His Arg Pro Pro His Ala Asn Pro Pro Thr
      130     135     140
Pro Pro Pro Ala Gly Ile Arg Arg Pro Thr Pro Gly Pro His Arg Thr
145     150     155     160
Gly Leu Thr Ala Pro Pro Arg Pro Arg Thr Pro Pro Pro Leu Arg His
      165     170     175
Gln Pro Thr Pro Ala Pro Leu Pro His Pro Gln Arg Thr Ser Arg Pro
      180     185     190
Ala Pro Arg Gln Pro Gln Asn Pro Pro Ala Thr His Pro Ala Pro Pro
      195     200     205
Pro Thr Tyr Arg Pro Cys Ser Arg Pro Pro Ala Pro Ser Xaa Pro Xaa
      210     215     220
Xaa Xaa Xaa Xaa Xaa Xaa Phe Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
225     230     235     240
Xaa Xaa Xaa Xaa Thr Thr Gln Thr Gly Lys Gln Leu Ala Thr Leu Thr
      245     250     255
Leu Leu Thr Thr Val Leu Pro Thr
      260
```

(2) INFORMATION FOR SEQ ID NO:2799:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 116 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2799:

```

Ser Ile Ser Phe Asp Glu Thr Ala Ile Phe Gly Glu Leu Ile Arg Tyr
1           5           10           15
Leu Asp Gln Tyr Glu Asp Val Ile Leu Arg Glu Ile Lys Ala Gln Phe
          20           25           30
Pro Asp Val Ala Val Asp Lys Leu Met Glu Glu Tyr Ile Lys Ala Gly
          35           40           45
Leu Ile Leu Arg Glu Asn Lys Arg Tyr Tyr Leu Asn Phe Pro Thr Leu
          50           55           60
Glu Ser Leu Asp Ser Leu Glu Leu Asp Gln Glu Ile Phe Val Arg Glu
65           70           75           80
Ala Ser Pro Val Tyr Gln Ala Leu Leu Glu Gln Ser Phe Glu Thr Glu
          85           90           95
Leu Arg Asn Gln Ile Asn Ala Ala Ile Leu Val Glu Arg Arg Thr Leu
          100          105          110
Arg Ala Leu Lys
          115
  
```

(2) INFORMATION FOR SEQ ID NO:2800:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 75 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...75

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2800:

```

Phe Leu Ile Pro Ala Ile Val Lys Pro Glu Val Phe Ser Ser Ala Lys
1           5           10           15
Pro His Ser Val Phe Thr Thr Met Cys Pro Cys His His Glu Ser Pro
          20           25           30
Asn Asp Leu Thr Arg Lys Tyr Asp Phe Tyr Val Tyr Pro Asn Ser Ile
          35           40           45
Met Thr Phe Phe Ser Lys Val Asn Ile Ser His Phe Phe Asn Asp Lys
          50           55           60
Lys Glu Ala Ala Asn Arg Pro Thr Ser Cys Phe
65           70           75
  
```

(2) INFORMATION FOR SEQ ID NO:2801:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...143

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2801:

```
Phe Leu Ile Pro Ala Ile Val Lys Pro Glu Val Phe Ser Ser Ala Lys
1           5           10           15
Pro His Ser Val Phe Thr Thr Met Cys Pro Cys His His Glu Ser Pro
20           25           30
Asn Asp Leu Thr Arg Lys Tyr Asp Phe Tyr Val Tyr Pro Asn Ser Ile
35           40           45
Met Thr Phe Phe Ser Lys Val Asn Ile Ser His Phe Phe Asn Asp Lys
50           55           60
Lys Glu Ala Thr Asn Arg Pro Thr Ser Tyr Ser Glu Pro Ile Thr Pro
65           70           75           80
Ser Leu Phe Ser Phe Ile Arg Phe Leu Ser Asp Cys Asn Leu Val Phe
85           90           95
Asp Leu Val Ile Pro Leu Thr Gly Thr Thr Met Ser Asn Cys Ser Arg
100          105          110
Ser Tyr Leu Met Arg Tyr Phe Asn Gln Phe Phe Arg Asn Gln Arg Ala
115          120          125
Ala Gln Gly Arg Tyr Gln Gly Ile Leu Leu Phe Ile Ile Gly Met
130          135          140
```

(2) INFORMATION FOR SEQ ID NO:2802:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

(B) LOCATION 1...73

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2802:

```
Lys Pro Ile Pro Asn Ile Ile Ser Leu Ala Ala Glu Lys Pro Ser Phe
1          5          10          15
Leu Ala Ser Lys Asn Asn Ile Lys Asp Asp Val Ser Pro Gln Val Ile
          20          25          30
Glu Ile Ile Pro Val Val Lys Leu Phe Val Phe Asn Thr Asn Met Gln
          35          40          45
Lys Thr Ala Ala Ile Asp Glu Glu Leu Val Thr Pro Ile Ile Ser Gly
          50          55          60
Leu Ala Arg Gly Phe Leu Asn Ile Val
65          70
```

(2) INFORMATION FOR SEQ ID NO:2803:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...127

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2803:

```
Gln Lys Ile Pro Thr Ile Gln Ser Ser Ser Asn Lys Glu Lys Asn Met
1          5          10          15
Ser Asn Ile Tyr Asp Ser Ala Asn Glu Leu Ser Arg Gly Leu Arg Gly
          20          25          30
Leu Pro Glu Tyr Lys Ala Val Lys Ala Ala Lys Asp Ala Ile Ala Ala
          35          40          45
Asp Ala Glu Ala Ser Lys Ile Phe Thr Glu Tyr Leu Ala Phe Gln Glu
          50          55          60
Glu Ile Gln Lys Leu Ala Gln Thr Gly Gln Met Pro Asp Ala Ser Phe
65          70          75          80
Gln Ala Lys Met Glu Gly Phe Gly Lys Gln Ile Gln Gly Asn Ser Leu
          85          90          95
Leu Ser Glu Phe Phe Thr Lys Gln Gln Gln Leu Ala Ile Tyr Leu Ser
          100          105          110
Asp Ile Glu Lys Ile Val Phe Glu Pro Val Ser Glu Leu Leu Lys
          115          120          125
```

(2) INFORMATION FOR SEQ ID NO:2804:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 612 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...612

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2804:

```

Thr Ser Ile Pro Ala Gln Asn Leu Arg Ala Val Ser Leu Leu Ala Asn
1      5      10      15
Leu Ser Lys Lys Ile Ala Gln Ser Thr Ile Ser Asn Ile Ser Asn Ser
20      25      30
Cys Leu Thr Asn Cys Ser Ile Thr Lys Lys Lys Leu Ala Pro Ser Lys
35      40      45
Leu Arg Ser Ser Asn Met Ala Tyr Thr Leu Lys Pro Glu Glu Val Gly
50      55      60
Val Phe Ala Ile Gly Gly Leu Gly Glu Ile Gly Lys Asn Thr Tyr Gly
65      70      75      80
Ile Glu Tyr Gln Asp Glu Ile Ile Ile Val Asp Ala Gly Ile Lys Phe
85      90      95
Pro Glu Asp Asp Leu Leu Gly Ile Asp Tyr Val Ile Pro Asp Tyr Ser
100     105     110
Tyr Ile Val Asp Asn Ile Asp Arg Val Lys Ala Val Leu Ile Thr His
115     120     125
Gly His Glu Asp His Ile Gly Gly Ile Pro Phe Leu Leu Lys Gln Ala
130     135     140
Asn Val Pro Ile Tyr Ala Gly Pro Leu Ala Leu Ala Leu Ile Arg Gly
145     150     155     160
Lys Leu Glu Glu His Gly Leu Leu Arg Asn Ala Lys Leu Tyr Glu Ile
165     170     175
Asn His Asn Thr Glu Leu Thr Phe Lys Asn Leu Lys Ala Thr Phe Phe
180     185     190
Arg Thr Thr His Ser Ile Pro Glu Pro Leu Gly Ile Val Ile His Thr
195     200     205
Pro Gln Gly Lys Ile Val Cys Thr Gly Asp Phe Lys Phe Asp Phe Thr
210     215     220
Pro Val Gly Glu Pro Ala Asp Leu His Arg Met Ala Ala Leu Gly Glu
225     230     235     240
Glu Gly Val Leu Cys Leu Leu Ser Asp Ser Thr Asn Ala Glu Val Pro
245     250     255
Thr Phe Thr Asn Ser Glu Lys Val Val Gly Gln Ser Ile Met Lys Ile
260     265     270
Ile Gln Gly Ile Glu Gly Arg Ile Ile Phe Ala Ser Phe Ala Ser Asn
275     280     285
Ile Phe Arg Leu Gln Gln Ala Thr Glu Ala Ala Val Lys Thr Gly Arg
290     295     300
Lys Ile Ala Val Phe Gly Arg Ser Met Glu Lys Ala Ile Val Asn Gly
305     310     315     320
Ile Asp Leu Gly Tyr Ile Lys Ala Pro Lys Gly Thr Phe Ile Glu Pro

```

				325				330					335				
Asn	Glu	Ile	Lys	Asp	Tyr	Pro	Ala	Gly	Glu	Val	Leu	Ile	Leu	Cys	Thr		
			340					345					350				
Gly	Ser	Gln	Gly	Glu	Pro	Met	Ala	Ala	Leu	Ser	Arg	Ile	Ala	Asn	Gly		
		355					360					365					
Thr	His	Arg	Gln	Val	Gln	Leu	Gln	Pro	Gly	Asp	Thr	Val	Ile	Phe	Ser		
	370					375					380						
Ser	Ser	Pro	Ile	Pro	Gly	Asn	Thr	Thr	Ser	Val	Asn	Lys	Leu	Ile	Asn		
385				390						395					400		
Ile	Ile	Ser	Glu	Ala	Gly	Val	Glu	Val	Ile	His	Gly	Lys	Val	Asn	Asn		
			405					410					415				
Ile	His	Thr	Ser	Gly	His	Gly	Gly	Gln	Gln	Glu	Gln	Lys	Leu	Met	Leu		
		420					425					430					
Cys	Leu	Ile	Lys	Pro	Lys	Tyr	Phe	Met	Pro	Val	His	Gly	Glu	Tyr	Arg		
	435					440					445						
Met	Gln	Lys	Val	His	Ala	Gly	Leu	Ala	Val	Asp	Thr	Gly	Val	Glu	Lys		
	450					455				460							
Asp	Asn	Ile	Phe	Ile	Met	Ser	Asn	Gly	Asp	Val	Leu	Ala	Leu	Thr	Ala		
465				470					475						480		
Asp	Ser	Ala	Arg	Ile	Ala	Gly	His	Phe	Asn	Ala	Gln	Asp	Ile	Tyr	Val		
		485					490						495				
Asp	Gly	Asn	Arg	Ile	Gly	Glu	Ile	Gly	Ala	Ala	Val	Leu	Lys	Asp	Arg		
	500					505						510					
Arg	Asp	Leu	Ser	Glu	Asp	Gly	Val	Val	Leu	Ala	Val	Ala	Thr	Val	Asp		
	515					520					525						
Phe	Lys	Ser	Gln	Met	Ile	Leu	Ser	Gly	Pro	Asp	Ile	Leu	Ser	Arg	Gly		
	530				535					540							
Phe	Val	Tyr	Met	Arg	Glu	Ser	Gly	Asp	Leu	Ile	Arg	Gln	Ser	Gln	Arg		
545				550					555						560		
Ile	Leu	Phe	Asn	Ala	Ile	Arg	Ile	Ala	Leu	Lys	Asn	Lys	Asp	Ala	Ser		
		565					570					575					
Val	Gln	Ser	Val	Asn	Gly	Ala	Ile	Val	Asn	Ala	Ile	Arg	Pro	Phe	Leu		
	580					585					590						
Tyr	Glu	Asn	Thr	Glu	Arg	Glu	Pro	Ile	Ile	Ile	Pro	Met	Ile	Leu	Thr		
	595					600					605						
Pro	Asp	Glu	Glu														
	610																

(2) INFORMATION FOR SEQ ID NO:2805:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...81

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2805:

Ser	Ile	Val	Pro	Gly	Met	Met	Val	Ile	Pro	Leu	Pro	Val	Pro	Ala	Ser
1				5					10					15	
Pro	Arg	Ile	Glu	Ala	Asn	Pro	Pro	Pro	Ile	Ala	Pro	Ala	Ile	Asn	Glu
			20					25					30		
Arg	Lys	Asn	Gly	Leu	Arg	Lys	Arg	Lys	Phe	Thr	Pro	Lys	Ile	Ala	Gly
		35					40					45			
Ser	Val	Ile	Pro	Arg	Lys	Ala	Glu	Arg	Ala	Ala	Gly	Lys	Ala	Ser	Val
	50					55					60				
Phe	Ser	Phe	Gly	Phe	Phe	Val	Leu	Thr	Pro	Thr	Ala	Thr	Val	Ala	Ala
65					70					75					80
Pro															

(2) INFORMATION FOR SEQ ID NO:2806:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 247 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...247

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2806:

Gly	Asp	Ser	Phe	Arg	Arg	Ser	Lys	Pro	Ser	Met	Thr	Glu	Thr	Ile	Lys
1				5				10						15	
Leu	Met	Lys	Ala	His	Thr	Ser	Val	Arg	Arg	Phe	Lys	Glu	Gln	Val	Leu
			20					25					30		
Pro	Gln	Glu	Asp	Leu	Thr	Glu	Ile	Leu	Thr	Ala	Ala	Gln	Met	Ala	Ser
		35					40					45			
Ser	Trp	Lys	Asn	Phe	Gln	Ser	Tyr	Ser	Val	Ile	Val	Val	Arg	Ser	Gln
	50					55					60				
Glu	Lys	Lys	Asp	Ala	Leu	Tyr	Glu	Leu	Val	Pro	Gln	Glu	Ala	Ile	Arg
65					70					75					80
Gln	Ser	Ala	Val	Phe	Leu	Leu	Phe	Val	Gly	Asp	Leu	Asn	Arg	Ala	Glu
				85					90					95	
Lys	Gly	Ala	Arg	Leu	His	Thr	Asp	Thr	Phe	Gln	Pro	Gln	Gly	Val	Glu
			100					105						110	
Gly	Leu	Leu	Ile	Ser	Ser	Val	Asp	Ala	Ala	Leu	Ala	Gly	Gln	Asn	Ala
		115					120					125			
Leu	Leu	Ala	Ala	Glu	Ser	Leu	Gly	Tyr	Gly	Gly	Val	Ile	Ile	Gly	Leu
		130					135				140				
Val	Arg	Tyr	Lys	Ser	Glu	Glu	Val	Ala	Glu	Leu	Phe	Asn	Leu	Pro	Asp
145					150					155					160
Tyr	Thr	Tyr	Ser	Val	Phe	Gly	Met	Ala	Leu	Gly	Val	Pro	Asn	Gln	Thr
				165					170					175	
His	Asp	Val	Lys	Pro	Arg	Leu	Pro	Leu	Asp	Asn	Val	Val	Phe	Glu	Glu

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...155
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2808:

Asp	Tyr	Pro	Pro	Gln	Glu	Pro	Phe	Ile	Thr	Ala	Thr	Met	Lys	Glu	Val
1				5					10					15	
Asp	Glu	Leu	Ala	Glu	Leu	Asp	Ile	Glu	Val	Ile	Ser	Leu	Asp	Cys	Thr
			20					25					30		
Lys	Arg	Glu	Arg	Tyr	Asp	Gly	Leu	Glu	Ile	Gln	Glu	Phe	Ile	Arg	Gln
			35				40					45			
Val	Lys	Glu	Lys	Tyr	Pro	Asn	Gln	Leu	Leu	Met	Ala	Asp	Thr	Ser	Ile
	50				55					60					
Phe	Glu	Glu	Gly	Leu	Ala	Val	Glu	Ala	Gly	Ile	Asp	Phe	Val	Gly	
65				70				75						80	
Thr	Thr	Leu	Ser	Gly	Tyr	Thr	Ser	Tyr	Ser	Pro	Lys	Val	Asp	Gly	Pro
			85				90						95		
Asp	Phe	Glu	Leu	Ile	Lys	Lys	Leu	Cys	Asp	Ala	Gly	Val	Asp	Val	Ile
			100				105					110			
Ala	Glu	Gly	Lys	Ile	His	Thr	Pro	Glu	Gln	Ala	Lys	Gln	Ile	Leu	Glu
			115				120					125			
Tyr	Gly	Val	Arg	Gly	Ile	Val	Val	Gly	Gly	Ala	Ile	Thr	Arg	Pro	Lys
	130				135						140				
Glu	Ile	Thr	Glu	Arg	Phe	Val	Ala	Ser	Leu	Lys					
145					150					155					

(2) INFORMATION FOR SEQ ID NO:2809:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 301 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...301
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2809:

Met	Thr	Ala	Phe	Gln	Gln	Leu	Pro	Ser	Ser	Val	Leu	Gln	Thr	Gly	Ala
1				5				10						15	

Ile	Phe	Leu	Ser	Ile	Ile	Ile	Glu	Ala	Leu	Pro	Phe	Val	Leu	Ile	Gly
		20						25					30		
Ser	Ile	Val	Ser	Gly	Leu	Ile	Glu	Val	Tyr	Ile	Thr	Pro	Asp	Lys	Val
		35					40					45			
Tyr	His	Phe	Leu	Pro	Arg	Asn	Arg	Trp	Gly	Arg	Ile	Phe	Phe	Gly	Thr
	50					55					60				
Phe	Val	Gly	Ile	Leu	Phe	Pro	Ser	Cys	Glu	Cys	Gly	Ile	Val	Pro	Ile
65					70					75					80
Ile	Asn	Arg	Phe	Leu	Glu	Lys	Lys	Val	Pro	Ser	Tyr	Thr	Ala	Val	Pro
			85						90					95	
Phe	Leu	Val	Thr	Ala	Pro	Val	Ile	Asn	Pro	Ile	Val	Leu	Phe	Ala	Thr
			100					105						110	
Tyr	Ser	Ala	Phe	Gly	Asn	Ser	Phe	His	Val	Ala	Leu	Leu	Arg	Ala	Leu
		115					120					125			
Gly	Ser	Ile	Val	Val	Ala	Val	Ile	Leu	Gly	Ile	Phe	Leu	Gly	Phe	Phe
	130					135					140				
Trp	Gln	Glu	Pro	Ile	Gln	Lys	Glu	Asn	Arg	Leu	Ala	Cys	His	Glu	His
145					150					155					160
Asp	Phe	Ser	His	Leu	Ser	Pro	Ala	Lys	Lys	Val	Phe	Gln	Val	Phe	Val
			165						170					175	
Gln	Ala	Ile	Asp	Glu	Phe	Phe	Asp	Thr	Gly	Arg	Tyr	Leu	Val	Phe	Gly
		180					185					190			
Cys	Leu	Phe	Ala	Ser	Val	Ile	Gln	Val	Tyr	Val	Pro	Thr	Arg	Ile	Leu
	195						200					205			
Thr	Ser	Ile	Ser	Ala	Thr	Pro	Leu	Phe	Ala	Ile	Leu	Leu	Leu	Met	Ile
	210					215					220				
Leu	Ala	Phe	Leu	Leu	Ser	Leu	Cys	Ser	Glu	Ala	Asp	Ala	Phe	Ile	Gly
225					230					235					240
Ala	Ser	Leu	Leu	Ser	Ser	Phe	Gly	Leu	Ala	Pro	Val	Leu	Ala	Phe	Leu
			245						250					255	
Val	Ile	Gly	Pro	Met	Leu	Asp	Ile	Lys	Asn	Ile	Leu	Met	Met	Lys	Asn
		260						265					270		
Tyr	Leu	Lys	Ala	Arg	Phe	Ile	Ser	His	Phe	Ile	Thr	Ile	Val	Thr	Leu
	275						280					285			
Val	Val	Leu	Ala	Tyr	Ser	Leu	Leu	Ile	Gly	Val	Ile	Leu			
	290					295					300				

(2) INFORMATION FOR SEQ ID NO:2810:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 118 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...118

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2810:

Phe	Ser	Ser	Leu	Thr	Leu	Thr	Ile	Pro	Arg	Ser	Ile	Arg	Pro	Glu	Ala
1				5					10					15	
Thr	Val	Pro	Arg	Pro	Val	Ile	Glu	Asn	Thr	Ser	Ser	Thr	Gly	Arg	Ser
			20					25					30		
Asn	Gly	Leu	Ser	Val	Ser	Arg	Ser	Gly	Ser	Gly	Ile	Tyr	Ser	Ser	Thr
		35					40					45			
Val	Phe	Ile	Asn	Ser	Ile	Thr	Met	Ser	Ser	Tyr	Leu	Glu	Ser	Pro	Ser
	50					55					60				
Arg	Ala	Leu	Ser	Ala	Glu	Pro	Trp	Ile	Thr	Gly	Arg	Ser	Ser	Pro	Gly
65					70					75					80
Lys	Ser	Tyr	Ser	Asp	Asn	Arg	Ser	Arg	Ile	Ser	Ile	Ser	Thr	Asn	Ser
				85				90						95	
Ser	Asn	Ser	Ser	Ser	Ser	Thr	Lys	Ser	Thr	Leu	Phe	Met	Lys	Thr	Ile
			100					105					110		
Arg	Cys	Leu	Thr	Pro	Thr										
			115												

(2) INFORMATION FOR SEQ ID NO:2811:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 523 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...523

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2811:

Leu	Thr	Thr	Pro	Gly	His	Val	Asp	Phe	Thr	Tyr	Glu	Val	Ser	Arg	Ser
1				5					10					15	
Leu	Ala	Ala	Cys	Glu	Gly	Ala	Ile	Leu	Val	Val	Asp	Ala	Ala	Gln	Gly
			20					25					30		
Ile	Glu	Ala	Gln	Thr	Leu	Ala	Asn	Val	Tyr	Leu	Ala	Leu	Asp	Asn	Asp
		35					40					45			
Leu	Glu	Ile	Met	Pro	Ile	Ile	Asn	Lys	Ile	Asp	Leu	Pro	Ala	Ala	Asp
	50					55				60					
Pro	Glu	Arg	Val	Arg	Thr	Glu	Ile	Glu	Asp	Val	Ile	Gly	Leu	Asp	Ala
65				70					75					80	
Ser	Glu	Ala	Val	Leu	Ala	Ser	Ala	Lys	Ala	Gly	Ile	Gly	Ile	Glu	Glu
				85				90						95	
Ile	Leu	Glu	Gln	Ile	Val	Glu	Lys	Val	Pro	Ala	Pro	Thr	Gly	Asp	Val
			100					105					110		
Thr	Ala	Pro	Leu	Lys	Ala	Leu	Ile	Phe	Asp	Ser	Val	Tyr	Asp	Ala	Tyr
		115				120						125			
Arg	Gly	Val	Ile	Leu	Gln	Val	Arg	Val	Met	Asp	Gly	Val	Val	Lys	Pro
	130				135					140					
Gly	Asp	Lys	Ile	Gln	Leu	Met	Ser	Asn	Ser	Lys	Thr	Phe	Asp	Val	Ala
145					150					155					160

Glu	Val	Gly	Ile	Phe	Thr	Pro	Lys	Ala	Val	Gly	Arg	Asp	Phe	Leu	Ala
				165					170					175	
Thr	Gly	Asp	Val	Gly	Tyr	Ile	Ala	Ala	Ser	Ile	Lys	Thr	Val	Gln	Asp
			180					185						190	
Thr	Arg	Val	Gly	Asp	Thr	Val	Thr	Leu	Ala	Thr	Asn	Pro	Ala	Ala	Glu
		195					200					205			
Pro	Leu	His	Gly	Tyr	Lys	Gln	Met	Asn	Pro	Met	Val	Phe	Ala	Gly	Leu
	210					215					220				
Tyr	Pro	Ile	Glu	Ser	Asn	Lys	Tyr	Asn	Asp	Leu	Arg	Glu	Ala	Leu	Glu
225					230					235					240
Lys	Met	Gln	Leu	Asn	Asp	Ala	Ser	Leu	Gln	Phe	Glu	Pro	Glu	Thr	Ser
				245					250					255	
Gln	Ala	Leu	Gly	Phe	Gly	Phe	Arg	Cys	Gly	Phe	Leu	Gly	Leu	Leu	His
		260						265					270		
Met	Asp	Val	Ile	Gln	Glu	Arg	Leu	Glu	Arg	Glu	Phe	Asn	Ile	Asp	Leu
	275						280					285			
Ile	Met	Thr	Ala	Pro	Ser	Val	Ile	Tyr	Lys	Val	Asn	Leu	Thr	Asp	Gly
	290					295					300				
Glu	Ser	Met	Asp	Val	Ser	Asn	Pro	Ser	Glu	Phe	Pro	Asp	Pro	Thr	Lys
305					310					315					320
Ile	Ala	Thr	Ile	Glu	Glu	Pro	Tyr	Val	Lys	Ala	Gln	Ile	Met	Val	Pro
			325						330					335	
Gln	Glu	Phe	Val	Gly	Ala	Val	Met	Glu	Leu	Ala	Gln	Arg	Lys	Arg	Gly
		340						345					350		
Asp	Phe	Val	Thr	Met	Asp	Tyr	Ile	Asp	Asp	Asn	Arg	Val	Asn	Val	Ile
	355						360					365			
Tyr	Gln	Ile	Pro	Leu	Ala	Glu	Ile	Val	Phe	Asp	Phe	Phe	Asp	Lys	Leu
	370					375					380				
Lys	Ser	Ser	Thr	Arg	Gly	Tyr	Ala	Ser	Phe	Asp	Tyr	Glu	Leu	Ser	Glu
385					390					395					400
Tyr	Arg	Pro	Ser	Lys	Leu	Val	Lys	Met	Asp	Ile	Leu	Leu	Asn	Gly	Asp
			405						410					415	
Lys	Val	Asp	Ala	Leu	Ser	Phe	Ile	Val	His	Lys	Asp	Phe	Ala	Tyr	Glu
		420						425					430		
Arg	Gly	Lys	Leu	Ile	Val	Asp	Lys	Leu	Lys	Lys	Ile	Ile	Pro	Arg	Gln
	435					440						445			
Gln	Phe	Glu	Val	Pro	Ile	Gln	Ala	Ala	Ile	Gly	His	Lys	Ile	Val	Ala
	450					455					460				
Arg	Thr	Asp	Ile	Lys	Ala	Leu	Arg	Lys	Asn	Val	Leu	Ala	Lys	Cys	Tyr
465					470					475					480
Gly	Gly	Asp	Val	Ser	Arg	Lys	Arg	Lys	Leu	Leu	Glu	Lys	Gln	Lys	Ala
			485						490					495	
Gly	Lys	Lys	Arg	Met	Lys	Ser	Ile	Gly	Ser	Val	Glu	Val	Pro	Gln	Glu
		500						505					510		
Ala	Phe	Leu	Ser	Val	Leu	Ser	Met	Asp	Glu	Glu					
	515						520								

(2) INFORMATION FOR SEQ ID NO:2812:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...63

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2812:

Ser	Tyr	Arg	Pro	Ile	His	Xaa	Cys	Xaa	Ile	Phe	Thr	Phe	Pro	Lys	Leu
1				5					10					15	
Glu	His	Val	Lys	Phe	Ile	Gly	Leu	Thr	His	Cys	Gly	Arg	Ile	Trp	Glu
			20					25					30		
Gly	Trp	Gly	Val	Pro	Xaa	Glu	Arg	Ile	Ile	Val	Val	Lys	Pro	Gly	Asp
		35					40					45			
His	Ile	Gly	Ile	Lys	Arg	Tyr	Glu	Asp	Ser	Cys	Ser	Arg	Ile	Ile	
	50					55					60				

(2) INFORMATION FOR SEQ ID NO:2813:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 172 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...172

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2813:

Glu	Gly	Arg	Pro	Ile	Tyr	Ile	Arg	Leu	Glu	Val	Asp	Lys	Lys	Asp	Arg
1				5					10					15	
Ile	Trp	Gly	Leu	Leu	Ala	Tyr	Gln	Glu	Asp	Phe	Gln	Arg	Leu	Ala	Arg
			20					25					30		
Pro	Ala	Tyr	Asn	Asn	Met	Gln	Asn	Gln	Asn	Trp	Pro	Ala	Ile	Val	Tyr
		35					40					45			
Arg	Leu	Lys	Leu	Ser	Gly	Thr	Phe	Val	Tyr	Leu	Pro	Glu	Asn	Asn	Met
	50					55					60				
Leu	Gly	Phe	Ile	His	Pro	Ser	Glu	Arg	Tyr	Ala	Glu	Pro	Arg	Leu	Gly
65				70					75					80	
Gln	Val	Leu	Asp	Ala	Arg	Val	Ile	Gly	Phe	Arg	Glu	Val	Asp	Arg	Thr
			85					90					95		
Leu	Asn	Leu	Ser	Leu	Lys	Pro	Arg	Ser	Phe	Glu	Met	Leu	Glu	Asn	Asp
		100					105						110		
Ala	Gln	Met	Ile	Leu	Thr	Tyr	Leu	Glu	Ser	Asn	Gly	Gly	Phe	Met	Thr
		115					120					125			
Leu	Asn	Asp	Lys	Ser	Ser	Pro	Asp	Asp	Ile	Lys	Ala	Thr	Phe	Gly	Ile
	130					135					140				

Ser Lys Gly Gln Phe Lys Lys Ala Leu Gly Gly Leu Met Lys Ala Gly
 145 150 155 160
 Lys Ile Lys Gln Asp Gln Phe Gly Thr Glu Leu Ile
 165 170

(2) INFORMATION FOR SEQ ID NO:2814:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...172

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2814:

Gly Thr Arg Pro Arg Lys Val Ala Leu Phe Leu Lys Asn Phe Asn Ser
 1 5 10 15
 Leu Lys His Leu Ala Pro Val Tyr Ile Asp Glu Thr Gly Ile Asp Arg
 20 25 30
 Tyr Leu Tyr Arg Pro Tyr Ala Arg Ala Pro Arg Gly Glu Lys Val Tyr
 35 40 45
 Glu Lys Ile Ser Gly Arg Arg Phe Glu Arg Thr Ser Ile Val Ala Gly
 50 55 60
 Gln Val Asp Gly Glu Phe Ile Ala Pro Met Ile Tyr Lys Lys Ser Met
 65 70 75 80
 Thr Ser Asp Phe Phe Val Glu Trp Phe Lys Thr Gln Leu Leu Pro Ala
 85 90 95
 Leu Lys Thr Pro His Val Ile Val Met Gly Asn Ala Ser Phe His Pro
 100 105 110
 Lys Asn Ile Leu Asp Glu Leu Cys Ile Gln Asp Lys His Phe Phe Leu
 115 120 125
 Pro Leu Pro Pro Tyr Ser Pro Asp Leu Asn Pro Ile Glu Gln Ala Trp
 130 135 140
 Ala Ile Leu Lys Lys Lys Val Thr Asp Val Leu Arg Glu Val Ser Thr
 145 150 155 160
 Ile Phe Glu Cys Leu Glu Cys Phe Phe Lys Thr Arg
 165 170

(2) INFORMATION FOR SEQ ID NO:2815:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2815:

Lys	Gly	Gly	Pro	Ala	Met	Gln	Asp	Ser	Gly	Ile	Gln	Val	Leu	Phe	Gln
1				5					10					15	
Gly	Asn	Asn	Leu	Leu	Arg	Ile	Leu	Gln	Gly	Leu	Gly	Val	Thr	Ile	Gly
			20					25					30		
Ile	Ser	Ile	Leu	Ser	Val	Leu	Leu	Ser	Met	Met	Phe	Gly	Thr	Val	Met
		35					40					45			
Gly	Ile	Ile	Met	Thr	Ser	His	Ser	Arg	Ile	Ile	Arg	Phe	Leu	Thr	Arg
		50				55					60				
Leu	Tyr	Leu	Glu	Phe	Ile	Arg	Ile	Met	Pro	Gln	Leu	Val	Leu	Leu	Phe
65					70				75						80
Ile	Val	Tyr	Phe	Gly	Leu	Ala	Arg	Asn	Phe	Asn	Ile	Asn	Ile	Ser	Gly
			85					90						95	
Glu	Thr	Ser	Ala	Ile	Ile	Ile	Phe	Thr	Leu	Trp	Gly	Thr	Ala	Glu	Met
			100					105					110		
Gly	Asp	Leu	Val	Arg	Gly	Ala	Ile	Thr	Ser	Leu	Pro	Lys	His	Gln	Phe
		115					120					125			
Glu	Ser	Gly													
		130													

(2) INFORMATION FOR SEQ ID NO:2816:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 73 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...73

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2816:

Arg	Pro	Gly	Pro	Cys	Met	Leu	Leu	Ser	Ser	Thr	Ser	Thr	Ala	Leu	Phe
1				5					10					15	
Asp	Pro	Leu	Ile	Glu	Val	Thr	Gln	Asn	Phe	Ser	Thr	Leu	Gln	Thr	Ser
			20					25					30		
Met	Val	Ser	Ala	Gly	Arg	Val	Phe	Ala	Leu	Ile	Asp	Glu	Ser	Thr	Tyr
		35				40					45				
Glu	Pro	Leu	Gln	Glu	Asn	Gly	Gln	Ala	Lys	Val	Lys	Glu	Gly	Asn	Ile

50 55 60
Ser Phe Gly Thr Cys Val Tyr Leu Val
65 70

(2) INFORMATION FOR SEQ ID NO:2817:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 95 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Streptococcus pneumoniae

```
(ix) FEATURE:
      (A) NAME/KEY: misc_feature
      (B) LOCATION 1...95
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2817:

Pro	Ile	Ala	Leu	Leu	Pro	His	Met	Arg	Lys	His	Val	Lys	Arg	Phe	Val
1				5					10					15	
Phe	Asn	Lys	Arg	Lys	Arg	Phe	Tyr	Cys	Val	Arg	Ser	Arg	Ile	Lys	Ser
			20					25					30		
Phe	Ser	Ile	Val	Val	Gly	Arg	Phe	Thr	Ser	Phe	Ser	Pro	Glu	Ile	Glu
			35				40					45			
Phe	Leu	Pro	Ser	Arg	Phe	Ile	His	His	Leu	Lys	Thr	Val	Phe	Tyr	Thr
			50			55					60				
Leu	Arg	Lys	Ser	Leu	Gln	Ile	Thr	Ser	Ala	Ser	Pro	Tyr	Arg	Thr	Gln
65					70					75					80
Val	Gln	Pro	Glu	Ala	Ser	Phe	Leu	Val	Cys	Phe	Leu	Ile	Phe	Ile	
				85					90					95	

(2) INFORMATION FOR SEO ID NO:2818:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Streptococcus pneumoniae

```
(ix) FEATURE:
      (A) NAME/KEY: misc_feature
      (B) LOCATION 1...65
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2818:

```

Ile Pro Leu Pro Leu Lys Glu Ile Lys Pro Ser Phe Tyr Gln Ile Arg
1          5          10          15
Gln Met Val Trp Met Ile Ser Glu His Lys Ser Cys Gln Pro Phe Ala
          20          25          30
Leu Arg Arg Asn Asn Arg Leu Ile Leu Phe Glu Asn Leu Phe Lys Pro
          35          40          45
Arg Gln Arg Arg Leu Ala Val Tyr Leu Gln Pro Gln Asn Ser Val Leu
50          55          60
Ser
65

```

(2) INFORMATION FOR SEQ ID NO:2819:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 721 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...721

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2819:

```

Lys Glu Leu Pro Met Thr Ser Tyr Lys Arg Thr Phe Val Pro Gln Ile
1          5          10          15
Asp Ala Arg Asp Cys Gly Val Ala Ala Leu Ala Ser Ile Ala Lys Phe
          20          25          30
Tyr Gly Ser Asp Phe Ser Leu Ala His Leu Arg Glu Leu Ala Lys Thr
          35          40          45
Asn Lys Glu Gly Thr Thr Ala Leu Gly Ile Val Lys Ala Ala Asp Glu
50          55          60
Met Gly Phe Glu Thr Arg Pro Val Gln Ala Asp Lys Thr Leu Phe Asp
65          70          75          80
Met Ser Asp Val Pro Tyr Pro Phe Ile Val His Val Asn Lys Glu Gly
          85          90          95
Lys Leu Gln His Tyr Tyr Val Val Tyr Gln Thr Lys Lys Asp Tyr Leu
          100          105          110
Ile Ile Gly Asp Pro Asp Pro Ser Val Lys Ile Thr Lys Met Ser Lys
          115          120          125
Glu Arg Phe Phe Ser Glu Trp Thr Gly Val Ala Ile Phe Leu Ala Pro
          130          135          140
Lys Pro Ser Tyr Gln Pro His Lys Asp Lys Lys Asn Gly Leu Leu Ser
145          150          155          160
Phe Leu Pro Leu Ile Phe Lys Gln Lys Ser Leu Ile Ala Tyr Ile Val
          165          170          175
Leu Ser Ser Leu Leu Val Thr Ile Ile Asn Ile Gly Gly Ser Tyr Tyr
          180          185          190
Leu Gln Gly Ile Leu Asp Glu Tyr Ile Pro Asn Gln Met Lys Ser Thr

```

		195				200				205					
Leu	Gly	Ile	Ile	Ser	Val	Gly	Leu	Val	Ile	Thr	Tyr	Ile	Leu	Gln	Gln
210						215					220				
Val	Met	Ser	Phe	Ser	Arg	Asp	Tyr	Leu	Leu	Thr	Val	Leu	Ser	Gln	Arg
225					230					235					240
Leu	Ser	Ile	Asp	Val	Ile	Leu	Ser	Tyr	Ile	Arg	His	Ile	Phe	Glu	Leu
				245					250					255	
Pro	Met	Ser	Phe	Ala	Thr	Arg	Arg	Thr	Gly	Glu	Ile	Ile	Ser	Arg	
			260					265				270			
Phe	Thr	Asp	Ala	Asn	Ser	Ile	Ile	Asp	Ala	Leu	Ala	Ser	Thr	Ile	Leu
		275				280					285				
Ser	Leu	Phe	Leu	Asp	Val	Ser	Ile	Leu	Ile	Leu	Val	Gly	Gly	Val	Leu
290					295					300					
Leu	Ala	Gln	Asn	Pro	Asn	Leu	Phe	Leu	Leu	Ser	Leu	Leu	Ser	Ile	Pro
305				310					315						320
Ile	Tyr	Met	Phe	Ile	Ile	Phe	Ser	Phe	Met	Lys	Pro	Phe	Glu	Lys	Met
			325			330								335	
Asn	His	Asp	Val	Met	Gln	Ser	Asn	Ser	Met	Val	Ser	Ser	Ala	Ile	Ile
		340				345						350			
Glu	Asp	Ile	Asn	Gly	Ile	Glu	Thr	Ile	Lys	Ser	Leu	Thr	Ser	Glu	Glu
	355				360							365			
Asn	Arg	Tyr	Gln	Asn	Ile	Asp	Ser	Glu	Phe	Val	Asp	Tyr	Leu	Glu	Lys
370				375						380					
Ser	Phe	Lys	Leu	Ser	Lys	Tyr	Ser	Ile	Leu	Gln	Thr	Ser	Leu	Lys	Gln
385				390					395						400
Gly	Thr	Lys	Leu	Val	Leu	Asn	Ile	Leu	Ile	Leu	Trp	Phe	Gly	Ala	Gln
			405					410					415		
Leu	Val	Met	Ser	Ser	Lys	Ile	Ser	Ile	Gly	Gln	Leu	Ile	Thr	Phe	Asn
		420					425					430			
Thr	Leu	Phe	Ser	Tyr	Phe	Thr	Thr	Pro	Met	Glu	Asn	Ile	Ile	Asn	Leu
	435					440						445			
Gln	Thr	Lys	Leu	Gln	Ser	Ala	Lys	Val	Ala	Asn	Asn	Arg	Leu	Asn	Glu
450				455						460					
Val	Tyr	Leu	Val	Glu	Ser	Glu	Phe	Gln	Val	Gln	Glu	Asn	Pro	Val	His
465				470				475							480
Ser	His	Phe	Leu	Met	Gly	Asp	Ile	Glu	Phe	Asp	Asp	Leu	Ser	Tyr	Lys
			485			490						495			
Tyr	Gly	Phe	Gly	Arg	Asp	Thr	Leu	Thr	Asp	Ile	Asn	Leu	Thr	Ile	Lys
		500				505						510			
Gln	Gly	Asp	Lys	Val	Ser	Leu	Val	Gly	Val	Ser	Gly	Ser	Gly	Lys	Thr
	515					520						525			
Thr	Leu	Ala	Lys	Met	Ile	Val	Asn	Phe	Phe	Glu	Pro	Tyr	Lys	Gly	His
530				535						540					
Ile	Ser	Ile	Asn	Tyr	Gln	Asp	Ile	Lys	Asn	Ile	Asp	Lys	Lys	Val	Leu
545				550					555						560
Arg	Arg	His	Ile	Asn	Tyr	Leu	Pro	Gln	Gln	Ala	Tyr	Ile	Phe	Asn	Gly
			565					570						575	
Ser	Ile	Leu	Glu	Asn	Leu	Thr	Leu	Gly	Gly	Asn	His	Met	Ile	Ser	Gln
		580					585					590			
Glu	Asp	Ile	Leu	Arg	Ala	Cys	Glu	Leu	Ala	Glu	Ile	Arg	Gln	Asp	Ile
	595					600						605			
Glu	Arg	Met	Pro	Met	Gly	Tyr	Gln	Thr	Gln	Leu	Ser	Asp	Gly	Ala	Gly
610				615						620					
Leu	Ser	Gly	Gly	Gln	Lys	Gln	Arg	Ile	Ala	Leu	Ala	Arg	Ala	Leu	Leu
625				630					635						640
Thr	Lys	Ala	Pro	Val	Leu	Ile	Leu	Asp	Glu	Ala	Thr	Ser	Gly	Leu	Asp
			645					650						655	

Val	Leu	Thr	Glu	Lys	Lys	Val	Ile	Asp	Asn	Leu	Ile	Ser	Leu	Thr	Asp
			660					665					670		
Lys	Thr	Ile	Leu	Phe	Val	Ala	His	Arg	Leu	Ser	Ile	Ala	Glu	Arg	Thr
		675					680					685			
Asn	Arg	Val	Ile	Val	Leu	Asp	Gln	Gly	Lys	Ile	Ile	Glu	Val	Gly	Ser
	690					695				700					
His	Gln	Glu	Leu	Met	Gln	Ala	Gln	Gly	Phe	Tyr	His	His	Leu	Phe	Asn
705					710					715					720
Lys															

(2) INFORMATION FOR SEQ ID NO:2820:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...248

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2820:

Asp	Ser	Met	Pro	Met	Arg	Asp	Arg	Ile	Ser	Ala	Phe	Leu	Glu	Glu	Lys
1				5					10					15	
Gln	Gly	Leu	Ser	Val	Asn	Ser	Lys	Gln	Ser	Tyr	Lys	Tyr	Asp	Leu	Glu
		20						25					30		
Gln	Phe	Leu	Asp	Met	Val	Gly	Glu	Arg	Ile	Ser	Glu	Thr	Ser	Leu	Lys
		35					40					45			
Ile	Tyr	Gln	Ala	Gln	Leu	Ala	Asn	Leu	Lys	Ile	Ser	Ala	Gln	Lys	Arg
	50					55					60				
Lys	Ile	Ser	Ala	Cys	Asn	Gln	Phe	Leu	Tyr	Phe	Leu	Tyr	Gln	Lys	Gly
65				70						75				80	
Glu	Val	Asp	Ser	Phe	Tyr	Arg	Leu	Glu	Leu	Ala	Lys	Gln	Ala	Glu	Lys
			85						90					95	
Lys	Thr	Glu	Lys	Pro	Glu	Ile	Leu	Tyr	Leu	Asp	Ser	Phe	Trp	Gln	Glu
		100						105					110		
Ser	Asp	His	Pro	Glu	Gly	Arg	Leu	Leu	Ala	Leu	Leu	Ile	Leu	Glu	Met
	115					120						125			
Gly	Leu	Leu	Pro	Ser	Glu	Ile	Leu	Ala	Ile	Lys	Val	Ala	Asp	Ile	Asn
	130					135					140				
Leu	Asp	Phe	Gln	Val	Leu	Arg	Ile	Ser	Lys	Ala	Ser	Gln	Gln	Arg	Ile
145				150						155					160
Val	Thr	Ile	Pro	Thr	Ala	Leu	Leu	Ser	Glu	Leu	Glu	Pro	Leu	Met	Gly
			165						170					175	
Gln	Thr	Tyr	Leu	Phe	Glu	Arg	Gly	Gly	Lys	Pro	Tyr	Ser	Arg	Gln	Trp
		180					185					190			
Ala	Phe	Arg	Gln	Leu	Glu	Ser	Phe	Val	Lys	Glu	Lys	Gly	Phe	Pro	Ser
		195					200					205			

Leu	Ser	Ala	Gln	Val	Leu	Arg	Glu	Gln	Phe	Ile	Leu	Arg	Gln	Ile	Glu
210						215					220				
Asn	Lys	Val	Asp	Leu	Tyr	Glu	Ile	Ala	Lys	Lys	Leu	Gly	Leu	Lys	Thr
225					230					235					240
Val	Leu	Thr	Leu	Glu	Lys	Tyr	Arg								
				245											

(2) INFORMATION FOR SEQ ID NO:2821:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...221

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2821:

Ala	Val	Ser	Pro	Lys	Met	Gly	Leu	Gly	Ala	Tyr	His	Cys	Phe	Asn	Leu
1				5				10						15	
Ser	Ser	Gln	Tyr	Ser	Gly	Ala	Gly	Met	Gly	Ala	Ile	Leu	Glu	Thr	Gln
		20					25					30			
Arg	Glu	Leu	Arg	Glu	Val	Leu	Asn	Asp	Gly	Val	Lys	Pro	Cys	Asp	Leu
	35					40					45				
His	Ala	Glu	Ile	Leu	Pro	Ser	Gly	Gly	Asp	Lys	Lys	His	Tyr	Pro	Ile
	50				55					60					
Ala	Phe	Asn	Ala	Leu	Pro	Gln	Ile	Asp	Val	Phe	Thr	Asp	Asn	Asp	Tyr
65				70				75						80	
Thr	Tyr	Glu	Glu	Met	Lys	Met	Thr	Lys	Glu	Thr	Lys	Lys	Ile	Met	Glu
		85					90						95		
Asp	Asp	Ser	Ile	Ala	Val	Ser	Ala	Thr	Cys	Val	Arg	Ile	Pro	Val	Leu
	100					105						110			
Ser	Ala	His	Ser	Glu	Ser	Val	Tyr	Ile	Glu	Thr	Lys	Glu	Val	Ala	Pro
	115					120					125				
Ile	Glu	Glu	Val	Lys	Ala	Ala	Ile	Ala	Ala	Phe	Pro	Gly	Ala	Val	Leu
	130				135					140					
Glu	Asp	Asp	Val	Ala	His	Gln	Ile	Tyr	Pro	Gln	Ala	Ile	Asn	Ala	Val
145				150				155						160	
Gly	Ser	Arg	Asp	Thr	Phe	Val	Gly	Arg	Ile	Arg	Lys	Asp	Leu	Asp	Ala
		165					170						175		
Glu	Lys	Gly	Ile	His	Met	Trp	Val	Val	Ser	Asp	Asn	Leu	Leu	Lys	Gly
	180				185							190			
Ala	Ala	Trp	Asn	Ser	Val	Gln	Ile	Ala	Glu	Thr	Leu	His	Glu	Arg	Gly
	195				200						205				
Leu	Val	Arg	Pro	Thr	Ala	Glu	Leu	Lys	Phe	Glu	Leu	Lys			
	210				215					220					

(2) INFORMATION FOR SEQ ID NO:2822:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 68 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...68

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2822:

Ala	Phe	Ser	Pro	Asn	Val	Ile	Pro	Cys	Lys	Ile	Pro	Pro	Val	Pro	Phe
1				5					10					15	
Phe	Gln	Ser	Ser	Tyr	His	Leu	Leu	Ala	Phe	Ala	Tyr	Tyr	Ile	Ile	Ile
			20					25					30		
Cys	Val	His	Leu	Ser	Lys	His	Ser	Asp	Thr	Leu	Val	Ile	Glu	Lys	Ala
		35					40					45			
Ser	Leu	Lys	Leu	Thr	Leu	Lys	Gly	Pro	Ser	Leu	Val	Gln	Tyr	Arg	Thr
		50				55					60				
Gln	Ser	Ser	Phe												
65															

(2) INFORMATION FOR SEQ ID NO:2823:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 311 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2823:

Leu	Val	Ala	Pro	Met	Glu	Pro	Ala	Thr	Cys	Val	Arg	Val	Ser	Ser	Leu
1				5					10					15	
Thr	Phe	Leu	Phe	Trp	Glu	Pro	Met	Pro	Met	Pro	Trp	Tyr	Arg	Phe	Met
			20					25					30		
Ala	Met	Thr	Met	Arg	Leu	Ser	Arg	Leu	Thr	Leu	Arg	Pro	Thr	Lys	Ile
		35					40					45			

Val	Ser	Phe	Leu	Trp	Ile	Pro	Met	Ile	Pro	Phe	Ala	Ser	Val	Tyr	Gln
50						55					60				
Leu	Pro	Phe	Arg	Trp	Arg	Val	Ser	Trp	Val	Ile	Arg	Leu	Thr	Leu	Trp
65					70					75					80
Val	Cys	Gly	Leu	Thr	Leu	Gly	Ile	Leu	Pro	Thr	Phe	Leu	Arg	Lys	Ser
				85					90					95	
Val	Ser	Asn	Trp	Thr	Arg	Leu	Asp	Leu	Gln	Arg	Leu	Arg	Phe	Met	Leu
			100					105					110		
Leu	Met	Ile	Trp	Thr	Lys	Ile	Leu	Ser	Ser	Ile	Ser	Arg	Cys	Lys	Arg
		115					120					125			
Pro	Arg	Leu	Met	Ser	Gly	Val	Trp	Val	Pro	Gln	Leu	Ile	Thr	Ala	Tyr
		130					135					140			
Asp	Gln	Pro	Ala	Leu	Gly	Ala	Val	Tyr	Lys	Ile	Val	Ala	Ile	Glu	Asp
145					150					155					160
Glu	Thr	Gly	Gln	Met	Arg	Asn	Thr	Ile	Lys	Leu	Ser	Asn	Asn	Ala	Glu
				165					170					175	
Lys	Val	Ser	Thr	Pro	Gly	Lys	Lys	Gln	Val	Trp	Arg	Ile	Thr	Ser	Arg
			180					185					190		
Glu	Lys	Gly	Lys	Ser	Glu	Gly	Asp	Tyr	Ile	Thr	Tyr	Asp	Gly	Val	Asp
		195					200					205			
Ile	Ser	Asp	Met	Thr	Glu	Ile	Lys	Met	Phe	His	Pro	Thr	Tyr	Thr	Tyr
		210					215				220				
Ile	Lys	Lys	Thr	Val	Arg	Asn	Phe	Asp	Ala	Val	Pro	Leu	Leu	Val	Asp
225					230					235					240
Ile	Phe	Lys	Glu	Gly	Ile	Leu	Val	Tyr	Asn	Leu	Pro	Ser	Leu	Thr	Asp
				245					250					255	
Ile	Gln	Asp	Tyr	Ala	Arg	Lys	Glu	Phe	Asp	Lys	Leu	Trp	Asp	Glu	Tyr
			260					265					270		
Lys	Arg	Val	Leu	Asn	Pro	Gln	His	Tyr	Pro	Val	Asp	Leu	Ala	Arg	Asp
		275					280					285			
Val	Trp	Gln	Asp	Lys	Met	Asp	Leu	Ile	Asp	Lys	Met	Arg	Lys	Glu	Ala
		290				295					300				
Leu	Gly	Glu	Gly	Glu	Glu	Glu									
305						310									

(2) INFORMATION FOR SEQ ID NO:2824:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...143

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2824:

Ser	Pro	Gln	Pro	Arg	Tyr	Trp	Ile	Ser	Asn	Leu	Ala	Pro	Thr	Phe	Ser
1				5					10					15	


```

Ser Met Ile Leu Leu Ala Phe Ala Asn Asn Ser Ser Lys Leu Ser Gly
      20      25      30
Leu Ser Pro Ile Trp Tyr Ile Leu Ile Thr Gly Leu Ser Pro Glu Ser
      35      40      45
Ala Ala Phe Leu Leu Leu Pro Val Lys Phe Pro Gln Ala Ala Arg Pro
      50      55      60
Ala Ala Arg Ala Thr Thr Leu Ala Asp Ala Lys Ala Tyr Phe Phe Gln
      65      70      75      80
Phe Phe Met Ile Lys Thr Pro Phe Phe Ile Phe Lys Leu Ile Asn Asn
      85      90      95
Val Met Ile Leu Tyr Ser Met Lys Ile Lys Glu Gln Thr Arg Lys Leu
      100     105     110
Ala Ala Gly Cys Ser Lys His Cys Phe Glu Val Val Asp Lys Thr Asp
      115     120     125
Glu Val Ser Tyr Ile Tyr Leu Arg Gln Gly Asp Val Asp Thr Val
      130     135     140

```

(2) INFORMATION FOR SEQ ID NO:2825:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 197 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...197

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2825:

```

Pro Arg Gln Pro Thr Asn Trp Ala Ser Arg Leu Leu Arg Ser Met Leu
1      5      10      15
Phe His Thr Glu Asn Trp Thr Arg Pro Asp Gln Glu Val Lys Phe Ile
      20      25      30
Met Asn Leu Pro Val Glu Phe Tyr Asp Asn Tyr Val Pro Glu Leu His
      35      40      45
Ala Asn Asn Val Lys Ile Gln Met Ile Gly Glu Thr Asp Arg Leu Pro
      50      55      60
Lys Gln Thr Phe Glu Ala Leu Thr Lys Ala Glu Glu Leu Thr Lys Asn
      65      70      75      80
Asn Thr Gly Leu Ile Leu Asn Phe Ala Leu Asn Tyr Gly Gly Arg Ala
      85      90      95
Glu Ile Thr Gln Ala Leu Lys Leu Ile Ser Gln Asp Val Leu Asp Ala
      100     105     110
Lys Ile Asn Pro Gly Asp Ile Thr Glu Glu Leu Ile Gly Asn Tyr Leu
      115     120     125
Phe Thr Gln His Leu Pro Lys Asp Leu Arg Asp Pro Asp Leu Ile Ile
      130     135     140
Arg Thr Ser Gly Glu Leu Arg Leu Ser Asn Phe Leu Pro Trp Gln Gly

```

145		150		155		160									
Ala	Tyr	Ser	Glu	Leu	Tyr	Phe	Thr	Asp	Thr	Leu	Trp	Pro	Asp	Phe	Asp
		165		170		175									
Glu	Ala	Ala	Leu	Gln	Glu	Ala	Ile	Leu	Ala	Tyr	Asn	Arg	Arg	His	Arg
		180		185		190									
Arg	Phe	Gly	Gly	Val											
		195													

(2) INFORMATION FOR SEQ ID NO:2826:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 168 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...168
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2826:

Ser	Cys	Lys	Pro	Trp	Ser	Phe	Pro	Tyr	Arg	Lys	Pro	Phe	Lys	Ser	Leu
1				5				10					15		
Gly	Lys	Asp	Asp	Leu	Glu	Ile	Ile	Asn	Arg	Ser	Met	Val	Lys	Ala	Asn
		20						25					30		
Val	Glu	Asp	Leu	Ala	Asn	Asn	Leu	Val	Glu	Glu	Leu	Ser	Gly	Gly	Gln
		35					40					45			
Arg	Gln	Arg	Val	Trp	Ile	Ala	Leu	Ala	Leu	Ala	Gln	Asp	Thr	Ser	Ile
		50				55					60				
Leu	Leu	Leu	Asp	Glu	Pro	Thr	Thr	Tyr	Leu	Asp	Ile	Ser	Tyr	Gln	Ile
65				70				75						80	
Glu	Leu	Leu	Asp	Leu	Leu	Thr	Asp	Leu	Asn	Gln	Lys	Tyr	Lys	Thr	Thr
			85					90					95		
Ile	Cys	Met	Ile	Leu	His	Asp	Ile	Asn	Leu	Thr	Ala	Arg	Tyr	Ala	Asp
			100					105					110		
Tyr	Leu	Phe	Ala	Ile	Lys	Glu	Gly	Lys	Leu	Val	Ala	Glu	Gly	Lys	Pro
		115				120						125			
Glu	Asp	Ile	Leu	Asn	Asp	Lys	Leu	Val	Lys	Asp	Ile	Phe	Asn	Leu	Glu
	130					135					140				
Ala	Lys	Ile	Ile	Arg	Asp	Pro	Ile	Ser	Asn	Ser	Pro	Leu	Met	Ile	Pro
145				150				155							160
Ile	Gly	Lys	His	His	Val	Ser	Ser								
			165												

(2) INFORMATION FOR SEQ ID NO:2827:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 115 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...115
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2827:

```

Ile Ser Lys Pro Thr Gln Thr Pro Ser Val Phe Lys Val Lys Ser Val
1          5          10          15
Ile Ser Val Ile Pro Ile Ala Lys Ile Tyr Cys Lys His Ser Asn Asn
          20          25          30
Lys Leu Ile Lys Lys Pro Val Pro Thr Ile Leu Lys Leu Asp Lys Leu
          35          40          45
Val Phe Ile Lys Gly Lys Gln Thr Pro Asn Gly Ile Lys Lys Ile Arg
          50          55          60
Leu Asn Asn Ile Ser Ala Lys Thr Ile Phe Pro Ser Thr Ile Ser Gly
65          70          75          80
Ser Glu Asn Gly Ile Gln Leu Ile Tyr Leu Gly Ala Lys Lys Asn Ala
          85          90          95
Ile Asn Ser Gly Phe Val Ser Asn Leu Asn Lys Ile Pro Gln Val Asn
          100          105          110
Asn Ile Arg
          115

```

(2) INFORMATION FOR SEQ ID NO:2828:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 81 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...81

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2828:

```

Arg Arg Ala Leu Asn Gln Ser Phe Gln Lys Pro Arg Ala Val Lys Ser
1          5          10          15
Val Met Val Ala Ile Pro Gly Ser Asp Asn Gly Lys Gln Ile Trp Lys
          20          25          30
Lys Ile Arg Ala Ser Leu Ala Pro Ser Ile Arg Ala Asp Ser Arg Met
          35          40          45

```

Ala	Ser	Gly	Met	Val	Phe	Leu	Lys	Lys	Glu	Arg	Ile	Lys	Met	Met	Leu
50						55					60				
Asn	Gly	Glu	Arg	Ser	Ile	Gly	Thr	Ile	Lys	Ala	Gln	Thr	Val	Ser	Pro
65					70				75						80
Ser															

(2) INFORMATION FOR SEQ ID NO:2829:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 229 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...229

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2829:

His	Ala	Glu	Pro	Ala	Pro	Thr	Ser	Leu	Pro	Pro	Pro	Pro	Ile	His	Pro
1				5				10					15		
Arg	Ser	Pro	Ser	Ser	Arg	Ser	His	Arg	Asn	Phe	Ser	Leu	Cys	Ser	Gln
			20					25					30		
Thr	Pro	Trp	Pro	His	His	Gly	Thr	His	Pro	Cys	Ser	Pro	Tyr	Leu	Pro
			35					40					45		
Ala	Asp	Thr	Ala	Leu	Leu	Thr	Pro	Thr	Ala	Pro	His	Ser	Pro	His	Ser
50						55					60				
Thr	Arg	Pro	Arg	Thr	Ala	Pro	Ala	Ser	Thr	Pro	Ala	Thr	Pro	Leu	Pro
65					70					75				80	
Ser	Thr	Pro	Arg	Ser	Pro	Ala	Cys	Arg	Pro	Pro	Pro	Arg	Gly	Gln	Ser
				85					90					95	
Pro	Thr	Ala	Arg	Glu	Gln	Leu	Pro	Pro	Pro	Thr	Pro	Thr	Thr	Ala	Arg
			100					105					110		
Arg	Thr	Pro	Thr	Pro	Pro	Arg	Pro	Pro	Gln	Glu	Ser	Ala	Ala	Pro	
			115				120				125				
Pro	Arg	Ala	His	Thr	Ala	Pro	Ala	Ser	Pro	Pro	His	Pro	Ala	Pro	Ala
130						135					140				
His	Pro	Pro	His	Ser	Ala	Thr	Ser	Pro	His	Arg	Pro	Pro	Tyr	His	Thr
145				150					155					160	
Pro	Asn	Glu	Arg	Ala	Ala	Pro	Pro	His	Ala	Ser	Pro	Lys	Thr	Pro	Pro
				165					170					175	
Pro	Pro	Thr	Pro	Pro	Arg	Arg	Xaa	Pro	Thr	Ala	His	Ala	Arg	Asp	Pro
			180				185						190		
Pro	His	Arg	Ala	Ser	His	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Phe	Xaa	Xaa
			195				200					205			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Leu	His	Lys	Leu	Ala
210						215					220				
Ser	Ser	Trp	Arg	Pro											

(2) INFORMATION FOR SEQ ID NO:2830:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2830:

```

Gln Tyr Phe Leu Arg Gly Asp Ile Phe Met Ser Glu Arg Lys Leu Phe
1          5          10          15
Thr Ser Glu Ser Val Ser Glu Gly His Pro Asp Lys Ile Ala Asp Gln
          20          25          30
Ile Ser Asp Ala Ile Leu Asp Ala Ile Leu Ala Lys Asp Pro Glu Ala
          35          40          45
His Val Ala Ala Glu Thr Ala Val Tyr Thr Gly Ser Val His Val Phe
          50          55          60
Gly Glu Ile Ser Thr Asn Ala Tyr Val Asp Ile Asn Arg Val Val Arg
65          70          75          80
Asp Thr Ile Ala Glu Ile Gly Tyr Thr Asn Thr Glu Tyr Gly Phe Ser
          85          90          95
Ala Glu Thr Val Gly Val His Pro Ser Leu Val Glu Gln Ser Pro Asp
          100          105          110
Ile Ala Gln Gly Val Asn Glu Ala Leu Glu Val Arg Gly Asn Ala Asp
          115          120          125
Gln Asp Pro Leu Asp Leu Ile Gly Ala Gly Asp Gln Gly Leu Met Phe
          130          135          140
Gly Phe Ala Val Asp Glu Thr Glu Glu Leu Met Pro Leu Pro Ile Ala
145          150          155          160
Leu Ser His Lys Leu Val Arg Arg Leu Ala Glu Leu Arg Lys Ser Gly
          165          170          175
Glu Ile Ser Tyr Leu Arg Pro Asp Ala Lys Ser Gln Val Thr Val Glu
          180          185          190
Tyr Asp Glu Asn Asp Arg Pro Val Arg Val Asp Thr Val Val Ile Ser
          195          200          205
Thr Gln His Asp Pro Glu Ala Thr Asn Glu Gln Ile His Gln Asp Val
          210          215          220
Ile Asp Lys Val Ile Lys Glu Val Ile Pro Ser Ser Tyr Leu Asp Asp
225          230          235          240
Lys Thr Lys Phe Phe Ile Asn Pro Thr Gly Arg Phe Val Ile Gly Gly
          245          250          255
Pro Gln Gly Asp Ser Gly Leu Thr Gly Arg Lys Ile Ile Val Asp Thr
          260          265          270
Tyr Gly Gly Tyr Ser Arg His Gly Gly Gly Ala Phe Ser Gly Lys Asp

```


Ser	Val	Gln	Lys	Ala	Ile	Ala	Gln	Ala	Arg	Ala	Tyr	Ala	Pro	Phe	Val
145					150				155					160	
Lys	Met	Val	Glu	Val	Glu	Val	Glu	Ser	Leu	Ala	Ala	Ala	Glu	Glu	Ala
			165						170					175	
Ala	Ala	Ala	Gly	Ala	Asp	Ile	Ile	Met	Leu	Asp	Asn	Met	Ser	Leu	Glu
			180					185					190		
Gln	Ile	Glu	Gln	Ala	Ile	Thr	Leu	Ile	Ala	Gly	Arg	Ser	Arg	Ile	Glu
		195					200					205			
Cys	Ser	Gly	Asn	Ile	Asp	Met	Thr	Thr	Ile	Ser	Arg	Phe	Arg	Gly	Leu
	210				215					220					
Ala	Ile	Asp	Tyr	Val	Ser	Ser	Gly	Ser	Leu	Thr	His	Ser	Ala	Lys	Ser
225					230				235						240
Leu	Asp	Phe	Ser	Met	Lys	Gly	Leu	Thr	Tyr	Leu	Asp	Val			
				245					250						

(2) INFORMATION FOR SEQ ID NO:2832:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 68 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...68
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2832:

Asp	Leu	Ala	Phe	Val	Met	Glu	Ser	Asp	Ser	Arg	Ser	Phe	Phe	Leu	Cys
1			5					10						15	
His	Thr	Leu	Arg	Lys	Ser	Leu	Gln	Thr	Thr	Ser	Val	Leu	Ser	Glu	Thr
			20					25				30			
Ser	Lys	Leu	Cys	Phe	Glu	Gln	Pro	Ala	Thr	Ser	Phe	Leu	Val	Cys	Phe
	35					40					45				
Leu	Ile	Phe	Ile	Glu	Tyr	Gln	Phe	Glu	Trp	Lys	Met	Glu	Ser	Tyr	His
	50					55				60					
Leu	Val	Met	Ser												
65															

(2) INFORMATION FOR SEQ ID NO:2833:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 127 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...127

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2833:

```

Leu Leu Arg Pro Gly Ser Gln Gly Val Val Phe Gly Ala Leu Thr Ala
1          5          10          15
Asp Lys Lys Leu Asp Lys Pro Asn Leu Glu Lys Leu Ile Ala Ala Ser
          20          25          30
Lys Gly Met Glu Ile Val Phe His Met Ala Phe Asp Glu Leu Ser Asp
          35          40          45
Glu Asp Gln Pro Glu Ala Ile Asp Trp Leu Ser Gln Ala Gly Val Thr
          50          55          60
Arg Ile Leu Thr Arg Ala Gly Val Ser Gly Asp Ser Leu Glu Lys Arg
65          70          75          80
Phe Val His Tyr His Arg Ile Leu Glu Tyr Ala Lys Gly Lys Ile Glu
          85          90          95
Ile Leu Pro Gly Gly Gly Ile Asp Leu Asp Asn Arg Gln Thr Phe Ile
          100         105         110
Asp Gln Val Gly Val Thr Gln Leu His Gly Thr Lys Val Val Phe
          115         120         125

```

(2) INFORMATION FOR SEQ ID NO:2834:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 316 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...316

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2834:

```

Tyr Cys Gly Pro Gln Lys Thr Ser Gln Glu Leu Asn Val Leu Lys Asn
1          5          10          15
Thr Tyr Asn Thr Phe His Lys Met Glu Glu Leu Gln Asp Glu Val Glu
          20          25          30
Ile Leu Leu Asp Phe Leu Ala Glu Asp Glu Ser Val His Asp Glu Leu
          35          40          45
Val Ala Gln Leu Ala Glu Leu Asp Lys Ile Met Thr Ser Tyr Glu Met
          50          55          60
Thr Leu Leu Leu Ser Glu Pro Tyr Asp His Asn Asn Ala Ile Leu Glu
65          70          75          80
Ile His Pro Gly Ser Gly Gly Thr Glu Ala Gln Asp Trp Gly Asp Met

```


50	55	60
Thr Ser Ser Ser Ala Arg Gly Glu Ile Tyr Asp Ala Ser Gly Lys Pro		
65	70	75
Leu Val Glu Asn Thr Leu Lys Gln Val Val Ser Phe Thr Arg Ser Asn		
	85	90
Lys Met Thr Ala Thr Asp Leu Lys Glu Thr Ala Lys Lys Leu Leu Thr		
	100	105
Tyr Val Ser Ile Ser Ser Pro Asn Leu Thr Glu Arg Gln Leu Ala Asp		
	115	120
Tyr Tyr Leu Ala Asp Pro Glu Ile Tyr Lys Lys Thr Val Glu Ala Leu		
	130	135
Pro Ser Glu Lys Arg Leu Asp Ser Asp Gly Asn Arg Leu Ser Glu Ser		
145	150	155
Glu Leu Tyr Asn Asn Ala Val Asp Ser Val Gln Thr Ser Gln Leu Asn		
	165	170
Tyr Thr Glu Asp Glu Lys Lys Glu Ile Tyr Leu Phe Ser Gln Leu Asn		
	180	185
Ala Val Gly Asn Phe Ala Thr Gly Thr Ile Ala Thr Asp Pro Leu Asn		
	195	200
Asp Ser Gln Val Ala Val Ile Ala Ser Ile Ser Lys Glu Met Pro Gly		
	210	215
Ile Ser Ile Ser Thr Ser Trp Asp Arg Lys Val Leu Glu Thr Ser Leu		
225	230	235
Ser Ser Ile Val Gly Ser Val Ser Ser Glu Lys Ala Gly Leu Pro Ala		
	245	250
Glu Glu Ala Glu Ala Tyr Leu Lys Lys Gly Tyr Ser Leu Asn Asp Arg		
	260	265
Val Gly Thr Ser Tyr Leu Glu Lys Gln Tyr Glu Glu Thr Leu Gln Gly		
	275	280
Lys Arg Ser Val Lys Glu Ile His Leu Asp Lys Tyr Gly Asn Met Glu		
	290	295
Ser Val Asp Thr Ile Glu Glu Gly Ser Lys Gly Asn Asn Ile Lys Leu		
305	310	315
Thr Ile Asp Leu Ala Phe Gln Asp Ser Val Asp Ala Leu Leu Lys Ser		
	325	330
Tyr Phe Asn Ser Glu Leu Glu Asn Gly Gly Ala Lys Tyr Ser Glu Gly		
	340	345
Val Tyr Ala Val Ala Leu Asn Pro Lys Thr Gly Ala Val Leu Ser Met		
	355	360
Ser Gly Ile Lys His Asp Leu Lys Thr Gly Glu Leu Thr Pro Asp Ser		
	370	375
Leu Gly Thr Val Thr Asn Val Phe Val Pro Gly Ser Val Val Lys Ala		
385	390	395
Ala Thr Ile Ser Ser Gly Trp Glu Asn Gly Val Leu Ser Gly Asn Gln		
	405	410
Thr Leu Thr Asp Gln Ser Ile Val Phe Gln Gly Ser Ala Pro Ile Asn		
	420	425
Ser Trp Tyr Thr Gln Ala Tyr Gly Ser Phe Pro Ile Thr Ala Val Gln		
	435	440
Ala Leu Glu Tyr Ser Ser Asn Thr Tyr Met Val Gln Thr Ala Leu Gly		
	450	455
Leu Met Gly Gln Thr Tyr Gln Pro Asn Met Phe Val Gly Thr Ser Asn		
465	470	475
Leu Glu Ser Ala Met Glu Lys Leu Arg Ser Thr Phe Gly Glu Tyr Gly		
	485	490
Leu Gly Thr Ala Thr Gly Ile Asp Leu Pro Asp Glu Ser Thr Gly Phe		
	500	505
		510

Val	Pro	Lys	Glu	Tyr	Ser	Phe	Ala	Asn	Tyr	Ile	Thr	Asn	Ala	Phe	Gly
		515					520					525			
Gln	Phe	Asp	Asn	Tyr	Thr	Pro	Met	Gln	Leu	Ala	Gln	Tyr	Val	Ala	Thr
	530					535					540				
Ile	Ala	Asn	Asn	Gly	Val	Arg	Val	Ala	Pro	Arg	Ile	Val	Glu	Gly	Ile
545					550					555					560
Tyr	Gly	Asn	Asn	Asp	Lys	Gly	Gly	Leu	Gly	Asp	Leu	Ile	Gln	Gln	Leu
			565						570					575	
Gln	Pro	Thr	Glu	Met	Asn	Lys	Val	Asn	Ile	Ser	Asp	Ser	Asp	Met	Ser
			580					585					590		
Ile	Leu	His	Gln	Gly	Phe	Tyr	Gln	Val	Ala	His	Gly	Thr	Ser	Gly	Leu
	595						600					605			
Thr	Thr	Gly	Arg	Ala	Phe	Ser	Asn	Gly	Ala	Leu	Val	Ser	Ile	Ser	Gly
	610					615					620				
Lys	Thr	Gly	Thr	Ala	Glu	Ser	Tyr	Val	Ala	Asp	Gly	Gln	Gln	Ala	Thr
625					630					635					640
Asn	Thr	Asn	Ala	Val	Ala	Tyr	Ala	Pro	Ser	Asp	Asn	Pro	Gln	Ile	Ala
			645						650					655	
Val	Ala	Val	Val	Phe	Pro	His	Asn	Thr	Asn	Leu	Thr	Asn	Gly	Val	Gly
		660					665					670			
Pro	Ser	Ile	Ala	Arg	Asp	Ile	Ile	Asn	Leu	Tyr	Gln	Lys	Tyr	His	Pro
		675					680					685			
Met	Asn														
	690														

(2) INFORMATION FOR SEQ ID NO:2836:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...68

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2836:

Tyr	Asn	Lys	Phe	Met	Asn	Lys	Gln	Gln	Phe	Ile	Ile	Met	Ala	Leu	Phe
1				5					10					15	
Thr	Ala	Ala	Glu	Thr	Tyr	Phe	Phe	Asn	Glu	Ala	Trp	Met	Thr	Gly	Arg
			20					25					30		
Tyr	Ile	Met	Ala	Ala	Phe	Trp	Ala	Ile	Leu	Leu	Phe	Arg	Asn	Phe	Arg
		35					40					45			
Val	Ser	Tyr	Val	Met	Gly	Lys	Ile	Val	Asp	Val	Ile	Asp	Gln	His	Phe
	50					55					60				
Asn	Arg	Lys	Asp												
65															

(2) INFORMATION FOR SEQ ID NO:2837:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 80 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...80
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2837:

Val	Leu	Lys	Leu	Lys	Lys	Glu	Pro	Leu	Leu	Ile	Gln	Leu	Pro	Pro	Met
1				5					10					15	
Tyr	Glu	Ala	Leu	Glu	Val	Ala	Pro	Met	His	Pro	Thr	Gly	Pro	Thr	Pro
			20					25					30		
Ala	Thr	Glu	Thr	Val	Asp	Ser	Tyr	Arg	Asp	Met	Lys	His	Arg	Lys	Asn
			35				40					45			
Leu	Leu	Gln	Phe	Tyr	Lys	Lys	Tyr	Ser	Glu	Asn	Asn	Ile	Leu	Ser	Leu
			50			55					60				
Tyr	Ile	Pro	Ala	Ser	Arg	Arg	Trp	Cys	Glu	Ser	Cys	Ile	Pro	Tyr	Arg
65					70					75					80

(2) INFORMATION FOR SEQ ID NO:2838:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 99 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...99
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2838:

Gln	Ile	Phe	Thr	Val	Gln	Met	His	Arg	Arg	Ser	Leu	His	Leu	Leu	Thr
1				5					10				15		
Ala	Trp	Asn	Lys	Arg	Gln	Asp	Ser	Ala	Trp	Gln	Ile	Leu	Cys	Pro	Phe
			20					25					30		
Thr	Met	Gln	Cys	Ala	Thr	Ser	Trp	Leu	Leu	Ala	Gln	Leu	Thr	Ser	Phe
			35				40					45			
Phe	Val	Val	Pro	Thr	Ile	Cys	Ser	Leu	Cys	Val	Ile	Ala	Trp	Ile	Ala

50		55		60											
Ser	Leu	Ser	Gln	Phe	Trp	Met	Lys	Trp	Asp	Asp	Ser	Met	Thr	Gly	Gln
65					70					75					80
Lys	Lys	Lys	Lys	Gln	Leu	Thr	Val	Leu	Met	Ser	Lys	Gln	Leu	Ser	Leu
				85					90						95
Thr	Thr	Ile													

(2) INFORMATION FOR SEQ ID NO:2839:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 574 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...574

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2839:

Leu	Asn	Phe	Thr	Arg	Glu	Glu	Leu	Asn	Lys	Met	Asp	Lys	Leu	Ile	Ile
1				5					10					15	
Phe	Ile	Glu	Lys	Gly	Lys	Pro	Phe	Phe	Glu	Lys	Leu	Ser	Arg	Asn	Ile
			20					25					30		
Tyr	Leu	Arg	Ala	Ile	Lys	Asp	Gly	Phe	Ile	Ser	Ser	Met	Pro	Ala	Val
		35					40					45			
Leu	Phe	Ser	Ser	Ile	Phe	Ile	Leu	Ile	Ala	Ala	Val	Pro	Asn	Ile	Phe
	50					55					60				
Gly	Phe	Lys	Trp	Ser	Asp	Glu	Gln	Leu	Ala	Phe	Ile	Leu	Lys	Pro	Tyr
65					70					75					80
Asn	Tyr	Ser	Met	Gly	Ile	Leu	Ala	Leu	Leu	Val	Ala	Gly	Thr	Thr	Ala
			85						90					95	
Lys	Ser	Leu	Thr	Asp	Ser	Val	Asn	Thr	Arg	Ser	Met	Glu	Lys	Thr	Asn
		100						105					110		
Gln	Ile	Asn	Tyr	Met	Ser	Thr	Phe	Leu	Ala	Ala	Val	Val	Gly	Leu	Leu
	115					120						125			
Ile	Leu	Ala	Ala	Asp	Pro	Ile	Glu	Gly	Gly	Phe	Ala	Asn	Gly	Leu	Leu
	130					135					140				
Gly	Thr	Arg	Gly	Leu	Leu	Thr	Ala	Phe	Leu	Ala	Ala	Phe	Ile	Thr	Val
145					150					155					160
Asn	Ile	Tyr	Lys	Val	Cys	Ile	Lys	Asn	Asn	Val	Thr	Ile	Arg	Leu	Pro
			165					170						175	
Glu	Glu	Val	Pro	Pro	Asn	Ile	Ala	Gln	Val	Phe	Lys	Asp	Val	Ile	Pro
		180					185						190		
Phe	Ala	Leu	Ser	Val	Leu	Ser	Ile	Tyr	Gly	Leu	Asp	Leu	Ile	Val	Arg
	195					200						205			
Asn	Ile	Phe	Gly	Thr	Asn	Val	Ala	Glu	Ser	Val	Gly	Lys	Ile	Leu	Ala
	210				215						220				
Pro	Leu	Phe	Ser	Ala	Thr	Asp	Gly	Tyr	Ile	Gly	Leu	Ala	Ile	Val	Phe

225		230		235		240
Gly	Ala	Tyr	Ala	Phe	Phe	Val
				245		250
Val	Glu	Pro	Leu	Ile	Val	Ala
				255		260
Val	Gln	Leu	Val	Gln	Ala	Gly
				265		270
Val	Thr	Gln	Thr	Phe	Val	Val
				275		280
Val	Val	Pro	Phe	Met	Phe	Met
				285		290
Val	Val	Pro	Phe	Met	Phe	Met
				295		300
Val	Val	Pro	Phe	Met	Phe	Met
				305		310
Ile	Val	Gly	Arg	Ala	Ser	Val
				315		320
Pro	Ile	Leu	Phe	Gly	Ala	Pro
				325		330
Pro	Phe	Val	Thr	Ala	Pro	Ile
				335		340
Val	Asp	Val	Leu	Gln	Met	Asn
				345		350
Thr	Pro	Ala	Pro	Ile	Gly	Ile
				355		360
Ser	Phe	Val	Leu	Ala	Ile	Thr
				365		370
Tyr	Pro	Phe	Val	Lys	Val	Tyr
				375		380
Lys	Gly	Asn	Ser	Ser	Ser	Glu
				385		390
Asn	Thr	Val	Lys	Ala	Asp	Ala
				395		400
Ala	Gln	Asn	Thr	Ile	Thr	Glu
				405		410
Gly	Gly	Gly	Thr	Ser	Gly	Leu
				415		420
Ala	Glu	Tyr	Asn	Val	Pro	Val
				425		430
His	Arg	Glu	Met	Leu	Pro	Glu
				435		440
Val	Ala	Ser	Asn	Phe	Glu	Asp
				445		450
Ile	Lys	Leu	Ala	Lys	Thr	Glu
				455		460
Asp	Gly	Lys	Gly	Ala	Leu	Ala
				465		470
				475		480
				485		490
				495		500
				505		510
				515		520
				525		530
				535		540
				545		550
				555		560
				565		570

(2) INFORMATION FOR SEQ ID NO:2840:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...73

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2840:

Met	Ile	Phe	Thr	Met	Ala	His	Asp	Gln	Arg	Gly	Gly	Ser	Met	Lys	Asp
1				5				10						15	
Leu	Phe	Leu	Lys	Arg	Lys	Gln	Ala	Phe	Arg	Arg	Glu	Cys	Leu	Gly	Tyr
			20					25					30		
Leu	Arg	Tyr	Val	Leu	Asn	Asp	His	Phe	Val	Leu	Phe	Leu	Leu	Val	Leu
		35					40					45			
Leu	Gly	Phe	Leu	Ala	Thr	Ser	Thr	Val	Asn	Ser	Tyr	Asn	Ile	Phe	Leu
	50					55					60				
Lys	Ile	Ile	Gly	Leu	Ser	Phe	Cys	Leu							
65						70									

(2) INFORMATION FOR SEQ ID NO:2841:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 190 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...190

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2841:

Ser	Ser	Phe	Thr	Gly	Gly	Asn	Leu	Thr	Gly	Gln	Leu	Thr	Glu	Lys	Ile
1				5				10						15	
Gln	Glu	His	Glu	Leu	Ile	Lys	Thr	Asn	Gln	Ala	Glu	Lys	Ser	Val	Gln
			20					25					30		
Asp	Val	Leu	Asp	Asn	Cys	Ile	Glu	Arg	Val	Gln	Asn	Asn	Ser	Leu	Lys
		35					40					45			
Ser	Asp	Arg	Val	Thr	Ser	Phe	Glu	Thr	Pro	Phe	Ala	Leu	Leu	Phe	Ile
	50					55				60					
Phe	Ala	Thr	Ile	Ala	Val	Met	Leu	Thr	Tyr	Gly	Gly	Tyr	Arg	Val	Ser
65					70					75					80
Ala	Gly	Tyr	Ile	Ser	Val	Gly	Thr	Leu	Val	Ser	Phe	Leu	Ile	Tyr	Leu
			85					90					95		
Phe	Gln	Leu	Leu	Asn	Pro	Ile	Ser	Asn	Ile	Ala	Asn	Phe	Val	Thr	Val
			100					105					110		
Tyr	Ser	Arg	Ser	Lys	Gly	Ser	Ser	Val	Ala	Leu	Asp	Asn	Leu	Leu	Ala
		115					120					125			
Val	Pro	Lys	Glu	Lys	Phe	Glu	Gly	Gly	Lys	Ser	Val	Ser	Gly	Gln	Gly
		130					135					140			

Leu	Asn	Phe	Asn	His	Val	Tyr	Phe	Gly	Tyr	Asp	Glu	Asn	Arg	Pro	Val
145					150					155					160
Leu	Lys	Asp	Ile	Thr	Cys	Ser	Ile	Phe	Lys	Gly	Gln	Lys	Leu	Leu	Leu
			165						170						175
Leu	Asp	His	Leu	Asp	Gln	Glu	Asn	Gln	Arg	Leu	Cys	Val	Cys		
			180					185					190		

(2) INFORMATION FOR SEQ ID NO:2842:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2842:

Lys	Arg	Phe	Thr	Arg	Cys	Cys	Lys	Thr	Tyr	Ser	Trp	Ser	Thr	Met	Ile
1				5					10					15	
His	Leu	Thr	Ile	Glu	Tyr	Cys	Asp	Asn	Ile	Ile	Asp	Pro	Tyr	Thr	Asn
			20					25					30		
Leu	Gly	Glu	Gln	Gln	Arg	Ile	Ala	Ser	Glu	Leu	Asp	Leu	Leu	Ser	Lys
		35					40					45			
Leu	Ile	Leu	Arg	Arg	Gln	Glu	Gln	Leu	Glu	Glu	Leu	Asn	Leu	Leu	Val
	50					55					60				
Lys	Ser	Arg	Phe	Asn	Glu	Met	Phe	Gly	Glu	Asn	Lys	Ile	Phe	Glu	Ser
65					70				75					80	
Ile	Asp	Asn	Leu	Phe	Asp	Ile	Ile	Asp	Gly	Asp	Arg	Gly	Lys	Asn	Tyr
			85					90					95		
Pro	Lys	Ser	Asp	Glu	Leu	Phe	Ser	Glu	Glu	Tyr	Cys	Leu	Phe	Leu	Asn
			100					105					110		
Thr	Lys	Asn	Val	Thr	Lys	Asn	Gly	Phe	Ser	Phe	Asp	Thr	Lys	Gln	Phe
		115					120					125			
Ile	Thr	Lys	Thr	Lys	Asp	Lys	Leu	Leu	Arg	Lys	Gly	Lys	Leu	Glu	Arg
		130				135					140				
Tyr	Asp	Ile	Val	Leu	Thr	Thr	Arg	Gly	Thr	Val	Gly	Asn	Val	Ala	Tyr
145					150				155					160	
Tyr	Asp	Glu	Leu	Ile	Lys	Tyr	Lys	His	Leu	Arg	Ile	Asn	Ser	Gly	Met
			165					170						175	
Val	Ile	Leu	Arg	Pro	Lys	Thr	Pro	Asn	Leu	Asn	Gln	Lys	Phe	Ile	Ile
			180					185					190		
His	Val	Leu	Arg	Asn	Asn	Asn	Tyr	Ser	Arg	Val	Ile	Ser	Gly	Ser	Ala
		195					200					205			
Gln	Pro	Gln	Leu	Pro	Ile	Thr	Lys	Leu	Lys	Lys	Ile	Leu	Leu	Pro	Leu
	210					215					220				
Pro	Pro	Leu	Ala	Leu	Gln	Asn	Glu	Phe	Ala	Asp	Phe	Val	Val	Gln	Val
225					230				235						240

Asp Lys Ser Gln Phe Ala Cys Glu Ile Ala Ile Lys Val Trp Arg Asn
245 250 255
Ser Leu Lys Phe Ser Ile Ile
260

(2) INFORMATION FOR SEQ ID NO:2843:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 156 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2843:

Ile Thr Leu Thr Thr Ile Tyr Thr Val Asp Glu Arg Asp Gly Thr Ile
1 5 10 15
Glu Glu Thr Thr Ser Arg Gln Ile Thr Lys Glu Met Val Lys Arg Arg
20 25 30
Ile Arg Arg Gly Thr Arg Glu Pro Glu Lys Val Val Val Pro Glu Gln
35 40 45
Ser Ser Ile Pro Ser Tyr Pro Val Ser Val Thr Ser Asn Gln Gly Thr
50 55 60
Asp Val Ala Val Glu Pro Ala Lys Ala Val Ala Pro Thr Thr Gly Trp
65 70 75 80
Lys Gln Glu Asn Gly Met Trp Tyr Phe Tyr Asn Thr Asp Gly Ser Met
85 90 95
Ala Thr Gly Trp Val Gln Val Asn Gly Ser Trp Tyr Tyr Leu Asn Ser
100 105 110
Asn Gly Ser Met Lys Val Asn Gln Trp Phe Gln Val Gly Gly Lys Trp
115 120 125
Tyr Tyr Val Asn Ala Ser Gly Glu Leu Ala Val Asn Thr Ser Ile Asp
130 135 140
Gly Tyr Arg Val Asn Asp Asn Gly Glu Trp Val Arg
145 150 155

(2) INFORMATION FOR SEQ ID NO:2844:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 180 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...180

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2844:

Ile	Met	Lys	Leu	Leu	Ser	Ile	Ala	Ile	Pro	Ser	Tyr	Asn	Ala	Ala	Ala
1				5					10					15	
Tyr	Leu	His	Tyr	Cys	Val	Glu	Ser	Leu	Val	Ile	Gly	Gly	Glu	Gln	Val
			20					25					30		
Gly	Ile	Leu	Ile	Ile	Asn	Asp	Gly	Ser	Gln	Asp	Gln	Thr	Gln	Glu	Ile
		35					40					45			
Ala	Glu	Cys	Leu	Ala	Ser	Lys	Tyr	Pro	Asn	Ile	Val	Arg	Ala	Ile	Tyr
	50					55					60				
Gln	Glu	Asn	Lys	Cys	His	Gly	Gly	Ala	Val	Asn	Arg	Gly	Leu	Ala	Glu
65					70					75					80
Ala	Ser	Gly	Arg	Tyr	Phe	Lys	Val	Val	Asp	Ser	Asp	Asp	Trp	Val	Asp
			85						90				95		
Pro	Arg	Ala	Tyr	Leu	Lys	Ile	Leu	Glu	Thr	Leu	Gln	Glu	Leu	Glu	Ser
		100						105					110		
Lys	Gly	Gln	Glu	Val	Asp	Val	Phe	Val	Thr	Asn	Phe	Val	Tyr	Glu	Lys
		115				120						125			
Glu	Gly	Gln	Ser	Arg	Lys	Lys	Ser	Met	Ser	Tyr	Asp	Ser	Val	Leu	Pro
	130					135					140				
Val	Arg	Gln	Ile	Phe	Gly	Trp	Asp	Gln	Val	Gly	Asn	Phe	Ser	Lys	Gly
145					150					155					160
Gln	Tyr	Thr	Met	Met	His	Ser	Leu	Ile	Tyr	Arg	Thr	Asp	Leu	Leu	Arg
				165					170					175	
Ala	Ser	Gln	Phe												
			180												

(2) INFORMATION FOR SEQ ID NO:2845:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 651 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...651

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2845:

Lys	Thr	Leu	Thr	Gly	Glu	Arg	Glu	Tyr	Met	Asp	Asn	Arg	Glu	Ala	Leu
1				5				10					15		
Lys	Thr	Phe	Met	Thr	Gly	Glu	Asn	Phe	Tyr	Leu	Gln	His	Tyr	Leu	Gly

			20					25				30					
Ala	His	Arg	Glu	Glu	Leu	Asn	Gly	Glu	Tyr	Gly	Tyr	Thr	Phe	Arg	Val		
		35					40					45					
Trp	Ala	Pro	Asn	Ala	Gln	Ala	Val	His	Leu	Val	Gly	Asp	Phe	Thr	Asn		
	50					55					60						
Trp	Ile	Glu	Asn	Gln	Ile	Pro	Met	Val	Arg	Asn	Asp	Phe	Gly	Val	Trp		
65					70					75					80		
Glu	Val	Phe	Thr	Asn	Met	Ala	Gln	Glu	Gly	His	Ile	Tyr	Lys	Tyr	His		
				85					90					95			
Val	Thr	Arg	Gln	Asn	Gly	His	Gln	Leu	Met	Lys	Ile	Asp	Pro	Phe	Ala		
			100					105					110				
Val	Arg	Tyr	Glu	Ala	Arg	Pro	Gly	Thr	Gly	Ala	Ile	Val	Thr	Glu	Leu		
	115						120					125					
Pro	Asp	Lys	Lys	Trp	Arg	Asp	Gly	Leu	Trp	Leu	Ala	Arg	Arg	Lys	Arg		
	130					135					140						
Trp	Gly	Phe	Ala	Glu	Arg	Pro	Val	Asn	Ile	Tyr	Glu	Val	His	Ala	Gly		
145					150					155					160		
Ser	Trp	Lys	Arg	Asn	Pro	Asp	Gly	Ser	Pro	Tyr	Ser	Phe	Ala	Gln	Leu		
				165				170						175			
Lys	Asp	Glu	Leu	Ile	Pro	Tyr	Leu	Val	Glu	Met	Asn	Tyr	Thr	His	Ile		
		180						185				190					
Glu	Phe	Met	Pro	Leu	Met	Ser	His	Pro	Leu	Gly	Leu	Ser	Trp	Gly	Tyr		
	195						200					205					
Gln	Leu	Met	Gly	Tyr	Phe	Ala	Leu	Glu	His	Ala	Tyr	Gly	Arg	Pro	Glu		
	210					215					220						
Glu	Phe	Gln	Asp	Phe	Val	Glu	Glu	Cys	His	Thr	His	Asn	Ile	Gly	Val		
225					230					235					240		
Ile	Val	Asp	Trp	Val	Pro	Gly	His	Phe	Thr	Ile	Asn	Asp	Asp	Ala	Leu		
				245					250					255			
Ala	Tyr	Tyr	Asp	Gly	Thr	Pro	Thr	Phe	Glu	Tyr	Gln	Asp	His	Asn	Lys		
			260					265					270				
Ala	His	Asn	His	Gly	Trp	Gly	Ala	Leu	Asn	Phe	Asp	Leu	Gly	Lys	Asn		
	275						280					285					
Glu	Val	Gln	Ser	Phe	Leu	Ile	Ser	Cys	Ile	Lys	His	Trp	Ile	Asp	Ile		
	290					295					300						
Tyr	His	Leu	Asp	Gly	Ile	Arg	Val	Asp	Ala	Val	Ser	Asn	Met	Leu	Tyr		
305					310					315					320		
Leu	Asp	Tyr	Asp	Asp	Ala	Pro	Trp	Thr	Pro	Asn	Lys	Asp	Gly	Gly	Asn		
			325						330					335			
Leu	Asn	Tyr	Glu	Gly	Tyr	Tyr	Phe	Leu	Gln	Arg	Leu	Asn	Glu	Val	Ile		
			340					345					350				
Lys	Leu	Glu	Tyr	Pro	Asp	Val	Met	Ile	Ala	Glu	Glu	Ser	Ser	Ser			
	355					360					365						
Ala	Thr	Lys	Ile	Thr	Gly	Met	Lys	Glu	Ile	Gly	Gly	Leu	Gly	Phe	Asp		
	370					375					380						
Tyr	Lys	Trp	Asn	Met	Gly	Trp	Met	Asn	Asp	Ile	Leu	Arg	Phe	Tyr	Glu		
385					390					395					400		
Glu	Asp	Pro	Ile	Tyr	Arg	Lys	Tyr	Asp	Phe	Asn	Leu	Val	Thr	Phe	Ser		
			405						410					415			
Phe	Met	Tyr	Val	Phe	Lys	Glu	Asn	Tyr	Leu	Leu	Pro	Phe	Ser	His	Asp		
			420					425					430				
Glu	Val	Val	His	Gly	Lys	Lys	Ser	Met	Met	His	Lys	Met	Trp	Gly	Asp		
	435						440					445					
Arg	Tyr	Asn	Gln	Phe	Ala	Gly	Leu	Arg	Asn	Leu	Tyr	Thr	Tyr	Gln	Ile		
	450					455					460						
Cys	His	Pro	Gly	Lys	Lys	Leu	Leu	Phe	Met	Gly	Ser	Glu	Tyr	Gly	Gln		
465					470					475					480		

Phe	Leu	Glu	Trp	Lys	Ser	Glu	Glu	Gln	Leu	Glu	Trp	Ser	Asn	Leu	Glu
				485					490					495	
Asp	Pro	Met	Asn	Ala	Lys	Met	Lys	Tyr	Phe	Thr	Ser	Gln	Leu	Asn	Gln
			500					505					510		
Phe	Tyr	Lys	Asp	His	Arg	Cys	Leu	Trp	Glu	Ile	Asp	Thr	Ser	Tyr	Asp
		515					520				525				
Gly	Ile	Glu	Ile	Ile	Asp	Ala	Asp	Asn	Arg	Asp	Gln	Ser	Val	Leu	Ser
	530					535					540				
Phe	Ile	Arg	Lys	Gly	Lys	Lys	Gly	Glu	Met	Leu	Val	Cys	Ile	Phe	Asn
545					550					555					560
Met	Val	Pro	Val	Glu	Arg	Lys	Asp	Phe	Thr	Ile	Gly	Leu	Pro	Val	Ala
			565					570						575	
Gly	Ile	Tyr	Glu	Glu	Val	Trp	Asn	Thr	Glu	Leu	Glu	Glu	Trp	Gly	Gly
		580					585						590		
Val	Trp	Lys	Glu	His	Asn	Gln	Thr	Val	Gln	Thr	Gln	Glu	Gly	Leu	Trp
		595				600					605				
Lys	Asp	Tyr	Glu	Gln	Thr	Leu	Thr	Phe	Thr	Leu	Pro	Ala	Met	Gly	Ala
	610					615					620				
Ser	Val	Trp	Lys	Ile	Lys	Arg	Arg	Leu	Lys	Ser	Thr	Lys	Thr	Val	Thr
625					630					635					640
Asn	Lys	Asn	Gln	Lys	Gly	Val	Glu	Asn	Glu	Lys					
			645						650						

(2) INFORMATION FOR SEQ ID NO:2846:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2846:

Arg	Ser	Ile	Thr	Lys	Arg	Arg	Lys	Asp	Lys	Lys	Ala	Glu	Gly	Phe	Pro
1				5				10						15	
Arg	Leu	Phe	Thr	Tyr	Tyr	Leu	Trp	Leu	Tyr	Asn	Ile	Val	Val	Gly	Asn
			20				25						30		
Pro	Pro	Met	Asp	Ile	Met	Glu	Pro	Ile	Leu	Cys	Arg	Lys	Lys	Val	Pro
		35				40						45			
Tyr	Val	Pro	Ile	Met	Lys	Ser	Asp	Lys	Thr	Thr	His				
50					55						60				

(2) INFORMATION FOR SEQ ID NO:2847:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...461

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2847:

Ser	Leu	Ile	Thr	Cys	Met	Arg	Ala	Ile	Met	Val	Glu	His	Phe	Ser	Ser
1				5					10					15	
Val	Ser	Lys	Ile	Leu	Thr	Val	Asn	Ala	Met	Ser	Arg	Met	Val	Asn	Val
			20					25					30		
Pro	Gln	Leu	Glu	Asn	Leu	Arg	Trp	Leu	Gly	Met	Asp	Trp	Asp	Glu	Ser
		35					40					45			
Pro	Glu	Ser	His	Glu	Asn	Tyr	Arg	Gln	Ser	Glu	Arg	Leu	Asp	Leu	Tyr
	50					55				60					
Gln	Lys	Tyr	Ile	Asp	Gln	Leu	Leu	Ala	Glu	Gly	Lys	Ala	Tyr	Lys	Ser
65					70					75					80
Tyr	Val	Thr	Glu	Glu	Glu	Leu	Ala	Ala	Glu	Arg	Glu	Arg	Gln	Glu	Val
				85					90					95	
Ala	Gly	Glu	Thr	Pro	Arg	Tyr	Ile	Asn	Glu	Tyr	Leu	Gly	Met	Ser	Glu
			100					105					110		
Glu	Glu	Lys	Ala	Ala	Tyr	Ile	Ala	Glu	Arg	Glu	Ala	Ala	Gly	Ile	Ile
		115					120					125			
Pro	Thr	Val	Arg	Leu	Ala	Val	Asn	Glu	Ser	Gly	Ile	Tyr	Lys	Trp	His
	130					135					140				
Asp	Met	Val	Lys	Gly	Asp	Ile	Glu	Phe	Glu	Gly	Gly	Asn	Ile	Gly	Gly
145					150					155				160	
Asp	Trp	Ile	Ile	Gln	Lys	Lys	Asp	Gly	Tyr	Pro	Thr	Tyr	Asn	Phe	Ala
			165					170					175		
Val	Ala	Ile	Asp	Asp	His	Asp	Met	Gln	Ile	Ser	His	Val	Ile	Arg	Gly
		180						185					190		
Asp	Asp	His	Ile	Ala	Asn	Thr	Pro	Lys	Gln	Leu	Met	Val	Tyr	Glu	Ala
		195					200					205			
Leu	Gly	Trp	Glu	Ala	Pro	Glu	Phe	Gly	His	Met	Thr	Leu	Ile	Ile	Asn
	210					215					220				
Ser	Glu	Thr	Gly	Lys	Lys	Leu	Ser	Lys	Arg	Asp	Thr	Asn	Thr	Leu	Gln
225					230					235					240
Phe	Ile	Glu	Asp	Tyr	Arg	Lys	Lys	Gly	Tyr	Leu	Ala	Glu	Ala	Val	Phe
			245						250					255	
Asn	Phe	Ile	Ala	Leu	Leu	Gly	Trp	Asn	Pro	Gly	Ser	Glu	Asp	Glu	Ile
		260						265					270		
Phe	Ser	Arg	Glu	Glu	Leu	Ile	Lys	Leu	Phe	Asp	Glu	Asn	Arg	Leu	Ser
		275					280					285			
Lys	Ser	Pro	Ala	Ala	Phe	Asp	Gln	Lys	Lys	Leu	Asp	Trp	Met	Ser	Asn
	290					295					300				
Asp	Tyr	Ile	Lys	Asn	Ala	Asp	Leu	Glu	Thr	Ile	Leu	Glu	Met	Ala	Lys
305					310					315					320
Pro	Phe	Leu	Glu	Glu	Ala	Gly	Arg	Leu	Thr	Asp	Lys	Ala	Glu	Lys	Leu

				325					330					335	
Val	Glu	Leu	Tyr	Lys	Pro	Gln	Met	Lys	Ser	Val	Asp	Glu	Ile	Ile	Pro
			340					345					350		
Leu	Thr	Asp	Leu	Phe	Phe	Ser	Asp	Phe	Pro	Glu	Leu	Thr	Glu	Ala	Glu
		355					360					365			
Arg	Glu	Val	Met	Thr	Gly	Glu	Thr	Val	Pro	Thr	Val	Leu	Glu	Ala	Phe
	370					375					380				
Lys	Ala	Lys	Leu	Glu	Ala	Met	Thr	Asp	Asp	Lys	Phe	Val	Thr	Glu	Asn
385					390					395					400
Ile	Phe	Pro	Gln	Ile	Lys	Ala	Val	Gln	Lys	Glu	Thr	Gly	Ile	Lys	Gly
			405					410					415		
Lys	Asn	Leu	Phe	Met	Pro	Ile	Arg	Ile	Ala	Val	Ser	Gly	Glu	Met	His
		420					425					430			
Gly	Pro	Glu	Leu	Pro	Asp	Thr	Ile	Phe	Leu	Leu	Gly	Arg	Glu	Lys	Ser
		435				440					445				
Ile	Gln	His	Ile	Glu	Asn	Met	Leu	Lys	Glu	Ile	Ser	Lys			
	450					455					460				

(2) INFORMATION FOR SEQ ID NO:2848:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*.

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...145

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2848:

Glu	Ile	Ile	Thr	Ile	His	Asp	Ser	Asn	Asp	Val	Asn	Arg	Ser	Asp	Val
1				5					10					15	
Phe	Val	Asp	Leu	Val	Ser	Ile	Thr	Phe	Ser	Leu	Met	Asn	Phe	Phe	Lys
		20					25					30			
Ile	Leu	Ile	Asn	Leu	Thr	Ala	Gln	Val	Ser	Pro	Gln	Val	Ile	Asp	Glu
	35					40					45				
Lys	Ile	Leu	Met	Met	Asp	Leu	Asn	Leu	Asn	Asn	Tyr	Leu	Ser	Thr	Val
	50				55					60					
Ile	Gln	Leu	Arg	Gln	Asp	Val	Tyr	Thr	Gly	Ile	Lys	Ile	Leu	His	Arg
65				70					75					80	
Val	Gly	His	Gly	Arg	Gln	Asp	Met	Asn	Val	Thr	Ser	Leu	Gln	Asn	Ser
		85						90				95			
His	Ile	Phe	Gly	Trp	Gln	Val	Gln	His	Ile	Ala	Asp	Lys	Leu	Thr	Ser
		100				105						110			
Asp	Phe	Trp	Val	Ala	Glu	Asn	Phe	Leu	Ser	Asn	Gln	Val	Ile	Gly	Arg
	115					120					125				
Ala	Asn	Ser	Gln	Met	Ser	Glu	Asn	His	Pro	Phe	Pro	Pro	Ser	Ile	Val
	130					135					140				
Asn															

(2) INFORMATION FOR SEQ ID NO:2849:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 568 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...568

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2849:

```

Glu Lys Ile Thr Gln Thr Ser Leu Trp Lys Val Ser Thr Leu Val Leu
1          5          10          15
Leu Val Glu Lys Arg Arg Leu Arg Met Arg Leu Lys Val Ile Asn Lys
          20          25          30
Leu Val Asp Ile Asn Ile Leu Tyr Ser Ser Gln Glu Ala Asn Leu Ala
          35          40          45
Asn Leu Arg Lys Lys Gln Ala Lys Asn Pro Gly Lys Lys Val Asn Val
          50          55          60
Ser Ala Arg Val Leu Ser Ser Tyr Ile Phe Ser Ser Leu Leu Met Leu
65          70          75          80
Ile Cys Phe Ser Asn Ile Ala Phe Arg Phe Pro Phe Glu Glu Met Pro
          85          90          95
Ser Phe Phe Ser Thr Met Val Ala Ile Leu Leu Val Leu Ala Phe Ser
          100         105         110
Thr Ser Phe Thr Ala Phe Tyr Asn Val Phe Tyr Glu Ser Lys Asp Leu
          115         120         125
Ala Ser Tyr Arg Pro Tyr Ala Phe Lys Glu Ser Glu Ile Ile Met Ala
          130         135         140
Lys Gly Leu Ser Val Leu Leu Pro Ala Leu Thr Gly Ile Val Pro Ile
145         150         155         160
Leu Ala Tyr Phe Leu Val Leu Tyr Ile Arg Leu Ala Pro Ser Leu Trp
          165         170         175
Leu Gly Leu Pro Leu Met Leu Leu Ser Leu Thr Leu Leu Phe Val Ser
          180         185         190
Val Thr Leu Val Thr Val Val Ala Val His Phe Leu Ala Gln Thr Arg
          195         200         205
Val Phe Arg Lys Tyr Gln Ser Ile Phe Ser Asn Val Met Ile Gly Ile
          210         215         220
Gly Val Leu Ile Pro Leu Ile Phe Ile Phe Phe Leu Gln Ser Thr Phe
225         230         235         240
Gly Ser Ile Val Asp Lys Val Arg Asp Ile Pro Phe Leu Leu Tyr Pro
          245         250         255
Leu His Ile Phe Tyr Lys Ile Ala Val Glu Pro Phe Ser Thr Glu Ala
          260         265         270
Leu Val Gly Leu Leu Ala Trp Ile Gly Leu Thr Leu Phe Leu Leu Tyr

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[illegible]

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2850:

Arg	Leu	Ser	Thr	Arg	Phe	Phe	Lys	Ser	Ile	Ile	Val	Ser	Cys	Ser	His
1				5					10					15	
Leu	Leu	Phe	Phe	Lys	Glu	Lys	Trp	Trp	Gly	Glu	Phe	Phe	Gln	Phe	Phe
			20					25					30		
Lys	Ala	Leu	Leu	Ser	Ser	Ile	Cys	Ile	Phe	Thr	Asp	Asp	Lys	Thr	Asp
		35					40					45			
Ile	Ile	Thr	Thr	Lys	Gly	Ser	Asp	Ser	Val	Arg	Glu	Ala	Gln	Ser	Ile
	50					55					60				
Asn	Asp	Arg	Thr	Lys	Gly	Leu	Ser	Gln	Ser	Arg	Lys	Gly	Phe		
65					70					75					

(2) INFORMATION FOR SEQ ID NO:2851:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 80 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...80
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2851:

Arg	Phe	Glu	Phe	Ala	Gly	Phe	Thr	Trp	Ser	Leu	Cys	Leu	Arg	Ile	Tyr
1				5				10						15	
Leu	His	Gly	Pro	Leu	Ile	Ile	Thr	Val	Ser	Gln	Asp	Phe	Thr	Ser	Leu
			20					25					30		
Ser	Asp	Ile	Ser	Ala	Thr	His	Phe	Glu	Gln	Leu	His	Ile	Met	Thr	Ile
		35					40					45			
Val	His	Ser	Asp	Ile	Gln	Arg	Asn	Asn	Ser	Pro	Leu	Thr	Cys	Asp	Asn
	50					55					60				
Arg	Leu	Ser	Leu	His	Ser	Val	Ala	Phe	Leu	Phe	Thr	Arg	Ile	Ile	Arg
65					70					75					80

(2) INFORMATION FOR SEQ ID NO:2852:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 80 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...80

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2852:

Arg	Leu	Glu	Phe	Ala	Gly	Phe	Thr	Trp	Ser	Leu	Tyr	Leu	Arg	Ile	Tyr
1				5				10						15	
Leu	His	Glu	Ser	Leu	Ile	Thr	Thr	Val	Ser	Gln	Asp	Phe	Thr	Ser	Leu
			20					25					30		
Ser	Asp	Ile	Ser	Ala	Thr	His	Phe	Glu	Gln	Leu	His	Ile	Met	Thr	Ile
		35					40					45			
Val	His	Ser	Asp	Ile	Gln	Arg	Asn	Asn	Ser	Pro	Leu	Thr	Cys	Asp	Asn
	50					55				60					
Arg	Leu	Ser	Leu	His	Ser	Val	Ala	Phe	Leu	Phe	Thr	Arg	Ile	Ile	Arg
65					70				75						80

(2) INFORMATION FOR SEQ ID NO:2853:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 80 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...80

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2853:

Arg	Leu	Glu	Phe	Ala	Gly	Phe	Thr	Trp	Ser	Leu	Cys	Leu	Arg	Ile	Tyr
1				5				10						15	
Leu	His	Glu	Pro	Leu	Ile	Thr	Thr	Val	Ser	Gln	Asp	Phe	Thr	Ser	Leu
			20					25					30		
Ser	Asp	Ile	Ser	Ala	Thr	His	Phe	Glu	Gln	Leu	His	Ile	Met	Thr	Ile
		35					40					45			
Val	His	Ser	Asp	Ile	Gln	Arg	Asn	Asn	Ser	Pro	Leu	Thr	Cys	Asp	Asn
	50					55				60					
Arg	Leu	Ser	Leu	His	Ser	Val	Lys	Phe	Leu	Phe	Thr	Arg	Met	Ile	Arg
65					70				75						80

(2) INFORMATION FOR SEQ ID NO:2854:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 83 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...83

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2854:

Arg	Leu	Glu	Phe	Ala	Gly	Phe	Thr	Trp	Ser	Leu	Cys	Leu	Arg	Ile	Tyr
1				5					10					15	
Leu	His	Glu	Pro	Leu	Ile	Thr	Thr	Val	Ser	Gln	Asp	Phe	Thr	Ser	Leu
			20					25					30		
Ser	Asp	Ile	Ser	Ala	Thr	His	Phe	Glu	Gln	Leu	His	Ile	Met	Thr	Ile
		35					40					45			
Val	His	Ser	Asp	Ile	Gln	Arg	Asn	Asn	Ser	Pro	Leu	Thr	Cys	Asp	Asn
	50					55					60				
Arg	Leu	Ser	Leu	His	Ser	Val	Ala	Phe	Phe	Tyr	Lys	Asn	Asn	Ser	Leu
65					70					75					80
Ile	Leu	Phe													

(2) INFORMATION FOR SEQ ID NO:2855:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 80 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...80

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2855:

Arg	Leu	Glu	Phe	Ala	Gly	Phe	Thr	Trp	Ser	Leu	Cys	Leu	Arg	Ile	Tyr
1				5					10					15	
Leu	His	Gly	Pro	Leu	Ile	Thr	Thr	Val	Ser	Gln	Asp	Phe	Thr	Ser	Leu
			20					25					30		
Ser	Asp	Ile	Ser	Ala	Thr	His	Phe	Glu	Gln	Leu	His	Ile	Met	Thr	Ile
		35					40					45			
Val	His	Ser	Asp	Ile	Gln	Arg	Asn	Asn	Ser	Pro	Leu	Thr	Cys	Asp	Asn
	50					55					60				
Arg	Leu	Ser	Leu	His	Ser	Val	Lys	Phe	Leu	Phe	Thr	Lys	Ile	Ile	Arg
65					70					75					80

(2) INFORMATION FOR SEQ ID NO:2856:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...105
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2856:

Val	Gly	Ser	Thr	Cys	Lys	Arg	Leu	Pro	Gly	Lys	Pro	Thr	Phe	Thr	Asp
1				5					10					15	
Leu	Ile	Glu	Met	Pro	Ala	Phe	Ser	Ser	Ala	Trp	Glu	Met	Ala	Asp	Leu
		20					25						30		
Ile	Ala	Val	Ala	Ala	Val	Ser	Ile	Ser	Thr	Ile	Ile	Pro	Ser	Phe	Thr
		35				40						45			
Pro	Leu	Leu	Leu	Ala	Leu	Leu	Thr	Pro	Ile	Thr	Phe	Asn	Ser	Pro	Phe
	50				55					60					
Leu	Cys	Ser	Ala	Thr	Ser	Thr	Leu	Thr	Glu	Leu	Val	Pro	Ile	Ser	Arg
65				70					75					80	
Pro	Val	Lys	Lys	Pro	Ser	Leu	Ala	Ile	Thr	Ser	Leu	Pro	Leu	Tyr	Leu
		85				90							95		
Pro	Ser	Phe	Ala	Leu	Arg	Ile	Ile	Pro							
		100				105									

(2) INFORMATION FOR SEQ ID NO:2857:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 75 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...75
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2857:

Tyr	Thr	Ser	Thr	Ser	Lys	Thr	Leu	Leu	Glu	Ile	Asp	Leu	Thr	Val	Leu
1				5				10					15		
Ile	Asp	Leu	Ser	Tyr	Tyr	Phe	Ile	Leu	Leu	Tyr	Ser	Val	Asn	Leu	

		20					25					30			
Tyr	Glu	Phe	Lys	Pro	Ile	Ser	Ser	Leu	Thr	Ser	Ser	Lys	Ala	Val	Ser
		35					40					45			
Asn	Ile	Cys	Leu	Arg	Val	Phe	Asp	Ser	Leu	Gln	Leu	Thr	Asp	Lys	Leu
	50					55					60				
Ser	Asp	Lys	Ile	Cys	Thr	Thr	Ser	Glu	Thr	Glu					
65					70				75						

(2) INFORMATION FOR SEQ ID NO:2858:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...86

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2858:

Tyr	Thr	Ser	Thr	Ser	Lys	Thr	Phe	Leu	Glu	Ile	Asp	Leu	Thr	Val	Leu
1				5					10					15	
Ile	Asp	Leu	Ser	Cys	Ser	Cys	Phe	Ile	Leu	Leu	Tyr	Arg	Ser	His	Ser
		20						25				30			
Lys	Glu	Phe	Val	Pro	Lys	Leu	Leu	Gly	Ser	Phe	Phe	Ser	Trp	Thr	Thr
		35					40					45			
Lys	Glu	Leu	Met	Gly	Ile	Ile	Phe	Phe	Asn	Asn	Phe	Pro	Thr	Val	Tyr
	50				55						60				
Lys	Asn	Asn	Met	Met	Gly	Tyr	Ile	Ser	Ser	Lys	Thr	Tyr	Leu	Ile	Lys
65				70					75					80	
Leu	Ile	Lys	Asn	Ser	Ile										
				85											

(2) INFORMATION FOR SEQ ID NO:2859:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

(B) LOCATION 1...63

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2859:

Tyr	Thr	Ser	Thr	Ser	Lys	Ile	Leu	Leu	Glu	Ile	Asp	Leu	Thr	Ile	Leu
1				5					10					15	
Ile	Tyr	Leu	Ser	Cys	Ser	Tyr	Phe	Ile	Ser	Leu	Tyr	Leu	Lys	Leu	Ser
			20					25					30		
Met	Thr	Lys	Cys	Ala	Pro	Met	Ser	Trp	Glu	Arg	Thr	Phe	Phe	Ile	Phe
		35					40					45			
Phe	Ile	Phe	Leu	Asn	Pro	Ser	Ile	Lys	Thr	Ile	Gly	Met	Asn	Phe	
	50					55					60				

(2) INFORMATION FOR SEQ ID NO:2860:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 861 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...861

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2860:

Pro	Thr	Glu	Phe	Ser	Ile	Ile	Leu	Arg	Gly	Asn	Met	Lys	Ser	Phe	Leu
1				5					10					15	
Lys	Thr	Tyr	Arg	Thr	Tyr	Phe	Ile	Ser	Phe	Ile	Ile	Pro	Val	Val	Ile
			20					25					30		
Met	Ser	Gly	Val	Tyr	Leu	Ser	Gln	Gly	Ile	Tyr	Trp	Asn	Ser	Asp	Asn
		35					40					45			
Ser	Pro	Leu	Leu	Gly	Asp	Gly	Phe	His	Gln	Tyr	Val	Ile	Phe	Asp	Ile
	50					55					60				
Ala	Leu	Arg	Asn	Ile	Leu	His	Gly	Asn	Ser	Ser	Leu	Phe	Tyr	Thr	Phe
65					70				75						80
Thr	Ser	Gly	Leu	Gly	Leu	Asn	Phe	Tyr	Ala	Leu	Ser	Ser	Tyr	Tyr	Leu
				85					90					95	
Gly	Ser	Phe	Leu	Ala	Pro	Leu	Val	Tyr	Phe	Phe	Asp	Leu	Thr	Asn	Met
			100					105					110		
Pro	Asp	Ala	Ile	Tyr	Leu	Thr	Thr	Leu	Leu	Lys	Phe	Gly	Leu	Ile	Gly
	115						120					125			
Leu	Ser	Thr	Phe	Phe	Ser	Leu	Asn	Lys	Leu	Phe	Gln	Ser	Ile	Pro	Gln
	130					135					140				
Thr	Leu	Lys	Leu	Ala	Leu	Ser	Thr	Ser	Tyr	Ala	Leu	Met	Ser	Phe	Thr
145					150				155						160
Val	Ser	Gln	Leu	Glu	Ile	Lys	Thr	Trp	Leu	Asp	Val	Phe	Ile	Leu	Ile
			165					170					175		
Pro	Leu	Ile	Ile	Thr	Gly	Leu	His	Leu	Leu	Ile	Thr	Glu	Lys	Lys	Leu
			180					185					190		

(2) INFORMATION FOR SEQ ID NO:2862:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2862:

Met	Ile	Glu	Phe	Glu	Lys	Pro	Asn	Ile	Thr	Lys	Ile	Asp	Glu	Asn	Lys
1				5					10					15	
Asp	Tyr	Gly	Lys	Phe	Val	Ile	Glu	Pro	Leu	Glu	Arg	Gly	Tyr	Gly	Thr
			20					25					30		
Thr	Leu	Gly	Asn	Ser	Leu	Arg	Arg	Val	Leu	Leu	Ala	Ser	Leu	Pro	Gly
		35					40					45			
Ala	Ala	Val	Thr	Ser	Ile	Asn	Ile	Asp	Gly	Val	Leu	His	Glu	Phe	Asp
	50					55					60				
Thr	Val	Pro	Gly	Val	Arg	Glu	Asp	Val	Met	Gln	Ile	Ile	Leu	Asn	Ile
65					70					75					80
Lys	Gly	Ile	Ala	Val	Lys	Ser	Tyr	Val	Glu	Asp	Glu	Lys	Ile	Ile	Glu
				85					90					95	
Leu	Asp	Val	Glu	Gly	Pro	Ala	Glu	Val	Thr	Ala	Gly	Asp	Ile	Leu	Thr
			100					105					110		
Asp	Ser	Asp	Ile	Glu	Ile	Val	Asn	Pro	Asp	His	Tyr	Leu	Phe	Thr	Ile
	115						120					125			
Gly	Glu	Gly	Ser	Ser	Leu	Lys	Ala	Thr	Met	Thr	Val	Asn	Ser	Gly	Arg
	130					135					140				
Gly	Tyr	Val	Pro	Ala	Asp	Glu	Asn	Lys	Lys	Asp	Asn	Ala	Pro	Val	Gly
145					150					155					160
Thr	Leu	Ala	Val	Asp	Ser	Ile	Tyr	Thr	Pro	Val	Thr	Lys	Val	Asn	Tyr
				165					170					175	
Gln	Val	Glu	Pro	Ala	Arg	Val	Gly	Ser	Asn	Asp	Gly	Phe	Asp	Lys	Leu
			180				185						190		
Thr	Leu	Glu	Ile	Leu	Thr	Asn	Gly	Thr	Ile	Ile	Pro	Glu	Asp	Ala	Leu
	195					200						205			
Gly	Leu	Ser	Ala	Arg	Ile	Leu	Thr	Glu	His	Leu	Asp	Leu	Phe	Thr	Asn
	210					215					220				
Leu	Thr	Glu	Ile	Ala	Lys	Ser	Thr	Glu	Val	Met	Lys	Glu	Ala	Asp	Thr
225					230					235					240
Glu	Ser	Asp	Asp	Arg	Ile	Leu	Asp	Arg	Thr	Ile	Glu	Glu	Leu	Asp	Leu
				245					250					255	
Ser	Val	Arg	Ser	Tyr	Asn	Cys	Leu	Lys	Arg	Ala	Gly	Ile	Asn	Thr	Val
			260				265						270		
His	Asp	Leu	Thr	Glu	Lys	Ser	Glu	Ala	Glu	Met	Met	Lys	Val	Arg	Asn
		275					280						285		

Leu	Gly	Arg	Lys	Ser	Leu	Glu	Glu	Val	Lys	Leu	Lys	Leu	Ile	Asp	Leu
290						295					300				
Gly	Leu	Gly	Leu	Lys	Asp	Lys									
305					310										

(2) INFORMATION FOR SEQ ID NO:2863:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 440 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...440

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2863:

Cys	Glu	Thr	Thr	Ser	Asp	Leu	Leu	Tyr	Gly	Arg	Asn	Arg	Met	Thr	Lys
1				5					10					15	
Val	Val	Phe	Glu	Glu	Lys	Tyr	Tyr	Pro	Ala	Val	Lys	Glu	Met	Val	Tyr
		20					25						30		
Arg	Thr	Arg	Leu	Ala	Asn	Gly	Leu	Thr	Val	Ala	Leu	Leu	Pro	Lys	Lys
		35				40						45			
Glu	Phe	Lys	Glu	Val	Tyr	Gly	Ser	Val	Thr	Val	Gln	Phe	Gly	Ser	Val
	50					55					60				
Asp	Thr	Phe	Val	Thr	Glu	Val	Asp	Gly	Asp	Val	Lys	Gln	Tyr	Pro	Gly
65					70				75					80	
Gly	Ile	Ala	His	Phe	Leu	Glu	His	Lys	Leu	Phe	Glu	Arg	Glu	Asp	Ser
			85					90					95		
Ser	Asp	Leu	Met	Ser	Ala	Phe	Thr	Ser	Leu	Gly	Ala	Asp	Ser	Asn	Ala
		100						105					110		
Phe	Thr	Ser	Phe	Thr	Lys	Thr	Asn	Tyr	Leu	Phe	Ser	Ala	Thr	Asp	Tyr
		115				120						125			
Phe	Leu	Glu	Asn	Leu	Asp	Leu	Leu	Asp	Glu	Leu	Val	Thr	Ser	Ala	His
	130					135					140				
Phe	Thr	Glu	Ala	Ser	Ile	Leu	Thr	Glu	Gln	Asp	Ile	Ile	Gln	Gln	Glu
145					150					155					160
Arg	Glu	Met	Tyr	Gln	Asp	Asp	Pro	Asp	Ser	Cys	Leu	Phe	Phe	Ser	Thr
				165				170						175	
Leu	Ala	Asn	Leu	Tyr	Pro	Gly	Thr	Pro	Leu	Ala	Thr	Asp	Ile	Val	Gly
		180					185					190			
Ser	Glu	Glu	Ser	Ile	Ser	Gln	Ile	Asn	Leu	Thr	Asn	Leu	Gln	Glu	Asn
	195					200					205				
Phe	Thr	Lys	Phe	Tyr	Lys	Pro	Val	Asn	Met	Ser	Leu	Phe	Leu	Val	Gly
	210					215					220				
Asn	Phe	Asp	Val	Glu	Arg	Val	Gln	Asp	Tyr	Phe	Glu	Ser	Lys	Glu	Leu
225					230					235					240
Lys	Asp	Ser	Asp	Phe	Gln	Glu	Val	Ala	Arg	Glu	Lys	Leu	Phe	Leu	Gln
				245					250						255

Pro	Val	Lys	Leu	Thr	Asp	Ser	Met	Arg	Met	Glu	Val	Ser	Ser	Pro	Lys
			260					265					270		
Leu	Ala	Ile	Gly	Val	Arg	Gly	Lys	Arg	Glu	Val	Ser	Glu	Ala	Asp	Cys
		275					280					285			
Tyr	Arg	His	His	Ile	Leu	Leu	Lys	Leu	Leu	Phe	Ala	Met	Met	Phe	Gly
	290					295					300				
Trp	Thr	Ser	Asp	Arg	Phe	Gln	Lys	Cys	Tyr	Glu	Ser	Gly	Lys	Ile	Asp
305					310					315					320
Ala	Ser	Leu	Ser	Leu	Glu	Val	Glu	Ile	Thr	Ser	Arg	Phe	His	Phe	Val
				325					330					335	
Met	Leu	Thr	Met	Asp	Thr	Lys	Glu	Pro	Val	Ala	Leu	Ser	His	Gln	Phe
			340					345					350		
Arg	Lys	Ala	Ile	Arg	Asn	Phe	Thr	Lys	Asp	Leu	Asp	Ile	Thr	Glu	Glu
		355					360					365			
His	Leu	Asp	Ile	Ile	Lys	Arg	Glu	Met	Phe	Gly	Glu	Phe	Phe	Ser	Ser
	370					375					380				
Met	Asn	Ser	Leu	Glu	Phe	Ile	Ala	Thr	Gln	Tyr	Asp	Ala	Phe	Glu	Asn
385					390					395					400
Gly	Glu	Thr	Ile	Phe	Asp	Leu	Pro	Lys	Ile	Leu	Gln	Glu	Ile	Thr	Leu
			405						410					415	
Glu	Asp	Val	Leu	Asp	Ala	Gly	His	His	Leu	Ile	Asp	Asp	Gly	Asp	Ile
		420						425					430		
Val	Asp	Phe	Thr	Ile	Phe	Pro	Ser								
		435					440								

(2) INFORMATION FOR SEQ ID NO:2864:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2864:

Lys	Gln	Thr	Thr	Tyr	Arg	Leu	Ala	Gln	Val	Gly	Val	Gln	Pro	Tyr	Arg
1				5				10					15		
Gln	Val	His	Ala	His	Ser	Thr	Gly	Asn	Arg	Asn	Ser	Thr	Val	Gln	Asn
		20					25					30			
Glu	Ala	Asp	Tyr	His	Trp	Arg	Lys	Asp	Pro	Glu	Leu	Gly	Phe	Phe	Ser
		35				40						45			
His	Val	Val	Gly	Asn	Gly	Arg	Ile	Met	Gln	Val	Gly	Pro	Val	Asn	Asn
	50				55				60						
Gly	Ser	Trp	Asp	Val	Gly	Gly	Gly	Trp	Asn	Ala	Glu	Thr	Tyr	Ala	Ala
65				70				75						80	
Val	Glu	Leu	Ile	Glu	Ser	His	Ser	Thr	Lys	Glu	Glu	Phe	Met	Ala	Asp
			85					90						95	

```

Tyr Arg Leu Tyr Ile Glu Leu Leu Arg Asn Leu Ala Asp Glu Ala Gly
    100                      105                      110
Leu Pro Lys Thr Leu Asp Thr Asp Asp Leu Ala Gly Ile Lys Thr His
    115                      120                      125
Glu Tyr Cys Thr Asn Asn Gln Pro Asn Asn His Ser Asp His Val Asp
    130                      135                      140
Pro Tyr Pro Tyr Leu Ala Ser Trp Gly Ile Ser Arg Glu Gln Phe Lys
    145                      150                      155                      160
Gln Asp Ile Glu Asn Gly Leu Ser Ala Ala Thr Gly Trp Gln Lys Asn
    165                      170                      175
Gly Thr Gly Tyr Trp Tyr Val His Ser Asp Gly Phe Tyr Pro Lys Asp
    180                      185                      190
Lys Phe Glu Lys Ile Asn Gly Thr Trp Tyr Tyr Phe Asp Gly Ser Gly
    195                      200                      205
Tyr Met Leu Ser Asp Arg Trp Lys Lys His Thr Asp Gly Asn Trp Tyr
    210                      215                      220
Trp Phe Asp Asn Ser Gly Glu Met Ala Thr Gly Trp Lys Lys Ile Ala
    225                      230                      235                      240
Glu Lys Trp Tyr Tyr Phe Asp Val Glu Gly Ala Met Lys Thr Gly Trp
    245                      250                      255
Val Lys Tyr Lys Asp Thr Trp Tyr Tyr Leu Asp Ala Lys Glu Gly Ala
    260                      265                      270
Met Val Ser Asn Ala Phe Ile Gln Ser Ala Asp Gly Thr Gly Trp Tyr
    275                      280                      285
Tyr Leu Lys Pro Asp Gly Ser Met Ala Asp Lys Pro Glu Phe Thr Val
    290                      295                      300
Glu Pro Asp Gly Leu Ile Thr Val Lys
    305                      310

```

(2) INFORMATION FOR SEQ ID NO:2865:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 417 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...417

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2865:

```

Asn Lys Thr Thr Met Lys Lys Ile Phe Leu Thr Leu Leu Thr Val Ser
1      5      10      15
Leu Leu Gly Gly Ala Ser Thr Ala Val Ala Gln Asp Phe Thr Ile Ala
    20      25      30
Ala Lys His Ala Ile Ala Val Glu Ala Asn Thr Gly Lys Ile Leu Tyr
    35      40      45
Glu Lys Asp Ala Thr Gln Pro Val Glu Ile Ala Ser Ile Thr Lys Leu
    50      55      60

```

Ile	Thr	Val	Tyr	Leu	Val	Tyr	Glu	Ala	Leu	Glu	Asn	Gly	Ser	Ile	Thr
65					70					75					80
Leu	Ser	Thr	Pro	Val	Asp	Ile	Ser	Asp	Tyr	Pro	Tyr	Gln	Leu	Thr	Thr
				85					90						95
Asn	Ser	Glu	Ala	Ser	Asn	Ile	Pro	Met	Glu	Ala	Arg	Asn	Tyr	Thr	Val
			100					105					110		
Glu	Glu	Leu	Leu	Glu	Ala	Thr	Leu	Val	Ser	Ser	Ala	Asn	Ser	Ala	Ala
		115					120					125			
Ile	Ala	Leu	Ala	Glu	Lys	Ile	Ala	Gly	Ser	Glu	Lys	Asp	Phe	Val	Asp
	130					135					140				
Met	Met	Arg	Ala	Lys	Leu	Leu	Glu	Trp	Gly	Ile	Gln	Asp	Ala	Thr	Val
145					150					155					160
Val	Asn	Thr	Thr	Gly	Leu	Asn	Asn	Glu	Thr	Leu	Gly	Asp	Asn	Ile	Tyr
				165					170					175	
Pro	Gly	Ser	Lys	Lys	Asp	Glu	Glu	Asn	Lys	Leu	Ser	Ala	Tyr	Asp	Val
			180					185					190		
Ala	Ile	Val	Ala	Arg	Asn	Leu	Ile	Lys	Lys	Tyr	Pro	Gln	Val	Leu	Glu
		195					200					205			
Ile	Thr	Lys	Lys	Pro	Ser	Ser	Thr	Phe	Ala	Gly	Met	Thr	Ile	Thr	Ser
	210					215					220				
Thr	Asn	Tyr	Met	Leu	Glu	Gly	Met	Pro	Ala	Tyr	Arg	Gly	Gly	Phe	Asp
225					230					235					240
Gly	Leu	Lys	Thr	Gly	Thr	Thr	Asp	Lys	Ala	Gly	Glu	Ser	Phe	Val	Gly
				245					250					255	
Thr	Thr	Val	Glu	Lys	Gly	Met	Arg	Val	Ile	Thr	Val	Val	Leu	Asn	Ala
		260						265					270		
Asp	His	Gln	Asp	Asn	Asn	Pro	Tyr	Ala	Arg	Phe	Thr	Ala	Thr	Ser	Ser
	275						280					285			
Leu	Met	Asp	Tyr	Ile	Ser	Ser	Thr	Phe	Thr	Leu	Arg	Lys	Ile	Val	Gln
	290					295					300				
Gln	Gly	Asp	Ala	Tyr	Gln	Asp	Ser	Lys	Ala	Pro	Val	Gln	Asp	Gly	Lys
305					310					315					320
Glu	Asp	Thr	Val	Thr	Ala	Val	Ala	Pro	Glu	Asp	Ile	Tyr	Leu	Ile	Glu
				325					330					335	
Gln	Ile	Gly	Asn	Gln	Ser	Ser	Gln	Ser	Val	Gln	Phe	Thr	Pro	Asp	Ser
			340					345					350		
Lys	Ala	Ile	Pro	Ala	Pro	Leu	Glu	Ala	Gly	Thr	Val	Val	Gly	His	Leu
	355						360					365			
Thr	Tyr	Lys	Asp	Lys	Asp	Leu	Ile	Gly	Gln	Gly	Tyr	Ile	Thr	Thr	Glu
	370					375					380				
Arg	Pro	Ser	Phe	Glu	Met	Val	Ala	Asp	Lys	Lys	Ile	Glu	Lys	Ala	Phe
385					390					395					400
Phe	Leu	Lys	Val	Trp	Trp	Asn	Gln	Phe	Val	Arg	Phe	Val	Asn	Glu	Lys
				405					410					415	

Leu

(2) INFORMATION FOR SEQ ID NO:2866:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2866:

```
Leu His Tyr Thr Arg Phe Gly Glu Asn Met Leu Glu Ile Lys Asn Leu
1          5          10          15
Thr Gly Gly Tyr Val His Val Pro Val Leu Lys Asp Val Ser Phe Thr
          20          25          30
Val Glu Ser Gly Gln Leu Val Gly Leu Ile Gly Leu Asn Gly Ala Gly
          35          40          45
Lys Ser Thr Thr Ile Asn Glu Ile Ile Gly Leu Leu Ala Pro Tyr Ser
          50          55          60
Gly Ser Ile Asn Ile Asn Gly Leu Thr Leu Gln Gly Asp Ala Thr Ser
65          70          75          80
Tyr Arg Lys Gln Ile Gly Tyr Ile Pro Glu Thr Pro Ser Leu Tyr Glu
          85          90          95
Glu Leu Thr Leu Arg Glu His Ile Glu Thr Val Ala Met Ala Tyr Gly
          100          105          110
Ile Glu Gln Lys Val Ala Phe Glu Arg Val Glu Pro Leu Leu Lys Met
          115          120          125
Phe Arg Leu Asp Arg Asn
          130
```

(2) INFORMATION FOR SEQ ID NO:2867:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 112 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2867:

```
Lys Asn Tyr Thr Pro Glu Gln Gln Lys Leu His Asp Gln Phe Glu Ala
1          5          10          15
Glu Ala Thr Glu Asp Ala Lys Lys Gln Gly Asp Ile Val Leu Asn Val
          20          25          30
Asp Gln Asp Phe Met Ser Ile Ser Lys Ser Asn Lys Ser Gly Ser Asp
          35          40          45
Trp Lys Lys Thr Phe Thr Val Arg Thr Thr Asn Arg Leu Ala Asn Asp
          50          55          60
```

Leu	Asn	Asn	Val	Leu	Lys	Gln	Ala	Asp	Lys	Asp	Thr	Pro	Asn	Thr	Pro
65					70					75					80
Thr	Trp	Leu	Asn	Ser	Ala	Ala	Ser	Lys	Ala	Lys	Asp	Asp	Asp	Arg	Ala
			85						90					95	
Tyr	Lys	Leu	Leu	Lys	Thr	Leu	Ile	Pro	Gly	Glu	Asn	Tyr	Leu	Ser	Cys
			100					105					110		

(2) INFORMATION FOR SEQ ID NO:2868:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 109 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...109

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2868:

Ser	Leu	Tyr	Thr	Arg	Ile	Ser	Leu	Leu	Leu	Trp	Thr	His	Thr	Gly	Glu
1				5					10					15	
Ser	Phe	Phe	Leu	Ile	Ala	Gly	Gly	Cys	Asn	Thr	Glu	Trp	Met	Asn	Val
			20					25					30		
Phe	Leu	Glu	Glu	Leu	Ser	Gln	Ala	Tyr	Pro	Asp	Asp	Tyr	Leu	Leu	Phe
		35				40						45			
Val	Met	Asp	Asn	Ala	Ile	Trp	His	Lys	Ser	Ser	Thr	Leu	Lys	Ile	Pro
	50				55						60				
Thr	Asn	Ile	Gly	Phe	Ala	Phe	Ile	Pro	Pro	Tyr	Thr	Pro	Glu	Met	Asn
65					70					75					80
Pro	Ile	Glu	Gln	Val	Trp	Lys	Glu	Ile	Arg	Lys	Arg	Gly	Phe	Lys	Asn
			85					90					95		
Lys	Ala	Phe	Gln	Thr	Leu	Glu	Asp	Val	Met	Asn	Gln	Leu			
			100					105							

(2) INFORMATION FOR SEQ ID NO:2869:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2869:

```
Leu Gly Glu Leu Ser Ile Pro Leu Arg Gln Ser Ser Thr Leu Ile Thr
1          5          10          15
Thr Lys Asn Ile Phe His Cys Asn Val Ile Ala Pro Ser Val Ile Leu
20          25          30
Ser Ala Ser Ile Leu Thr Met Cys Leu Leu Met Trp Ile Leu Arg Val
35          40          45
Asn Gly Lys Gln Met Lys Val Val Ser Val Ala Leu Ala Lys Leu Leu
50          55          60
Leu Thr Val Phe Val Lys Lys Ser Lys Val Val Leu Lys Met Leu Ala
65          70          75          80
Trp Lys Ser Leu Lys His Val Ser Leu Thr Tyr Leu Met Leu Gln Lys
85          90          95
Leu Leu Pro Leu Cys Phe Asn Ala Asn Lys His Leu Pro Leu Leu Met
100          105          110
His Glu Lys
115
```

(2) INFORMATION FOR SEQ ID NO:2870:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 93 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...93

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2870:

```
Phe Gln Tyr Thr Ile Thr Val Pro Ser Gln Pro Ala Ser Pro Val Pro
1          5          10          15
Ala Pro Ser Ser Ala Pro Thr Gln Asp Pro Arg Val Val Ala Ser Ala
20          25          30
Ser Ala Ser Ser Thr Ser Thr Gln Ala Gln Glu Gln Val Asp Lys Ser
35          40          45
Glu Leu Arg Ala Leu Ser Gln Glu Leu Asp Gln Arg Leu Lys Ala Leu
50          55          60
Ala Thr Ile Ser Asp Pro Lys Ile Asp Ala Thr Lys Ala Val Leu Leu
65          70          75          80
Asp Ala Gln Lys Ala Pro Glu Asp Ser Ala Leu Thr Glu
85          90
```

(2) INFORMATION FOR SEQ ID NO:2871:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 273 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...273
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2871:

Ala	Arg	Tyr	Thr	Arg	Phe	Tyr	Tyr	Lys	Ser	Phe	Ser	Phe	Ser	Glu	Leu
1				5					10					15	
Ile	Gly	Ile	Phe	Leu	Ala	Asn	Asp	Lys	Val	Leu	Gly	Pro	Ile	Gln	Ser
			20					25					30		
Ile	Ala	Tyr	Ser	Leu	Asn	Lys	Ile	Asn	Thr	Thr	Lys	Asp	Leu	Arg	Lys
		35					40					45			
Pro	Phe	Leu	Lys	Tyr	Leu	Ser	Gly	Glu	Lys	Asn	Phe	Ile	Asp	Ala	Glu
	50					55					60				
His	Asp	Asn	Asn	Gly	Leu	Tyr	Thr	Ser	Ser	Ile	Asp	Val	Ile	His	Met
65				70						75				80	
Lys	Asp	Val	Val	Tyr	Ser	Ile	Thr	Pro	Glu	Asn	Lys	Leu	Ser	Ile	Asp
			85						90					95	
Phe	Ser	Phe	Lys	Ser	Pro	Phe	Arg	Val	Leu	Leu	Thr	Gly	Thr	Ser	Gly
			100					105					110		
Ser	Gly	Lys	Thr	Thr	Ile	Leu	Asn	Leu	Ile	Asn	Gly	Ser	Leu	Lys	Pro
		115					120					125			
Gln	Lys	Gly	Tyr	Val	Asn	Leu	Leu	Ser	His	Gly	Lys	Lys	Ser	Ser	Asp
	130					135					140				
Ser	Ile	Pro	Thr	Val	Asp	Gln	Thr	Pro	Tyr	Ile	Phe	Asp	Thr	Thr	Ile
145				150						155				160	
Arg	Glu	Asn	Val	Thr	Leu	Phe	Gln	Asn	Glu	Tyr	Phe	Ser	Asp	Asp	Gln
			165						170					175	
Ile	Ile	Glu	Val	Leu	Lys	Lys	Val	Asn	Leu	Tyr	Glu	Glu	Leu	Glu	Lys
		180						185					190		
Ile	Asp	Ile	Leu	Asn	Tyr	Gln	Cys	Gly	Glu	Asn	Gly	Ser	Asn	Leu	Ser
	195						200					205			
Gly	Gly	Gln	Lys	Gln	Lys	Ile	Ala	Leu	Ala	Arg	Ala	Leu	Ile	Arg	Asn
	210					215					220				
Asn	Lys	Val	Tyr	Leu	Phe	Asp	Glu	Ile	Ser	Ala	Asn	Leu	Asp	Asn	Asp
225				230						235				240	
Asn	Ser	Asn	Ser	Ile	His	Asp	Ile	Leu	Phe	Asn	Leu	Gly	Ile	Ser	Phe
			245						250					255	
Ile	Glu	Val	Ser	His	His	Tyr	Asp	Leu	Asn	Asp	Lys	Arg	Tyr	Thr	Asp
		260						265					270		
Ile															

(2) INFORMATION FOR SEQ ID NO:2872:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 501 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...501
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2872:

Thr	Lys	Tyr	Thr	Ser	Asn	Pro	Phe	Cys	Gly	Val	Leu	Val	Gly	Ile	Gly
1				5					10					15	
Met	Thr	Ala	Leu	Ile	Gln	Ser	Ser	Ser	Gly	Val	Thr	Val	Ile	Thr	Val
			20					25					30		
Gly	Leu	Val	Ser	Ala	Gly	Leu	Leu	Thr	Leu	Arg	Gln	Ala	Ile	Gly	Ile
		35				40					45				
Val	Met	Gly	Ala	Asn	Ile	Gly	Thr	Thr	Val	Thr	Ser	Phe	Leu	Ile	Gly
	50					55					60				
Phe	Lys	Leu	Gly	Asn	Tyr	Ala	Leu	Pro	Met	Leu	Phe	Ile	Gly	Ala	Val
65				70						75				80	
Cys	Leu	Phe	Phe	Thr	Lys	Asn	Arg	Thr	Val	Asn	Asn	Ile	Gly	Arg	Ile
			85					90					95		
Leu	Phe	Gly	Val	Gly	Gly	Ile	Phe	Phe	Ala	Leu	Asn	Leu	Met	Ser	Gly
		100					105					110			
Ala	Met	Ala	Pro	Leu	Lys	Asp	Leu	Gln	Val	Phe	Lys	Asp	Tyr	Met	Ile
		115				120						125			
Glu	Leu	Ser	Lys	Asn	Pro	Val	Leu	Gly	Val	Phe	Val	Gly	Thr	Gly	Leu
130						135					140				
Thr	Leu	Leu	Ile	His	Ala	Ser	Ser	Ala	Thr	Ile	Gly	Ile	Leu	Gln	Asn
145				150						155				160	
Leu	Tyr	Ala	Gly	Asn	Leu	Ile	Asp	Leu	Gln	Gly	Ala	Leu	Pro	Val	Leu
			165					170					175		
Phe	Gly	Asp	Asn	Ile	Gly	Thr	Thr	Ile	Thr	Ala	Ile	Ile	Ala	Ser	Leu
		180					185					190			
Gly	Ala	Asn	Ile	Ala	Ala	Lys	Arg	Val	Ala	Gly	Ala	His	Val	Ala	Phe
		195				200						205			
Asn	Val	Ile	Gly	Thr	Val	Val	Cys	Val	Ile	Phe	Leu	Val	Pro	Phe	Thr
210						215					220				
Val	Leu	Ile	His	Trp	Phe	Glu	Ala	Thr	Leu	Asn	Leu	Ala	Pro	Glu	Met
225				230						235				240	
Thr	Ile	Ala	Phe	Ala	His	Gly	Thr	Phe	Asn	Ile	Thr	Asn	Thr	Ile	Val
			245					250					255		
Gln	Phe	Pro	Phe	Ile	Gly	Ala	Leu	Ala	Tyr	Phe	Val	Thr	Lys	Ile	Ile
		260					265					270			
Pro	Gly	Glu	Asp	Glu	Val	Val	Lys	Tyr	Glu	Pro	Leu	Tyr	Leu	Asp	Glu
		275				280					285				
His	Phe	Ile	Lys	Gln	Ala	Pro	Ser	Ile	Ala	Leu	Gly	Asn	Ala	Lys	Lys
290						295					300				

Glu	Leu	Leu	His	Leu	Gly	Asn	Tyr	Ala	Ala	Lys	Ala	Phe	Asp	Leu	Ser
305					310					315					320
Tyr	Lys	Tyr	Ile	Ile	Asp	Leu	Asp	Glu	Lys	Val	Ala	Glu	Lys	Gly	His
			325						330					335	
Lys	Thr	Glu	Glu	Ala	Ile	Asn	Thr	Ile	Asp	Glu	Gln	Leu	Thr	Arg	Tyr
		340						345					350		
Leu	Ile	Ala	Leu	Ser	Ser	Glu	Ala	Leu	Ser	Gln	Lys	Glu	Ser	Glu	Val
	355					360					365				
Leu	Thr	Asn	Ile	Leu	Asp	Ser	Ser	Arg	Asp	Leu	Glu	Arg	Ile	Gly	Asp
370					375					380					
His	Thr	Glu	Ala	Leu	Leu	Asn	Leu	Thr	Asp	Tyr	Leu	Gln	Arg	Lys	Asn
385				390					395					400	
Val	Glu	Phe	Ser	Asp	Ala	Ala	Leu	Lys	Glu	Leu	Glu	Glu	Val	Tyr	Arg
			405					410					415		
Gln	Thr	Ser	Asp	Phe	Ile	Lys	Asp	Ala	Leu	Asp	Ser	Val	Glu	Asn	Asn
		420					425					430			
Asp	Ile	Glu	Lys	Ala	Arg	Ser	Leu	Val	Glu	Arg	His	Glu	Ala	Ile	Asn
	435					440					445				
Lys	Ile	Glu	Arg	Val	Leu	Arg	Lys	Thr	His	Ile	Lys	Arg	Leu	Asn	Lys
450					455					460					
Gly	Glu	Cys	Ser	Thr	Gln	Ala	Gly	Val	Asn	Phe	Ile	Asp	Ile	Ile	Ser
465				470					475					480	
His	Tyr	Thr	Arg	Val	Ser	Asp	His	Ala	Met	Asn	Leu	Ala	Glu	Lys	Val
			485					490					495		
Phe	Ala	Glu	Gln	Ile											
			500												

(2) INFORMATION FOR SEQ ID NO:2873:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...66

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2873:

Phe	Phe	His	Thr	Asn	Val	Phe	Leu	Thr	Asp	Asn	Ser	Pro	Phe	Tyr	Tyr
1				5				10						15	
Ile	Lys	Lys	Ser	Pro	Leu	Ser	His	Ser	Lys	Thr	Xaa	Leu	Glu	Ser	Ile
			20					25					30		
Trp	Glu	Phe	Phe	Arg	Gln	Arg	Phe	Ser	Val	Leu	Ala	Ala	Asn	Leu	Gly
		35				40					45				
Gln	Asp	Lys	Glu	Lys	Ser	Pro	Ile	Lys	Gly	Phe	Leu	Gly	Cys	Leu	His
50					55						60				
Pro	Pro														
65															

(2) INFORMATION FOR SEQ ID NO:2874:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 417 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...417

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2874:

Ile	Met	Glu	Leu	Val	His	Gly	Ile	Ser	Thr	His	Phe	Ile	Gln	Ser	Lys	
1				5					10				15			
Lys	Phe	Lys	Thr	Asn	Lys	Ile	Thr	Val	Arg	Phe	Thr	Ala	Pro	Leu	Ser	
			20					25					30			
Leu	Asp	Thr	Ile	Ala	Gly	His	Met	Leu	Ser	Ala	Ser	Met	Leu	Glu	Thr	
		35					40					45				
Ala	Asn	Gln	Met	Tyr	Pro	Thr	Ser	Gln	Asp	Leu	Arg	Arg	His	Leu	Ala	
	50					55					60					
Ser	Leu	Tyr	Gly	Thr	Asp	Met	Ser	Thr	Asn	Cys	Phe	Arg	Arg	Gly	Gln	
65				70					75						80	
Ser	His	Ile	Ile	Glu	Leu	Thr	Phe	Thr	Tyr	Val	Arg	Asp	Glu	Phe	Leu	
			85					90					95			
Ser	Arg	Lys	Asn	Val	Leu	Thr	Ser	Gln	Ile	Leu	Glu	Leu	Val	Lys	Glu	
			100					105					110			
Thr	Leu	Phe	Ser	Pro	Val	Val	Val	Asp	Asn	Gly	Phe	Asp	Pro	Ala	Leu	
		115					120					125				
Phe	Glu	Ile	Glu	Lys	Lys	Gln	Leu	Leu	Ala	Ser	Leu	Ala	Ala	Asp	Met	
	130					135					140					
Asp	Asp	Ser	Phe	Tyr	Phe	Ala	His	Lys	Glu	Leu	Asp	Lys	Leu	Phe	Phe	
145				150					155						160	
His	Asp	Glu	Arg	Leu	Gln	Leu	Glu	Tyr	Ser	Asp	Leu	Arg	Asn	Arg	Ile	
			165					170					175			
Leu	Ala	Glu	Thr	Pro	Gln	Ser	Ser	Tyr	Ser	Cys	Phe	Gln	Glu	Phe	Leu	
		180						185				190				
Ala	Asn	Asp	Arg	Ile	Asp	Phe	Phe	Phe	Leu	Gly	Asp	Phe	Asn	Glu	Val	
	195						200					205				
Glu	Ile	Gln	Asn	Val	Leu	Glu	Ser	Phe	Gly	Phe	Lys	Gly	Arg	Lys	Gly	
	210					215					220					
Asp	Val	Lys	Val	Gln	Tyr	Cys	Gln	Pro	Tyr	Ser	Asn	Ile	Leu	Gln	Glu	
225				230					235						240	
Gly	Met	Val	Arg	Lys	Asn	Val	Gly	Gln	Ser	Ile	Leu	Glu	Leu	Gly	Tyr	
			245					250						255		
His	Tyr	Arg	Ser	Lys	Tyr	Gly	Asp	Glu	Gln	His	Leu	Pro	Met	Ile	Val	
		260					265					270				
Met	Asn	Gly	Leu	Leu	Gly	Gly	Phe	Ala	His	Ser	Lys	Leu	Phe	Thr	Asn	
		275					280					285				

Val	Arg	Glu	Asn	Ala	Gly	Leu	Ala	Tyr	Thr	Ile	Ser	Ser	Glu	Leu	Asp
290						295					300				
Leu	Phe	Ser	Gly	Phe	Leu	Arg	Met	Tyr	Ala	Gly	Ile	Asn	Arg	Glu	Asn
305					310					315					320
Arg	Asn	Gln	Ala	Arg	Lys	Met	Met	Asn	Asn	Gln	Leu	Leu	Asp	Leu	Lys
				325					330					335	
Lys	Gly	Tyr	Phe	Thr	Glu	Phe	Glu	Leu	Asn	Gln	Thr	Lys	Glu	Met	Ile
			340					345					350		
Arg	Trp	Ser	Leu	Leu	Leu	Ser	Gln	Asp	Asn	Gln	Ser	Ser	Leu	Ile	Glu
		355					360					365			
Arg	Ala	Tyr	Gln	Asn	Ala	Leu	Phe	Gly	Lys	Ser	Ser	Ala	Asp	Phe	Lys
	370					375						380			
Ser	Trp	Ile	Ala	Lys	Leu	Glu	Gln	Ile	Asp	Lys	Asp	Ala	Ile	Cys	Arg
385					390					395					400
Val	Ala	Asn	Asn	Val	Lys	Leu	Gln	Ala	Ile	Tyr	Phe	Met	Glu	Gly	Ile
				405					410					415	

Glu

(2) INFORMATION FOR SEQ ID NO:2875:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...111

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2875:

Gln	Ser	Glu	Phe	Gln	Val	Asn	Gly	Ser	Arg	Trp	Phe	Leu	Glu	Met	Arg
1				5					10					15	
Asn	Ile	Gly	Gln	Ala	Gly	Lys	Ile	Leu	Ala	Asp	Ser	Gly	Tyr	Gln	Gly
			20					25					30		
Leu	Met	Lys	Ile	Tyr	Pro	Gln	Ala	Gln	Thr	Pro	Arg	Lys	Ser	Ser	Lys
		35					40					45			
Leu	Lys	Pro	Leu	Thr	Leu	Glu	Asp	Lys	Ala	Cys	Asn	His	Ala	Leu	Ser
		50				55				60					
Lys	Glu	Arg	Ser	Lys	Val	Glu	Asn	Ile	Phe	Ala	Lys	Val	Lys	Thr	Phe
65				70					75					80	
Lys	Met	Phe	Ser	Thr	Thr	Tyr	Arg	Asn	His	Arg	Lys	Arg	Phe	Gly	Leu
			85					90						95	
Arg	Met	Asn	Leu	Ile	Ala	Gly	Ile	Ile	Asn	His	Glu	Leu	Gly	Phe	
			100				105						110		

(2) INFORMATION FOR SEQ ID NO:2876:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 63 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...63

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2876:

Phe	Gln	His	Thr	Ile	Lys	Ser	Gly	Asn	Thr	Thr	Ala	Lys	Lys	Phe	Glu
1				5				10						15	
Phe	Ile	Glu	Ile	Pro	Val	Gln	Lys	Leu	Lys	Lys	Ala	Ile	Tyr	Lys	Ala
			20				25						30		
His	Leu	Lys	Asp	Ser	Asp	Asp	Phe	Arg	Pro	Glu	Thr	Ser	Thr	Pro	Asn
		35				40						45			
Leu	Phe	Glu	Ser	Cys	Leu	Lys	Leu	Cys	Pro	Cys	Phe	Leu	Ser	Ser	
	50					55					60				

(2) INFORMATION FOR SEQ ID NO:2877:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 186 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2877:

His	Trp	His	Thr	Cys	Leu	Leu	Glu	Asp	Gly	Leu	Gln	Thr	Glu	Val	Phe
1				5				10						15	
Val	Met	Leu	Glu	Ser	Lys	Lys	Thr	Thr	Arg	Tyr	Val	Phe	Tyr	Val	Tyr
			20				25						30		
Leu	Met	Leu	Leu	Thr	Trp	Gly	Ile	Leu	Phe	Lys	Phe	Glu	Thr	Asn	Pro
		35				40						45			
Glu	Phe	Ile	Ala	Phe	Phe	Leu	Ala	Pro	Arg	Tyr	Ile	Asn	Trp	Ile	Pro
	50					55					60				
Phe	Ser	Glu	Pro	Leu	Ile	Val	Asp	Gly	Lys	Ile	Val	Phe	Ala	Glu	Met
65					70				75					80	
Leu	Phe	Asn	Leu	Ile	Phe	Phe	Ile	Pro	Leu	Gly	Val	Cys	Phe	Pro	Leu

				85					90					95			
Ile	Lys	Thr	Asn	Leu	Ser	Ser	Leu	Arg	Ile	Val	Gly	Thr	Gly	Phe	Leu		
			100					105					110				
Ile	Ser	Leu	Leu	Phe	Glu	Cys	Leu	Gln	Tyr	Ile	Leu	Ala	Ile	Gly	Ile		
		115					120					125					
Thr	Asp	Ile	Thr	Asp	Leu	Thr	Leu	Asn	Thr	Leu	Gly	Val	Cys	Val	Gly		
	130					135					140						
Leu	Leu	Ile	Tyr	Gln	Ile	Phe	Ile	Arg	Val	Phe	Lys	Ser	Gln	Thr	Arg		
145					150					155					160		
Lys	Trp	Ile	Asn	Ile	Leu	Gly	Met	Leu	Ser	Leu	Gly	Phe	Ala	Tyr	Leu		
			165					170						175			
Val	Leu	Leu	Leu	Leu	His	Leu	Ile	Gly	Val								
			180					185									

(2) INFORMATION FOR SEQ ID NO:2878:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 207 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2878:

Leu	Lys	Glu	Phe	His	Met	Ser	Asn	Glu	Lys	Asn	Thr	Asn	Thr	Asn	Val		
1				5				10						15			
Glu	Lys	Lys	Asp	Ala	Thr	Val	Val	Ala	His	Glu	Ile	Lys	Gly	Glu	Leu		
		20						25					30				
Thr	Tyr	Glu	Asp	Lys	Val	Ile	Gln	Lys	Ile	Ile	Gly	Leu	Ser	Leu	Glu		
	35					40					45						
Asn	Val	Ser	Gly	Leu	Leu	Gly	Ile	Asp	Gly	Gly	Phe	Phe	Ser	Asn	Leu		
50					55				60								
Lys	Glu	Lys	Ile	Val	Asn	Ser	Asp	Asp	Val	Thr	Ser	Gly	Val	Asn	Val		
65				70					75					80			
Glu	Val	Gly	Lys	Thr	Gln	Val	Ala	Val	Asp	Leu	Asn	Val	Ile	Val	Glu		
			85					90					95				
Tyr	Gln	Lys	Asn	Val	Pro	Ala	Leu	Tyr	Ser	Glu	Ile	Arg	Glu	Ile	Val		
		100					105					110					
Ser	Ser	Glu	Val	Ala	Lys	Met	Thr	Asp	Leu	Glu	Ile	Val	Glu	Ile	Asn		
	115					120						125					
Val	Asn	Val	Val	Asp	Ile	Lys	Thr	Lys	Glu	Gln	His	Glu	Ala	Asp	Ser		
	130					135					140						
Val	Ser	Leu	Gln	Asp	Arg	Val	Ser	Asp	Val	Ala	Glu	Ser	Thr	Gly	Glu		
145				150					155					160			
Phe	Thr	Ser	Glu	Gln	Phe	Glu	Lys	Ala	Lys	Ser	Gly	Leu	Gly	Ser	Gly		
		165						170						175			
Phe	Ser	Thr	Val	Gln	Glu	Lys	Val	Ser	Glu	Gly	Val	Glu	Ala	Val	Lys		

	180		185		190									
Gly	Ala	Ala	Asn	Gly	Val	Val	Ser	His	Glu	Asn	Thr	Arg	Val	Asn
	195		200		205									

(2) INFORMATION FOR SEQ ID NO:2879:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...78

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2879:

Ile	Lys	Glu	Leu	Ile	Met	Lys	Val	Val	Asn	Leu	Tyr	Asp	Leu	Lys	Gln
1			5						10					15	
Met	Gly	Asn	Lys	Gly	Gly	Cys	Thr	Ile	Gln	Leu	Ile	His	His	Phe	Pro
			20					25					30		
Phe	Gly	Met	Gly	Leu	Gly	His	Leu	Lys	Lys	Asp	Tyr	Ile	Glu	Phe	Lys
		35				40						45			
Arg	Val	Gly	Ile	Phe	Asp	Gly	Lys	Ala	Val	Glu	Val	Thr	Leu	Arg	Glu
	50				55					60					
Pro	Tyr	Ser	Arg	Asp	Leu	Leu	Gln	Val	Val	Lys	Ser	Ile	Lys		
65					70				75						

(2) INFORMATION FOR SEQ ID NO:2880:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...250

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2880:

Tyr	Asn	Asn	Thr	Thr	Phe	Phe	Tyr	Val	Phe	Tyr	Lys	Cys	Arg	Lys	Tyr
1			5					10						15	

Val	Cys	Ile	Cys	Asp	Arg	Leu	Met	Met	Cys	Gly	Met	Ala	Cys	Pro	Leu
50						55					60				
Phe	Ala	Ala	Val	Met	Phe	Ser	Val	Met	Leu	Ile	Asn	Ser	Asn	Gly	Ser
65					70				75					80	
Arg	Met	Ala	Leu												

(2) INFORMATION FOR SEQ ID NO:2882:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 145 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...145
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2882:

Tyr	Ser	Asn	Thr	Lys	Thr	Gly	Lys	Ala	Lys	Ser	Ala	Lys	Phe	Arg	Pro
1				5				10						15	
Ser	Phe	Phe	Asn	Leu	Lys	Ser	Leu	Val	Arg	Ile	Met	Gln	Thr	Thr	Lys
			20					25					30		
Val	Ser	Ile	Asn	Asn	Lys	Ile	Asp	Ala	Asn	Phe	Ile	Lys	Ile	Ile	Pro
			35				40					45			
Ile	Leu	Tyr	His	Lys	Lys	Arg	Leu	Met	Glu	Thr	Arg	Asn	Arg	Gly	Ile
			50			55					60				
Tyr	Arg	Lys	Val	Arg	Leu	Leu	Arg	Leu	Trp	Val	Ile	Phe	Val	Ile	Met
65					70				75					80	
Lys	Val	Ile	Lys	Ser	Tyr	Asn	Thr	Leu	Asn	Asp	Tyr	Tyr	Arg	Lys	Leu
				85				90						95	
Phe	Gly	Glu	Lys	Thr	Phe	Lys	Val	Pro	Ile	Asp	Ala	Gly	Phe	Asp	Cys
			100					105					110		
Pro	Asn	Arg	Asp	Gly	Thr	Val	Ala	His	Gly	Gly	Cys	Thr	Phe	Cys	Thr
			115				120					125			
Val	Ser	Gly	Ser	Gly	Asp	Ala	Ile	Val	Ala	Pro	Asp	Ala	Pro	Ile	Arg
			130			135					140				
Glu															
145															

(2) INFORMATION FOR SEQ ID NO:2883:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 117 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...117

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2883:

Tyr	Pro	Asn	Thr	Pro	Val	Arg	His	Lys	Pro	Pro	Trp	Thr	Arg	Tyr	Pro
1				5				10						15	
Pro	His	Lys	Gly	Ala	Lys	Asp	Ser	Leu	Gln	Glu	Leu	Pro	Tyr	Arg	Ser
			20					25						30	
Pro	Pro	Pro	Pro	Lys	Glu	Ala	Gly	Lys	Trp	Gln	Asp	Asn	Arg	Lys	Arg
			35					40						45	
Pro	His	Val	Pro	Leu	Leu	Lys	Leu	Ser	Tyr	Tyr	Val	Pro	Asp	Arg	His
			50					55						60	
Gln	Leu	Phe	Leu	Ser	Phe	Phe	Pro	Phe	Thr	Arg	Arg	Lys	Asn	Val	Leu
65					70					75					80
Phe	Phe	Ile	Gln	Val	Leu	Ile	Leu	Ser	Tyr	Leu	Phe	Tyr	Tyr	Ile	Phe
				85					90					95	
Thr	Lys	Lys	Ala	Ile	Val	Ser	Ile	His	Asn	Arg	Phe	Phe	His	Tyr	Arg
			100					105						110	
Thr	His	Ser	Pro	Leu											
				115											

(2) INFORMATION FOR SEQ ID NO:2884:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...92

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2884:

Thr	Glu	Asn	Thr	Met	Phe	Thr	Leu	Lys	Met	Arg	Pro	Met	Arg	Thr	Ile
1				5				10						15	
Phe	Gly	Gln	Lys	Lys	Arg	Leu	Asn	Val	Arg	Ser	Arg	Asn	Thr	Val	Ile
			20					25						30	
Ile	Ile	Thr	Gln	Glu	Gln	Ile	Met	Leu	Leu	Leu	Gln	Pro	Glu	Pro	Lys
			35					40						45	
Asp	Val	Ile	Gln	Arg	Met	Met	Gly	Ile	Ser	Ser	Met	His	Leu	Ile	Ser
			50					55						60	
Leu	Arg	Thr	Arg	Val	Met	Leu	Ile	Ser	Phe	Leu	Thr	Ala	Thr	Ile	Thr

65		70		75		80					
Ile	Thr	Phe	Leu	Arg	Met	Ser	Tyr	Gln	Leu	Ala	Ser
			85					90			

(2) INFORMATION FOR SEQ ID NO:2885:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...191

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2885:

Val	Met	Asn	Thr	Val	Lys	Asn	Lys	Gln	Glu	Ile	Leu	Glu	Ala	Phe	Arg
1				5					10					15	
Glu	Asn	Pro	Asp	Met	Met	Ala	Ile	Leu	Thr	Ile	Ile	Arg	Asp	Leu	Gly
			20					25				30			
Leu	Lys	Asp	Ser	Trp	Leu	Ala	Ala	Gly	Ser	Val	Arg	Asn	Phe	Ile	Trp
		35				40					45				
Asn	Leu	Leu	Ser	Asp	Lys	Ser	Pro	Phe	Asp	His	Glu	Thr	Asp	Ile	Asp
		50			55				60						
Val	Ile	Phe	Phe	Asp	Pro	Asp	Phe	Ser	Tyr	Glu	Glu	Thr	Leu	Leu	Leu
65				70				75						80	
Lys	Lys	Lys	Leu	Arg	Glu	Asp	Phe	Pro	Gln	Tyr	Gln	Trp	Glu	Leu	Lys
			85					90					95		
Asn	Gln	Val	Tyr	Met	His	Gln	His	Ser	Pro	His	Thr	Ala	Ser	Tyr	Thr
		100						105					110		
Ser	Ser	Arg	Asp	Ala	Met	Ser	Lys	Tyr	Pro	Glu	Arg	Cys	Thr	Ala	Val
		115					120					125			
Gly	Leu	Arg	Leu	Asn	Glu	Glu	Ser	Asp	Phe	Glu	Leu	Tyr	Val	Pro	Tyr
		130				135				140					
Gly	Leu	Glu	Asp	Ile	Leu	Asn	Phe	Gln	Val	Arg	Pro	Thr	Pro	His	Phe
145				150				155						160	
Leu	Glu	Asn	Glu	Asp	Arg	Met	Glu	Leu	Tyr	Gln	Thr	Arg	Leu	Ser	Lys
			165					170					175		
Lys	Asn	Trp	Gln	Glu	Lys	Trp	Lys	Asn	Leu	Ile	Phe	Lys	Asn	Thr	
		180					185						190		

(2) INFORMATION FOR SEQ ID NO:2886:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...88

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2886:

Thr	Met	Asn	Thr	Asn	Leu	Lys	Pro	Lys	Leu	Gln	Arg	Phe	Ala	Ser	Ala
1				5					10					15	
Thr	Ala	Phe	Ala	Cys	Pro	Ile	Cys	Gln	Glu	Asn	Leu	Thr	Leu	Leu	Glu
			20					25					30		
Thr	Asn	Phe	Lys	Cys	Cys	Asn	Arg	His	Ser	Phe	Asp	Leu	Ala	Lys	Phe
			35				40					45			
Gly	Tyr	Val	Asn	Leu	Ala	Pro	Gln	Ile	Lys	Gln	Ser	Ala	Asn	Tyr	Asp
	50					55				60					
Lys	Glu	Asn	Phe	Gln	Asn	Arg	Gln	Gln	Ile	Arg	Arg	Ser	Arg	Leu	Leu
65					70					75					80
Pro	Ser	Tyr	Leu	Arg	Cys	Cys	Ile								
					85										

(2) INFORMATION FOR SEQ ID NO:2887:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 413 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...413

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2887:

Ser	Gly	Asp	Thr	Met	Lys	Ile	Ser	Lys	Arg	His	Leu	Leu	Asn	Tyr	Ser
1				5					10					15	
Ile	Leu	Ile	Pro	Tyr	Leu	Leu	Leu	Ser	Ile	Leu	Gly	Leu	Ile	Val	Val
			20					25					30		
Tyr	Ser	Thr	Thr	Ser	Ala	Ile	Leu	Ile	Glu	Glu	Gly	Lys	Ser	Ala	Leu
			35				40					45			
Gln	Leu	Val	Arg	Asn	Gln	Gly	Ile	Phe	Trp	Ile	Val	Ser	Leu	Ile	Leu
	50					55				60					
Ile	Ala	Leu	Ile	Tyr	Lys	Leu	Arg	Leu	Asp	Phe	Leu	Arg	Asn	Glu	Arg
65					70					75				80	
Leu	Ile	Ile	Leu	Val	Ile	Leu	Ile	Glu	Met	Leu	Leu	Leu	Phe	Leu	Ala
				85					90					95	

Arg	Phe	Ile	Gly	Ile	Ser	Val	Asn	Gly	Ala	Tyr	Gly	Trp	Ile	Ser	Val	100	105	110
Ala	Gly	Val	Thr	Ile	Gln	Pro	Ala	Glu	Tyr	Leu	Lys	Ile	Ile	Ile	Ile	115	120	125
Trp	Tyr	Leu	Ala	His	Arg	Phe	Ser	Lys	Gln	Gln	Glu	Glu	Ile	Ala	Thr	130	135	140
Tyr	Asp	Phe	Gln	Val	Leu	Thr	Gln	Asn	Gln	Trp	Leu	Pro	Arg	Ala	Phe	145	150	155
Asn	Asp	Trp	Arg	Phe	Val	Leu	Leu	Val	Leu	Ile	Gly	Ser	Leu	Gly	Ile	165	170	175
Phe	Pro	Asp	Leu	Gly	Asn	Ala	Thr	Ile	Leu	Val	Leu	Val	Ser	Leu	Ile	180	185	190
Met	Tyr	Thr	Val	Ser	Gly	Ile	Ala	Tyr	Arg	Trp	Phe	Ser	Thr	Ile	Leu	195	200	205
Ala	Leu	Val	Ser	Ala	Thr	Ser	Val	Phe	Val	Leu	Thr	Thr	Ile	Ser	Leu	210	215	220
Ile	Gly	Val	Glu	Thr	Phe	Ser	Lys	Ile	Pro	Val	Phe	Gly	Tyr	Val	Ala	225	230	235
Lys	Arg	Phe	Ser	Ala	Phe	Phe	Asn	Pro	Phe	Ala	Asp	Arg	Ala	Asp	Ala	245	250	255
Gly	His	Gln	Leu	Ala	Asn	Ser	Tyr	Phe	Ala	Met	Val	Asn	Gly	Gly	Trp	260	265	270
Phe	Gly	Leu	Gly	Leu	Gly	Asn	Ser	Ile	Glu	Lys	Arg	Gly	Tyr	Leu	Pro	275	280	285
Glu	Ala	His	Thr	Asp	Phe	Val	Phe	Ser	Ile	Val	Ile	Glu	Glu	Phe	Gly	290	295	300
Phe	Val	Gly	Ala	Ser	Leu	Ile	Leu	Ala	Leu	Leu	Phe	Phe	Met	Ile	Leu	305	310	315
Arg	Ile	Ile	Leu	Val	Gly	Ile	Arg	Ala	Glu	Asn	Pro	Phe	Asn	Ala	Met	325	330	335
Val	Ala	Leu	Gly	Val	Gly	Gly	Met	Met	Leu	Val	Gln	Val	Phe	Val	Asn	340	345	350
Ile	Gly	Gly	Ile	Ser	Gly	Leu	Ile	Pro	Ser	Thr	Gly	Val	Thr	Phe	Pro	355	360	365
Phe	Leu	Ser	Gln	Gly	Gly	Asn	Ser	Leu	Leu	Val	Leu	Ser	Val	Ala	Val	370	375	380
Ala	Phe	Val	Leu	Asn	Ile	Asp	Ala	Ser	Glu	Lys	Arg	Ala	Lys	Leu	Tyr	385	390	395
Arg	Glu	Leu	Glu	Asn	Gln	Pro	Met	Asn	Leu	Leu	Lys					405	410	

(2) INFORMATION FOR SEQ ID NO:2888:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 503 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

(B) LOCATION 1...503

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2888:

Leu	Ile	Asp	Thr	Lys	Asn	Asn	Leu	Val	Met	Gln	Ser	Gln	Phe	Tyr	Asp	1	5	10	15
Gly	Glu	Leu	Arg	Glu	Leu	Thr	Glu	Gln	Ile	Leu	Asn	Ser	Val	Thr	Gly	20	25	30	
Asp	Glu	Lys	Lys	Ile	Ile	Glu	Phe	Phe	Arg	Asp	Ser	Ile	Phe	Asn	Phe	35	40	45	
Asn	Phe	Leu	Tyr	Arg	Lys	Leu	Glu	Thr	Ile	Asn	Glu	Leu	Phe	Asp	Glu	50	55	60	
Ile	Arg	Glu	Glu	His	Glu	Ser	Tyr	Arg	Arg	Gly	Gly	Trp	Ser	Ala	Asn	65	70	75	80
Asn	His	Leu	Phe	Asn	Ala	Glu	Phe	Thr	Val	Lys	Asn	Leu	Tyr	Asn	Phe	85	90	95	
Leu	Lys	Leu	Asn	Cys	Leu	Cys	Val	Glu	His	Tyr	Lys	Ile	Tyr	Lys	Ser	100	105	110	
Ile	Ile	Asn	Arg	Tyr	Leu	Glu	Ile	Leu	Leu	Leu	Ser	Tyr	Asp	Asn	Ser	115	120	125	
Tyr	Val	Asn	Pro	Asp	Ser	Ser	Ile	Phe	Asp	Arg	Thr	Ser	Ser	Trp	Leu	130	135	140	
Lys	Asn	Leu	Asp	Leu	Asp	Val	Lys	Leu	Ile	Leu	Pro	Asn	Ile	Asp		145	150	155	160
Phe	Lys	Val	Val	Asn	Leu	Tyr	Phe	Arg	Asn	Tyr	Ser	Phe	Gly	Lys	Ile	165	170	175	
Lys	Ile	Thr	Glu	Glu	Ala	Lys	Asp	Tyr	Leu	Leu	Asn	Arg	Ile	Thr	Tyr	180	185	190	
Leu	Gln	Glu	Arg	Leu	Glu	Ile	Thr	Glu	Asp	Glu	Asn	Leu	Arg	Glu	Leu	195	200	205	
Lys	Asn	Met	Leu	Ile	Phe	Leu	Pro	Leu	Val	Asp	Asp	Ile	Asp	Ile	Glu	210	215	220	
Lys	Val	Ile	Glu	Ile	Leu	Asn	Asn	Gln	Thr	Leu	Tyr	Tyr	Asn	Trp	Ser	225	230	235	240
Glu	Glu	Phe	Arg	Arg	Ile	Ile	Lys	Ile	Val	Leu	Asp	Asn	Met	Asp	Val	245	250	255	
Ile	Asp	Lys	Asp	Ser	Leu	Lys	Ser	Lys	Ile	Ile	Gly	Ile	Val	Asn	Lys	260	265	270	
His	Leu	Asn	Glu	Ile	Leu	Glu	Lys	Asn	Phe	Ser	Leu	Tyr	Asn	Ser	Val	275	280	285	
Tyr	Pro	Leu	Tyr	Ser	Gln	Leu	Leu	Glu	Tyr	Cys	Ser	Thr	Asp	Gln	Glu	290	295	300	
Thr	Ala	Ile	Ile	Val	Leu	Glu	Lys	Phe	Asn	Thr	Asp	Ile	Leu	Arg	Ile	305	310	315	320
Lys	Tyr	Lys	Asn	Asp	Asp	Ile	Lys	Asn	Ile	Ile	Glu	Tyr	Ser	Asp	Leu	325	330	335	
Ile	Cys	His	Leu	Phe	Lys	Tyr	Phe	Glu	Lys	Asp	Ile	Lys	Asp	Asp	Ile	340	345	350	
Leu	Asp	Thr	Leu	Lys	Val	Tyr	Glu	Glu	Ser	Glu	Asn	Ile	Ile	Tyr	His	355	360	365	
Lys	Val	Ile	Asp	Leu	Met	Ser	Tyr	Asn	Val	Tyr	Asp	Phe	Pro	Gln	Ile	370	375	380	
Gln	Asn	Lys	Ile	Tyr	His	Tyr	Leu	Ile	Lys	Arg	Ile	Asn	Asp	Lys	Arg	385	390	395	400
Val	Glu	Gly	Val	Lys	Thr	Phe	Pro	Asp	Pro	Arg	Glu	Lys	Ser	Val	Ser	405	410	415	

Asp Leu Tyr Asn Leu Ser Arg Lys Gly Tyr Phe Ser Asp Phe Glu Ile
 420 425 430
 Leu Lys Asp Ile Glu Glu Asp Ile Arg Gly Leu Tyr Pro Glu Val Asp
 435 440 445
 Trp Thr Trp Phe His Asp Arg Ser Asp Asp Val Ile His Arg Leu Leu
 450 455 460
 Glu His Arg Thr Pro Asn Asn Ile Lys Thr Tyr Phe Ser Lys Asn Glu
 465 470 475 480
 Glu Asp Asn Lys Leu Ile Asn Glu Tyr Ile Leu Lys Ala Phe Asp Glu
 485 490 495
 Asp Lys Leu Ile Leu Lys Lys
 500

(2) INFORMATION FOR SEQ ID NO:2889:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 73 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...73
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2889:

Thr Gly Asp Thr Ala Leu His Ser Gln Arg Gln Gln Ile Phe Leu Leu
 1 5 10 15
 Gln Lys Thr Asn Asp Leu Phe Asp Glu Leu Ala Ile Gln Ala Glu Ser
 20 25 30
 Arg His Ser Phe Leu Lys Lys Glu Asn Pro Thr Tyr Leu Glu Ser Lys
 35 40 45
 Asp Arg Tyr Leu Leu Phe Thr His Phe Pro Asn Ser Phe Phe Tyr Ile
 50 55 60
 Phe Cys Ile Arg Tyr Cys Arg Asn Asp
 65 70

(2) INFORMATION FOR SEQ ID NO:2890:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 85 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...85

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2890:

Glu	Leu	Asp	Thr	Lys	Ile	Gly	Ile	Ser	Lys	Asn	Thr	Ile	Arg	Asn	Tyr
1				5					10					15	
Glu	Lys	Arg	Val	Arg	Ser	Thr	Lys	Lys	Asn	Thr	Ile	Phe	Asp	Leu	Val
			20					25					30		
Lys	Val	Phe	Ser	Ser	Leu	Ile	Asp	Ala	Leu	Phe	Ser	Pro	Val	Gln	Lys
		35					40					45			
Asp	Ser	Pro	Ser	Asp	Ile	Gln	Ser	Ile	Tyr	Asp	Gln	Arg	Ala	Pro	Pro
	50					55				60					
Arg	Gln	Gly	Lys	Val	Leu	Thr	Tyr	Ala	Glu	Arg	Gln	Leu	Tyr	Asp	Gln
65					70				75						80
Lys	Asn	Glu	Val	Ser											
				85											

(2) INFORMATION FOR SEQ ID NO:2891:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 80 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...80

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2891:

Gln	Met	Asp	Thr	Ile	Glu	Asn	Leu	Ile	Ile	Ala	Ile	Val	Lys	Pro	Leu
1				5					10					15	
Ile	Ser	Gln	Pro	Asp	Ala	Leu	Thr	Ile	Lys	Ile	Glu	Asp	Thr	Pro	Glu
			20					25				30			
Phe	Leu	Glu	Tyr	His	Leu	Asn	Leu	Asp	Gln	Ser	Asp	Val	Gly	Arg	Val
		35				40					45				
Ile	Gly	Arg	Lys	Gly	Arg	Thr	Ile	Ser	Ala	Ile	Arg	Thr	Ile	Val	Tyr
	50					55				60					
Ser	Val	Pro	Thr	Glu	Tyr	Lys	Lys	Val	Arg	Ile	Val	Ile	Asp	Glu	Lys
65					70				75						80

(2) INFORMATION FOR SEQ ID NO:2892:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 146 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...146
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2892:

```

Arg Ile Gly Thr Tyr Gln Met Ile Asp Ile Gln Gly Ile Lys Glu Ala
1           5           10           15
Leu Pro His Arg Tyr Pro Met Leu Leu Val Asp Arg Val Leu Glu Val
20           25           30
Ser Glu Asp Thr Ile Val Ala Ile Lys Asn Val Thr Ile Asn Glu Pro
35           40           45
Phe Phe Asn Gly His Phe Pro Gln Tyr Pro Val Met Pro Gly Val Leu
50           55           60
Ile Met Glu Ala Leu Ala Gln Thr Ala Gly Val Leu Glu Leu Ser Lys
65           70           75           80
Pro Glu Asn Lys Gly Lys Leu Val Phe Tyr Ala Gly Met Asp Lys Val
85           90           95
Lys Phe Lys Lys Gln Val Val Pro Gly Asp Gln Leu Val Met Thr Ala
100          105          110
Thr Phe Val Lys Arg Arg Gly Thr Ile Ala Val Val Glu Ala Lys Ala
115          120          125
Glu Val Asp Gly Lys Leu Ala Ala Ser Gly Thr Leu Thr Phe Ala Ile
130          135          140
Gly Asn
145

```

(2) INFORMATION FOR SEQ ID NO:2893:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 187 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...187
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2893:

```

Lys Glu Gly Thr His Met Ile Lys Tyr Ser Ile Arg Gly Glu Asn Leu
1           5           10           15

```


Val	Ala	Gln	Gln	Glu	Asp	Phe	Ala	Val	Met	Met	Ala	Tyr	Phe	Glu	Asn
	115						120					125			
Gly	Gln	Gly	Gln	Phe	Gly	Leu	Ile	Tyr	Asp	Val	Val	Lys	Gly	Asp	Cys
	130					135					140				
Tyr	His	Gly	Gly	Gly	Glu	Phe	Pro	Val	Cys	Leu	Asn	Asp	Arg	Ser	Leu
145					150					155					160
Ala	Pro	Phe	Lys	Thr	Lys	Pro	Leu	Gly	Asp	Phe	Leu	Ile	Ala	Gly	Asn
			165					170						175	
Ser	Gly	Met	Leu	Glu	Thr	Asn	Glu	Trp	Gly	Leu	Ala	Asp	Leu	Ser	Arg
		180						185					190		
Ser	Val	Leu	Gly	Val	Arg	Val	Tyr	Gly	Ser	Ala	Ala	Ile	Ser	Phe	Ala
	195					200						205			
Lys	Ile	Leu	Ser	Gly	Arg	Leu	Leu	Thr	Tyr	Leu	Thr	Tyr	Leu	Gln	Pro
	210					215					220				
Trp	Asp	Tyr	Ala	Ala	Ala	Ser	Ile	Leu	Gly	Glu	Ser	Leu	Gly	Tyr	Arg
225					230					235					240
Val	Val	Thr	Leu	Phe	Gly	Glu	Ala	Pro	Asp	Phe	Gln	Thr	Arg	Gln	Pro
				245					250					255	
Val	Met	Met	Val	Pro	Leu	Glu	Met	Gln	Glu	Glu	Ile	Gln	Ser	Tyr	Ile
			260					265					270		
Tyr	Glu	Arg	Lys	Arg	Thr										
	275														

(2) INFORMATION FOR SEQ ID NO:2895:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 321 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...321

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2895:

Lys	Arg	Phe	Thr	Met	Ser	Glu	Ile	Glu	Ile	Ile	Asn	Ala	Lys	Lys	Ile
1				5				10					15		
Tyr	His	Asp	Val	Ser	Val	Ile	Glu	Asn	Leu	Asn	Ile	Thr	Ile	Pro	Lys
			20					25				30			
Gly	Ser	Leu	Phe	Thr	Leu	Leu	Gly	Ala	Ser	Gly	Cys	Gly	Lys	Thr	Thr
		35					40				45				
Leu	Leu	Arg	Met	Ile	Ala	Gly	Phe	Asn	Ser	Ile	Lys	Asp	Gly	Glu	Phe
		50				55					60				
Tyr	Phe	Asp	Asp	Thr	Lys	Ile	Asn	Asn	Met	Glu	Pro	Ser	Lys	Arg	Asn
65					70					75					80
Ile	Gly	Met	Val	Phe	Gln	Asn	Tyr	Ala	Ile	Phe	Pro	His	Leu	Thr	Val
			85					90					95		
Arg	Asp	Asn	Val	Ala	Phe	Gly	Leu	Met	Gln	Lys	Lys	Val	Pro	Lys	Glu
			100					105					110		

Glu	Leu	Ile	Gln	Gln	Thr	Asn	Lys	Tyr	Leu	Glu	Leu	Met	Gln	Ile	Ala
		115					120					125			
Gln	Tyr	Ala	Asp	Arg	Lys	Pro	Asp	Lys	Leu	Ser	Gly	Gly	Gln	Gln	Gln
	130					135					140				
Arg	Val	Thr	Leu	Ala	Cys	Ala	Leu	Ala	Val	Asn	Pro	Ser	Val	Leu	Leu
145					150					155					160
Met	Asp	Glu	Pro	Leu	Ser	Asn	Leu	Glu	Ala	Lys	Leu	Arg	Leu	Asp	Met
			165						170					175	
Arg	Gln	Ala	Ile	Arg	Glu	Ile	Gln	His	Glu	Val	Gly	Ile	Thr	Thr	Val
		180						185					190		
Tyr	Val	Thr	His	Asp	Gln	Glu	Glu	Ala	Met	Ala	Ile	Ser	Asp	Gln	Ile
	195					200						205			
Ala	Val	Met	Lys	Asp	Gly	Val	Ile	Gln	Gln	Ile	Gly	Arg	Pro	Lys	Glu
	210					215					220				
Leu	Tyr	His	Lys	Pro	Ala	Asn	Glu	Phe	Val	Ala	Thr	Phe	Ile	Gly	Arg
225					230					235					240
Thr	Asn	Ile	Ile	Pro	Ala	Asn	Leu	Glu	Lys	Arg	Ser	Asp	Gly	Ala	Tyr
				245					250					255	
Ile	Val	Phe	Ser	Asp	Gly	Tyr	Ala	Leu	Arg	Met	Pro	Ala	Leu	Asp	Gln
		260					265						270		
Val	Glu	Glu	Gln	Ala	Ile	His	Val	Ser	Ile	Arg	Pro	Glu	Glu	Phe	Ile
	275					280						285			
Lys	Asp	Glu	Ser	Gly	Asp	Ile	Glu	Gly	Thr	Ile	Ser	Asp	Ser	Val	Tyr
	290					295					300				
Leu	Gly	Leu	Asn	Thr	Lys	Tyr	Phe	Ile	Glu	Thr	Gly	Phe	Ala	Ser	Lys
305				310						315					320
Ile															

(2) INFORMATION FOR SEQ ID NO:2896:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2896:

Lys	Phe	Trp	Phe	His	Pro	Leu	Leu	Phe	Leu	Ala	Ile	Asp	Gln	Met	Gly
1				5					10					15	
Val	Lys	Ala	Thr	Leu	Cys	Lys	Gln	Ile	Ser	Met	Leu	Ser	Phe	Phe	Asp
		20					25						30		
Asn	Leu	Ala	Leu	Ile	Gln	Asp	Asn	Tyr	Leu	Leu	Cys	Pro	Leu	Ser	Asn
	35					40					45				
Ser	Gln	Ala	Val	Ser	Asn	Glu	Asn	Gln	Gly	Leu	Val	Gln	Ser	His	Glu
50					55					60					

Ile	Ile	Asp	Asn	Pro	Leu	Leu	Cys	Gln	Asn	Ile	Gln	Thr	Ala	Ser	Arg
65					70					75					80
Leu	Ile	Gln	Asn	Gln	Asp	Arg	Arg	Ile	Cys	Gln	Glu	Ser	Thr	Arg	Gln
			85						90					95	
Ser	Asp	Ser	Leu	Thr	Leu	Thr	Thr								
			100												

(2) INFORMATION FOR SEQ ID NO:2897:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 397 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...397

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2897:

Val	Ser	Ile	Thr	Ile	Thr	Leu	Arg	Lys	Trp	Gln	Ala	Glu	Ala	Ile	Lys
1				5					10					15	
Arg	Ser	Glu	His	Leu	Ser	Asn	Gly	Ile	Phe	Leu	Glu	Ala	Leu	Gly	Gly
			20					25					30		
Arg	Gly	Lys	Thr	Ile	Cys	Ala	Leu	Ala	Ile	Ala	Lys	His	Lys	Lys	Ala
		35					40					45			
Lys	Lys	Ile	Ile	Ile	Thr	Asn	Asn	Arg	Leu	Ala	Ile	Leu	Asn	Gly	Trp
		50				55					60				
Ile	Asp	Ala	Val	Lys	Phe	Met	Asn	Phe	Asp	Lys	Gly	Val	Glu	Ile	Ile
65					70				75					80	
Ile	Gln	Thr	Asp	Arg	Tyr	Leu	Gln	Asn	Gln	Val	Lys	Lys	Gly	His	Lys
				85					90					95	
Leu	Asp	Cys	Asp	Val	Leu	Ile	Val	Asp	Glu	Trp	Gln	Asn	Met	Ser	Ser
			100					105					110		
Asp	Lys	Gln	Val	Ala	Leu	Tyr	Arg	Lys	Ile	Lys	Arg	Lys	Tyr	Thr	Ile
		115					120					125			
Gly	Leu	Ser	Ala	Thr	Pro	Ile	Arg	Lys	Lys	Gly	Gln	Asn	Phe	Tyr	Pro
		130				135					140				
Leu	Glu	Lys	Thr	Val	Phe	Gly	Trp	Ala	Thr	Pro	Asn	Asn	Lys	Phe	Asp
145					150					155				160	
Trp	Gln	Lys	Thr	His	Gly	Lys	Met	Val	Tyr	Asp	Pro	Phe	Ser	Tyr	Ser
				165					170					175	
Lys	Glu	Lys	Trp	Glu	Asp	Phe	Gln	Asn	Tyr	Glu	Ser	Tyr	Ile	Ser	Ser
			180					185					190		
Leu	Pro	Asn	Phe	Phe	Arg	Trp	Glu	Glu	Ile	Glu	Gly	Ile	Glu	Asn	Ala
		195					200					205			
Val	Glu	Asn	Asn	Gly	Phe	Glu	Ile	Lys	Phe	Tyr	Gln	Lys	Arg	Val	Ala
	210					215					220				
Ser	Gly	Asn	Pro	Glu	Lys	Leu	Ala	Glu	Phe	Arg	Lys	Leu	Asn	Leu	Val
225						230				235					240

Thr	Val	Asp	Gly	Lys	Thr	Ala	Met	Ala	Lys	Gln	Ser	Phe	Gly	Arg	Lys	245	250	255
Thr	Phe	Glu	Arg	Tyr	Leu	Asn	Gln	Thr	Gly	Val	Ala	Val	Asp	Phe	Pro	260	265	270
Lys	Leu	Lys	Pro	Val	Asn	Ala	Asp	Thr	Pro	Leu	Met	Leu	Gln	Leu	Asp	275	280	285
Gly	Leu	Ile	Glu	Arg	Ala	Pro	His	Asp	Met	Leu	Ile	Val	Ser	Lys	Ser	290	295	300
Lys	Gln	Ile	Val	Asn	Val	Ile	Ser	Glu	Arg	His	Pro	Glu	Ile	Gly	Ile	305	310	315
Trp	Thr	Gly	Asp	Ile	Gln	Glu	Gly	Leu	Tyr	Lys	Lys	Phe	Val	Val	Ala	325	330	335
Thr	Ser	Gln	Val	Leu	Gly	Val	Gly	Val	Asp	Gly	Leu	Gln	His	Lys	Tyr	340	345	350
Gln	Thr	Ile	Val	Val	Leu	Asp	Pro	Val	Glu	Glu	Gly	Ser	Gly	Glu	Tyr	355	360	365
Asp	Asp	Tyr	Arg	Gln	Leu	Leu	Trp	Arg	Ile	Thr	Gly	Ser	Arg	Gln	Gln	370	375	380
His	Asp	Val	Asn	Val	Ile	Glu	Phe	Tyr	Tyr	Lys	Glu	Ser				385	390	395

(2) INFORMATION FOR SEQ ID NO:2898:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 364 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...364

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2898:

Arg	Arg	Trp	Leu	Lys	Thr	Lys	Thr	Glu	Glu	Cys	Phe	Met	Lys	Ala	Tyr	1	5	10	15
Thr	Tyr	Val	Lys	Pro	Gly	Leu	Ala	Ser	Phe	Val	Asp	Val	Asp	Lys	Pro	20	25	30	
Val	Ile	Arg	Lys	Pro	Thr	Asp	Ala	Ile	Val	Arg	Ile	Val	Lys	Thr	Thr	35	40	45	
Ile	Cys	Gly	Thr	Asp	Leu	His	Ile	Ile	Lys	Gly	Asp	Val	Pro	Thr	Cys	50	55	60	
Gln	Ser	Gly	Thr	Ile	Leu	Gly	His	Glu	Gly	Ile	Gly	Ile	Val	Glu	Glu	65	70	75	80
Val	Gly	Glu	Gly	Val	Ser	Asn	Phe	Lys	Lys	Gly	Asp	Lys	Val	Leu	Ile	85	90	95	
Ser	Cys	Val	Cys	Ala	Cys	Gly	Lys	Cys	Tyr	Tyr	Cys	Lys	Lys	Gly	Ile	100	105	110	
Tyr	Ala	His	Cys	Glu	Asp	Glu	Gly	Gly	Trp	Ile	Phe	Gly	His	Leu	Ile	115	120	125	

Asp	Gly	Met	Gln	Ala	Glu	Tyr	Leu	Arg	Val	Pro	His	Ala	Asp	Asn	Thr
130						135					140				
Leu	Tyr	His	Thr	Pro	Glu	Asp	Leu	Ser	Asp	Glu	Ala	Leu	Val	Met	Leu
145					150					155					160
Ser	Asp	Ile	Leu	Pro	Thr	Gly	Tyr	Glu	Ile	Gly	Val	Leu	Lys	Gly	Lys
			165					170						175	
Val	Glu	Pro	Gly	Cys	Ser	Val	Ala	Ile	Ile	Gly	Ser	Gly	Pro	Val	Gly
			180					185					190		
Leu	Ala	Ala	Leu	Leu	Thr	Ala	Gln	Phe	Tyr	Ser	Pro	Ala	Lys	Leu	Ile
	195					200						205			
Met	Val	Asp	Leu	Asp	Asp	Asn	Arg	Leu	Glu	Thr	Ala	Leu	Ser	Phe	Gly
	210					215					220				
Ala	Thr	His	Lys	Val	Asn	Ser	Ser	Asp	Pro	Glu	Lys	Ala	Ile	Lys	Glu
225					230					235					240
Ile	Tyr	Asp	Leu	Thr	Asp	Gly	Arg	Gly	Val	Asp	Val	Ala	Ile	Glu	Ala
			245					250						255	
Val	Gly	Ile	Pro	Ala	Thr	Phe	Asp	Phe	Cys	Gln	Lys	Ile	Ile	Gly	Val
		260					265						270		
Asp	Gly	Thr	Val	Ala	Asn	Cys	Gly	Val	His	Gly	Lys	Pro	Val	Glu	Phe
	275					280						285			
Asp	Leu	Asp	Lys	Leu	Trp	Ile	Arg	Asn	Ile	Asn	Val	Thr	Thr	Gly	Leu
	290					295					300				
Val	Ser	Thr	Asn	Thr	Thr	Pro	Gln	Leu	Leu	Lys	Ala	Leu	Glu	Ser	His
305					310					315					320
Lys	Ile	Glu	Pro	Glu	Lys	Leu	Val	Thr	His	Tyr	Phe	Lys	Leu	Ser	Glu
			325					330						335	
Ile	Glu	Lys	Ala	Tyr	Glu	Val	Phe	Ser	Lys	Ala	Ala	Asp	His	His	Ala
		340					345						350		
Ile	Lys	Val	Ile	Ile	Glu	Asn	Asp	Ile	Ser	Glu	Ala				
	355					360									

(2) INFORMATION FOR SEQ ID NO:2899:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...83

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2899:

Ala	Leu	Trp	Phe	Cys	Ser	Asn	Glu	Leu	Gly	Gly	Gly	Met	Ile	Leu	Ala
1				5					10					15	
Gly	Leu	Phe	Ser	Asn	Val	Leu	Ser	Pro	Val	Tyr	Glu	Leu	Ser	Phe	Thr
		20					25						30		
Leu	Asp	Ile	Trp	Ser	Ile	Leu	Ile	Cys	Leu	Ile	Ile	Ala	Phe	Phe	Gly
	35					40						45			

Thr	Ala	Phe	Ala	Phe	Phe	Ile	Ser	Met	Lys	Ala	Val	Ser	Leu	Val	Ser
50						55					60				
Pro	Leu	Val	Gly	Phe	Pro	Leu	Thr	Gln	Cys	Ala	Val	Asn	Leu	Ser	Leu
65					70					75					80
Leu	Leu	Ser													

(2) INFORMATION FOR SEQ ID NO:2900:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 266 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...266

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2900:

Gly	Pro	Ser	Thr	Glu	Leu	Arg	Phe	Glu	Leu	Ala	Arg	Leu	Val	Glu	Ile
1				5				10						15	
Cys	Gln	Pro	Xaa	Lys	Ile	Ser	Leu	Gly	Met	Val	Leu	Gly	Asn	Ala	Ser
			20					25					30		
Asn	Ile	Ile	Val	Arg	Asp	Gly	Gly	Ile	Arg	Gly	Phe	Val	Ile	Leu	Cys
			35				40					45			
Asp	Lys	Leu	Asn	Asn	Val	Ser	Val	Asp	Gly	Tyr	Thr	Ile	Glu	Ala	Glu
			50			55				60					
Ala	Gly	Ala	Asn	Leu	Ile	Glu	Thr	Thr	Arg	Ile	Ala	Leu	Arg	His	Ser
65				70				75						80	
Leu	Thr	Gly	Phe	Glu	Phe	Ala	Cys	Gly	Ile	Pro	Gly	Ser	Val	Gly	Gly
			85					90						95	
Ala	Val	Phe	Met	Asn	Ala	Gly	Ala	Tyr	Gly	Gly	Glu	Ile	Ala	His	Ile
			100				105					110			
Leu	Gln	Ser	Cys	Lys	Val	Leu	Thr	Lys	Asp	Gly	Glu	Ile	Glu	Thr	Leu
			115				120					125			
Ser	Ala	Lys	Asp	Leu	Ala	Phe	Gly	Tyr	Arg	His	Ser	Ala	Ile	Gln	Glu
			130			135					140				
Ser	Gly	Ala	Val	Val	Leu	Ser	Val	Lys	Phe	Ala	Leu	Ala	Pro	Gly	Thr
145				150					155					160	
His	Gln	Val	Ile	Lys	Gln	Glu	Met	Asp	Arg	Leu	Thr	His	Leu	Arg	Glu
			165					170						175	
Leu	Lys	Gln	Pro	Leu	Glu	Tyr	Pro	Ser	Cys	Gly	Ser	Val	Phe	Lys	Arg
			180				185					190			
Pro	Val	Gly	His	Phe	Ala	Gly	Gln	Leu	Ile	Ser	Glu	Ala	Gly	Leu	Lys
			195			200						205			
Gly	Tyr	Arg	Ile	Gly	Gly	Val	Glu	Val	Ser	Glu	Lys	His	Ala	Gly	Phe
210				215						220					
Met	Ile	Asn	Val	Ala	Asp	Gly	Thr	Ala	Lys	Asp	Tyr	Glu	Asp	Leu	Ile
225				230						235					240

Gln	Ser	Val	Ile	Glu	Lys	Val	Lys	Glu	His	Ser	Gly	Ile	Thr	Leu	Glu
				245					250					255	
Arg	Glu	Val	Arg	Ile	Leu	Gly	Glu	Ser	Lys						
				260					265						

(2) INFORMATION FOR SEQ ID NO:2901:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 69 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...69
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2901:

Ser	Asn	Ser	Thr	Ser	Ala	Phe	Ser	Leu	Pro	Thr	Ala	Ala	Thr	Ile	Ser
1				5					10					15	
Ser	Trp	Lys	Ala	Ile	Asn	Ser	Leu	Thr	Ala	Ser	Cys	Pro	Leu	Arg	Ser
			20					25					30		
Ala	Ser	Asn	Met	Ile	Ser	Ser	Asp	Asn	Ser	Leu	Ala	Pro	Asp	Ser	Thr
		35					40					45			
Met	Leu	Thr	Ala	Cys	Leu	Val	Pro	Ala	Thr	Val	Asn	Ser	Arg	Arg	Asp
	50					55					60				
Cys	Ser	Ala	Cys	Ser											
65															

(2) INFORMATION FOR SEQ ID NO:2902:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 72 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...72
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2902:

Leu Asn Ser Thr Ser Ser Lys Lys Phe Thr Leu Phe Leu Ile Met Asn

1				5					10					15	
Ile	Ser	Leu	Asn	Lys	His	Ile	Tyr	Lys	Tyr	Phe	Asn	Ile	Leu	Ser	Ile
			20					25					30		
Ser	Ser	Ser	Lys	Phe	Ser	Ser	Ile	Phe	Cys	Ile	Ser	Pro	Phe	Thr	Ile
		35					40					45			
Leu	Leu	Lys	Lys	Asp	Lys	Leu	Phe	Ile	Ser	Lys	Ile	Lys	Tyr	Phe	His
	50					55					60				
Thr	Thr	Val	Val	Ser	Arg	Asn	Ile								
65					70										

(2) INFORMATION FOR SEQ ID NO:2903:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...458

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2903:

Lys	Cys	Ser	Thr	Pro	Ser	Ser	Ser	Gly	Asp	Gln	Ser	Arg	Leu	Asp	Ala
1				5				10					15		
Thr	Ser	Leu	Gln	Gly	Thr	Asn	Glu	Lys	Asp	Val	Gly	Tyr	Gly	Val	Tyr
		20					25					30			
Asp	Leu	Phe	Asp	Leu	Gly	Glu	Phe	Asn	Gln	Lys	Gly	Thr	Val	Arg	Thr
	35					40					45				
Lys	Tyr	Gly	Phe	Lys	Glu	Asp	Tyr	Leu	Gln	Ala	Ile	Gln	Ala	Leu	Lys
	50				55					60					
Ala	Gln	Gly	Ile	Gln	Pro	Met	Ala	Asp	Val	Val	Leu	Asn	His	Lys	Ala
65				70					75					80	
Ala	Ala	Asp	His	Arg	Glu	Ala	Phe	Gln	Val	Ile	Glu	Val	Asp	Pro	Val
		85						90					95		
Asp	Arg	Thr	Val	Glu	Leu	Gly	Glu	Pro	Phe	Thr	Ile	Asn	Gly	Trp	Thr
		100					105					110			
Ser	Phe	Thr	Phe	Asp	Gly	Arg	Gln	Asp	Thr	Tyr	Asn	Asp	Phe	His	Trp
	115					120					125				
His	Trp	Tyr	His	Phe	Thr	Gly	Thr	Asp	Tyr	Asp	Ala	Lys	Arg	Arg	Lys
	130					135					140				
Ser	Gly	Ile	Tyr	Leu	Ile	Gln	Gly	Asp	Asn	Lys	Gly	Trp	Ala	Asn	Glu
145				150					155					160	
Glu	Leu	Val	Asp	Asn	Glu	Asn	Gly	Asn	Tyr	Asp	Tyr	Leu	Met	Tyr	Ala
		165						170					175		
Asp	Leu	Asp	Phe	Lys	His	Pro	Glu	Val	Ile	Gln	Asn	Ile	Tyr	Asp	Trp
	180						185					190			
Ala	Asp	Trp	Phe	Met	Glu	Thr	Thr	Gly	Val	Ala	Gly	Phe	Arg	Leu	Asp
	195					200					205				

Ala Val Lys His Ile Asp Ser Phe Phe Met Arg Asn Phe Ile Arg Asp
 210 215 220
 Met Lys Glu Lys Tyr Gly Asp Asp Phe Tyr Val Phe Gly Glu Phe Trp
 225 230 235 240
 Asn Pro Asp Lys Glu Ala Asn Leu Asp Tyr Leu Glu Lys Thr Glu Glu
 245 250 255
 His Phe Asp Leu Val Asp Val Arg Leu His Gln Asn Leu Phe Glu Ala
 260 265 270
 Ser Gln Ala Gly Ala Asn Tyr Asp Leu Arg Gly Ile Phe Thr Asp Ser
 275 280 285
 Leu Val Glu Leu Lys Pro Asp Lys Ala Val Thr Phe Val Asp Asn His
 290 295 300
 Asp Thr Gln Arg Gly Gln Ala Leu Glu Ser Thr Val Glu Glu Trp Phe
 305 310 315 320
 Lys Pro Ala Ala Tyr Ala Leu Ile Leu Leu Arg Gln Asp Gly Leu Pro
 325 330 335
 Cys Val Phe Tyr Gly Asp Tyr Tyr Gly Ile Ser Gly Gln Tyr Ala Gln
 340 345 350
 Glu Asp Phe Lys Glu Ile Leu Asp Arg Leu Leu Ala Ile Arg Lys Asp
 355 360 365
 Leu Ala Tyr Gly Glu Gln Asn Asp Tyr Phe Asp His Ala Asn Cys Ile
 370 375 380
 Gly Trp Val Arg Ser Gly Ala Glu Asn Gln Ser Pro Ile Ala Val Leu
 385 390 395 400
 Ile Ser Asn Asp Gln Glu Asn Ser Lys Ser Met Phe Val Gly Gln Glu
 405 410 415
 Trp Thr Asn Gln Thr Phe Val Asp Leu Leu Gly Asn His Gln Gly Gln
 420 425 430
 Val Thr Ile Asp Glu Glu Gly Tyr Gly Gln Phe Pro Val Ser Ala Arg
 435 440 445
 Ser Val Ser Val Trp Ala Val Asn Thr Ile
 450 455

(2) INFORMATION FOR SEQ ID NO:2904:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 511 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...511

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2904:

Arg Thr Thr Thr Leu Arg Arg Ser Asn Thr Arg Ser Leu Leu Gln Leu
 1 5 10 15
 Leu Phe Pro His Pro Pro Tyr Thr His Ala Pro Pro Pro Ala Asp Pro
 20 25 30

Ile	Ala	Thr	Ser	Pro	Phe	Val	Pro	Lys	Pro	Arg	Gly	Leu	Thr	Thr	Ala
	35						40					45			
His	Ile	Arg	Ala	Ala	His	Ile	Ser	Leu	Pro	Thr	Arg	Pro	Ser	Ser	His
	50					55					60				
Gln	Leu	Pro	Pro	Thr	His	Pro	Thr	Pro	Pro	Val	Pro	Gly	Pro	Pro	Pro
65					70					75					80
Pro	Gln	Pro	Arg	Pro	Pro	His	Phe	Pro	Pro	Pro	Pro	Val	Pro	Pro	His
				85					90					95	
Ala	Ala	Pro	Leu	His	Ala	Ala	Asn	Pro	Pro	Pro	Arg	Ala	Ser	Asn	Ser
			100					105					110		
Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Ala	Ala	Arg	Gln	Pro	Pro	His	Ala
			115					120				125			
Pro	Pro	Arg	Arg	Asn	Pro	Pro	Pro	His	Pro	Gly	Pro	Thr	Pro	His	Arg
					130			135			140				
Pro	His	Arg	Pro	Thr	Pro	Pro	Pro	His	Thr	Pro	Pro	Thr	Pro	Pro	Pro
145					150					155					160
Ala	His	Thr	Gly	Pro	Pro	Thr	Thr	Pro	Pro	Thr	Asn	Glu	Pro	Pro	Arg
				165						170					175
Pro	Thr	Pro	Ala	Pro	Lys	Pro	Pro	Arg	His	Pro	Pro	Arg	Pro	Ala	Ala
			180					185					190		
Xaa	Leu	Pro	Pro	Met	Leu	Ala	Thr	Pro	Arg	Thr	Glu	Xaa	Ala	Thr	Xaa
		195					200					205			
Xaa	Pro	Xaa	Xaa	Xaa	Phe	Ser	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
	210					215					220				
Xaa	Xaa	Xaa	Xaa	Tyr	Thr	Asn	Trp	Gln	Ala	Val	Gly	Asp	Leu	Asp	Phe
225					230					235					240
Ala	Asn	Asp	Arg	Thr	Ala	Tyr	Met	Met	Glu	Cys	Pro	Asn	Leu	Val	Phe
				245					250						255
Val	Glu	Glu	Gln	Pro	Val	Leu	Leu	Tyr	Cys	Pro	Gln	Gly	Leu	Asp	Lys
			260					265					270		
Lys	Val	Leu	Asp	Tyr	Asp	Asn	Ile	Phe	Pro	Asn	Met	Tyr	Lys	Ile	Gly
		275					280					285			
Ala	Ser	Phe	Asp	Pro	Lys	Asn	Ala	Lys	Met	Val	Asp	Val	Ser	Gln	Leu
					290		295				300				
Gln	Asn	Met	Asp	Tyr	Gly	Phe	Glu	Ala	Tyr	Ala	Thr	Gln	Ala	Phe	Asn
305					310					315					320
Ala	Pro	Asp	Gly	Arg	Ala	Leu	Ala	Val	Ser	Trp	Leu	Gly	Leu	Pro	Asp
				325					330					335	
Val	Ser	Tyr	Pro	Ser	Asp	Arg	Phe	Asp	His	Gln	Gly	Thr	Phe	Ser	Leu
			340					345					350		
Val	Lys	Glu	Leu	Thr	Ile	Lys	Asp	Asp	Lys	Leu	Tyr	Gln	Tyr	Pro	Val
		355					360					365			
Ala	Ala	Ile	Lys	Asp	Leu	Arg	Ala	Ser	Glu	Glu	Ala	Phe	Ser	Asn	Arg
					370		375				380				
Phe	Gln	Thr	Lys	Asn	Thr	Tyr	Glu	Leu	Glu	Leu	Asn	Leu	Glu	Ala	Asn
385					390					395					400
Ser	Gln	Ser	Glu	Ile	Val	Leu	Leu	Ala	Asp	Lys	Glu	Gly	Lys	Gly	Leu
				405					410					415	
Ser	Ile	Asn	Phe	Asp	Leu	Val	Asn	Gly	Gln	Val	Thr	Val	Asp	Arg	Ser
			420					425					430		
Gln	Ala	Gly	Glu	Gln	Tyr	Ala	Gln	Glu	Phe	Gly	Thr	Thr	Arg	Ser	Cys
		435					440					445			
Pro	Ile	Glu	Asn	Gln	Ala	Thr	Thr	Ala	Thr	Ile	Phe	Ile	Asp	Asn	Ser
		450				455					460				
Val	Phe	Glu	Ile	Phe	Ile	Asn	Lys	Gly	Glu	Lys	Val	Phe	Ser	Gly	Arg
465					470					475					480
Val	Phe	Pro	His	Ala	Asp	Gln	Asn	Gly	Ile	Leu	Ile	Lys	Ser	Gly	Asn

				485					490					495
Pro	Thr	Gly	Thr	Tyr	Tyr	Glu	Leu	Asp	Tyr	Gly	Arg	Lys	Thr	Asn
				500				505					510	

(2) INFORMATION FOR SEQ ID NO:2905:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 549 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2905:

Ile	Tyr	Tyr	Thr	Tyr	Arg	Arg	Lys	Ile	Leu	Leu	Thr	Val	Ser	Asp	Val
1				5				10						15	
Ser	Leu	Arg	Phe	Ser	Asp	Arg	Lys	Leu	Phe	Asp	Asp	Val	Asn	Ile	Lys
			20					25					30		
Phe	Thr	Glu	Gly	Asn	Thr	Tyr	Gly	Leu	Ile	Gly	Ala	Asn	Gly	Ala	Gly
		35					40					45			
Lys	Ser	Thr	Phe	Leu	Lys	Ile	Leu	Ala	Gly	Asp	Ile	Glu	Pro	Thr	Thr
	50				55					60					
Gly	His	Ile	Ser	Leu	Gly	Pro	Asp	Glu	Arg	Leu	Ser	Val	Leu	Arg	Gln
65				70				75						80	
Asn	His	Phe	Asp	Tyr	Glu	Asp	Glu	Arg	Ala	Ile	Asp	Val	Val	Ile	Met
			85					90					95		
Gly	Asn	Glu	Lys	Leu	Tyr	Ser	Ile	Met	Lys	Glu	Lys	Asp	Ala	Ile	Tyr
		100						105					110		
Met	Lys	Glu	Asp	Phe	Ser	Asp	Glu	Asp	Gly	Val	Arg	Ala	Ala	Glu	Leu
	115						120				125				
Glu	Gly	Glu	Phe	Ala	Glu	Leu	Gly	Gly	Trp	Glu	Ala	Glu	Ser	Glu	Ala
	130					135				140					
Ser	Gln	Leu	Leu	Gln	Asn	Leu	Asn	Ile	Pro	Glu	Glu	Leu	His	Tyr	Gln
145				150						155				160	
Asn	Met	Ser	Glu	Leu	Ala	Asn	Gly	Glu	Lys	Val	Lys	Val	Leu	Leu	Ala
			165					170					175		
Lys	Ala	Leu	Phe	Gly	Lys	Pro	Asp	Val	Leu	Leu	Leu	Asp	Glu	Pro	Thr
		180					185					190			
Asn	Gly	Leu	Asp	Ile	Gln	Ser	Ile	Thr	Trp	Leu	Glu	Asp	Phe	Leu	Ile
	195					200					205				
Asp	Phe	Asp	Asn	Thr	Val	Ile	Val	Val	Ser	His	Asp	Arg	His	Phe	Leu
	210				215					220					
Asn	Lys	Val	Cys	Thr	His	Met	Ala	Asp	Leu	Asp	Phe	Gly	Lys	Ile	Lys
225				230				235						240	
Leu	Tyr	Val	Gly	Asn	Tyr	Asp	Phe	Trp	Lys	Glu	Ser	Ser	Glu	Leu	Ala
			245					250					255		
Ala	Lys	Leu	Leu	Ala	Asp	Arg	Asn	Ala	Lys	Ala	Glu	Glu	Lys	Ile	Lys

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEO ID NO:2906:

Leu	Asn	Tyr	Thr	Pro	Lys	Val	Arg	Gln	Lys	Lys	Ser	Asn	Phe	Trp	Gly
1				5					10					15	
Val	Phe	Ile	Met	Lys	Leu	Ser	Tyr	Asp	Asp	Lys	Val	Gln	Ile	Tyr	Glu
		20						25					30		
Leu	Arg	Lys	Gln	Gly	Tyr	Ser	Leu	Glu	Lys	Leu	Ser	Asn	Lys	Phe	Gly
		35					40					45			
Ile	Asn	Asn	Ser	Asn	Phe	Arg	Tyr	Met	Ile	Lys	Leu	Ile	Asp	Arg	Tyr
	50					55					60				
Gly	Ile	Glu	Phe	Gly	Lys	Lys	Gly	Lys	Asn	Arg	Tyr	Tyr	Phe	Pro	Asp
65					70				75						80
Leu	Lys	Gln	Glu	Met	Ile	Tyr	Lys	Val							
					85										

(2) INFORMATION FOR SEQ ID NO:2907:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 72 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...72
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2907:

Phe	Gln	Tyr	Thr	Val	Thr	Cys	Asp	Glu	Asn	Ala	Ser	Asn	Asp	Thr	Glu
1				5					10					15	
Lys	Lys	Ala	Glu	Lys	Leu	Phe	Pro	Ala	Leu	Phe	Val	Ile	Val	Lys	Ala
		20						25					30		
Asn	Asp	Leu	Phe	Leu	Cys	Ile	Tyr	Met	Ser	Met	Asp	Pro	Lys	Gly	Tyr
		35				40						45			
Asn	Cys	Ser	Trp	Ser	Cys	Val	Ala	Asp	Ile	Gln	Ile	Ile	Asp	Asn	Arg
	50					55					60				
Asp	Ile	Val	Val	Asn	Asp	Ile	Gln								
65					70										

(2) INFORMATION FOR SEQ ID NO:2908:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 127 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...127

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2908:

Ile	Gln	Tyr	Thr	Ile	Asp	Cys	Asn	Gln	Thr	Thr	Ile	Trp	Arg	Asn	Val
1				5				10						15	
Lys	Lys	Tyr	Glu	Glu	Phe	Gly	Leu	Asp	Ser	Leu	Leu	Gln	Glu	Thr	Arg
			20				25						30		
Gly	Gly	Arg	Asn	His	Ala	Tyr	Met	Thr	Val	Gly	Glu	Glu	Lys	Ala	Phe
			35				40					45			
Leu	Ala	Arg	His	Leu	Lys	Ala	Thr	Glu	Ala	Gly	Glu	Phe	Val	Thr	Ile
			50				55				60				
Asp	Ala	Leu	Phe	Gln	Ala	Tyr	Lys	Lys	Glu	Leu	Gly	Arg	Ser	Tyr	Thr
65				70					75					80	
Arg	Asp	Ala	Phe	Tyr	Gln	Leu	Leu	Lys	Arg	His	Gly	Trp	Arg	Asn	Ile
			85					90						95	
Met	Pro	Arg	Pro	Glu	His	Pro	Arg	Lys	Thr	Asp	Ala	Gln	Thr	Ile	Val
			100					105					110		
Ala	Ser	Lys	Asn	Lys	Ile	Ser	Ile	Gln	Glu	Glu	Lys	Lys	Ala	Leu	
			115				120					125			

(2) INFORMATION FOR SEQ ID NO:2909:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 294 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...294

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2909:

Glu	Arg	Tyr	Thr	Ile	Met	Lys	Gly	Ile	Ile	Leu	Ala	Gly	Gly	Ser	Gly
1				5				10						15	
Thr	Arg	Leu	Tyr	Pro	Leu	Thr	Arg	Ala	Ala	Ser	Lys	Gln	Leu	Met	Pro
			20				25						30		
Val	Tyr	Asp	Lys	Pro	Met	Ile	Tyr	Tyr	Pro	Leu	Ser	Thr	Leu	Met	Leu
			35				40					45			
Ala	Gly	Ile	Lys	Asp	Ile	Leu	Ile	Ile	Ser	Thr	Pro	Gln	Asp	Leu	Pro
			50				55				60				
Arg	Phe	Lys	Asp	Leu	Leu	Leu	Asp	Gly	Ser	Glu	Phe	Gly	Ile	Lys	Leu
65				70				75						80	
Ser	Tyr	Ala	Glu	Gln	Pro	Ser	Pro	Asp	Gly	Leu	Ala	Gln	Ala	Phe	Leu
			85					90						95	

Ile	Gly	Glu	Glu	Phe	Ile	Gly	Asp	Asp	Ser	Val	Ala	Leu	Ile	Leu	Gly
			100					105						110	
Asp	Asn	Ile	Tyr	His	Gly	Pro	Gly	Leu	Ser	Lys	Met	Leu	Gln	Lys	Ala
		115					120					125			
Ala	Gln	Lys	Glu	Lys	Gly	Ala	Thr	Val	Phe	Gly	Tyr	Gln	Val	Lys	Asp
	130				135					140					
Pro	Glu	Arg	Phe	Gly	Val	Glu	Phe	Asp	Thr	Asp	Met	Asn	Ala	Ile	
145				150				155						160	
Ser	Ile	Glu	Glu	Lys	Pro	Glu	Asn	Pro	Arg	Ser	Asn	Tyr	Ala	Val	Thr
				165				170						175	
Gly	Leu	Tyr	Phe	Tyr	Asp	Asn	Asp	Val	Val	Glu	Ile	Ala	Lys	Gly	Ile
			180				185					190			
Lys	Pro	Ser	Ala	Arg	Gly	Glu	Leu	Glu	Ile	Thr	Asp	Ile	Asn	Lys	Ala
	195					200		205							
Tyr	Leu	Asn	Arg	Gly	Asp	Leu	Ser	Val	Glu	Leu	Met	Gly	Arg	Gly	Phe
	210				215			220							
Ala	Trp	Leu	Asp	Thr	Gly	Thr	His	Glu	Ser	Leu	Leu	Glu	Ala	Ser	Gln
225				230				235						240	
Tyr	Ile	Glu	Thr	Val	Gln	Arg	Met	Gln	Asn	Val	Gln	Val	Ala	Asn	Leu
			245					250						255	
Glu	Glu	Ile	Ala	Tyr	Arg	Met	Gly	Tyr	Ile	Ser	Cys	Glu	Asp	Val	Leu
		260					265					270			
Glu	Leu	Ala	Gln	Pro	Leu	Lys	Lys	Asn	Glu	Tyr	Gly	Gln	Tyr	Leu	Leu
	275					280						285			
Arg	Leu	Ile	Gly	Glu	Ala										
	290														

(2) INFORMATION FOR SEQ ID NO:2910:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2910:

Arg	Arg	His	Thr	Met	Thr	Phe	Leu	Asn	Lys	Ile	His	Glu	Thr	Ala	Thr
1			5					10						15	
Phe	Leu	Lys	Glu	Lys	Gly	Ile	Ala	Ala	Pro	Glu	Phe	Gly	Leu	Ile	Leu
		20					25					30			
Gly	Ala	Gly	Leu	Gly	Glu	Leu	Ala	Glu	Glu	Ile	Glu	Asn	Pro	Val	Val
	35				40						45				
Val	Asp	Tyr	Ala	Glu	Ile	Pro	Asn	Trp	Gly	Arg	Ser	Thr	Val	Val	Gly
	50				55			60							
His	Ala	Gly	Lys	Leu	Val	Tyr	Gly	Glu	Leu	Ala	Gly	Arg	Lys	Val	Leu
65				70				75						80	

Ala	Leu	Gln	Gly	Arg	Phe	His	Phe	Tyr	Glu	Gly	Asn	Pro	Leu	Glu	Val
				85					90					95	
Val	Thr	Phe	Pro	Val	Arg	Val	Met	Lys	Val	Leu	Gly	Cys	Glu	Gly	Val
			100					105					110		
Ile	Val	Thr	Asn	Ala	Ala	Gly	Gly	Ile	Arg	Phe	Gly	Pro	Gly	Thr	Leu
		115					120					125			
Met	Ala	Ile	Ser	Asp	His	Ile	Asn	Met	Thr	Gly	Gln	Asn	Pro	Leu	Met
	130					135					140				
Gly	Glu	Asn	Leu	Asp	Asp	Phe	Gly	Pro	Arg	Phe	Pro	Asp	Met	Ser	Arg
145					150					155					160
Ala	Tyr	Thr	Pro	Glu	Tyr	Arg	Ala	Thr	Ala	His	Glu	Val	Ala	Lys	Lys
				165					170					175	
Leu	Asn	Ile	Lys	Leu	Asp	Glu	Gly	Val	Tyr	Ile	Gly	Val	Thr	Gly	Pro
			180					185					190		
Thr	Tyr	Glu	Thr	Pro	Ala	Glu	Ile	Arg	Ser	Tyr	Lys	Thr	Leu	Gly	Ala
		195					200					205			
Asp	Ala	Val	Gly	Met	Ser	Thr	Val	Pro	Glu	Val	Ile	Val	Ala	Ala	His
	210					215					220				
Ser	Gly	Leu	Lys	Val	Leu	Gly	Ile	Ser	Cys	Ile	Thr	Asn	Phe	Ala	Ala
225					230				235						240
Gly	Phe	Gln	Glu	Glu	Leu	Asn	His	Glu	Glu	Ile	Val	Glu	Val	Thr	Glu
			245						250					255	
Arg	Val	Lys	Gly	Asp	Phe	Lys	Gly	Leu	Leu	Lys	Ala	Ile	Leu	Ala	Glu
			260					265					270		
Leu															

(2) INFORMATION FOR SEQ ID NO:2911:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...66

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2911:

Glu	Glu	Asn	Thr	Met	Ala	Lys	Val	Cys	Tyr	Phe	Thr	Gly	Arg	Lys	Thr
1				5				10						15	
Val	Ser	Gly	Asn	Asn	Arg	Ser	His	Ala	Met	Asn	Gln	Thr	Lys	Arg	Ala
			20					25					30		
Val	Lys	Pro	Asn	Leu	Gln	Lys	Val	Thr	Val	Leu	Ile	Asp	Gly	Lys	Pro
		35				40						45			
Lys	Lys	Val	Trp	Ala	Ser	Ala	Arg	Ala	Leu	Lys	Ser	Gly	Lys	Val	Glu
	50					55					60				
Arg	Val														
65															

(2) INFORMATION FOR SEQ ID NO:2912:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...515

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2912:

Arg	Gly	Asn	Thr	Ser	Arg	Ser	Leu	Ser	Gly	Gly	Gln	Tyr	Met	Ser	Gln	
1				5				10						15		
Glu	Lys	Tyr	Ile	Met	Ala	Ile	Asp	Gln	Gly	Thr	Thr	Ser	Ser	Arg	Ala	
			20				25						30			
Ile	Ile	Phe	Asn	Lys	Lys	Gly	Glu	Lys	Val	Ser	Ser	Ser	Gln	Lys	Glu	
		35				40						45				
Phe	Thr	Gln	Ile	Phe	Pro	Gln	Ala	Gly	Trp	Val	Glu	His	Asn	Ala	Asn	
	50				55				60							
Glu	Ile	Trp	Asn	Ser	Val	Gln	Ser	Val	Ile	Ala	Gly	Ala	Phe	Ile	Glu	
65			70				75							80		
Ser	Gly	Val	Lys	Pro	Asn	Gln	Ile	Glu	Ala	Ile	Gly	Ile	Thr	Asn	Gln	
			85				90						95			
Arg	Glu	Thr	Thr	Val	Val	Trp	Asp	Lys	Lys	Thr	Gly	Leu	Pro	Ile	Tyr	
		100				105						110				
Asn	Ala	Ile	Val	Trp	Gln	Ser	Arg	Gln	Thr	Ala	Pro	Leu	Ala	Glu	Gln	
	115				120						125					
Leu	Lys	Ser	Gln	Gly	Tyr	Val	Glu	Lys	Phe	His	Glu	Lys	Thr	Gly	Leu	
	130				135						140					
Ile	Ile	Asp	Ala	Tyr	Phe	Ser	Ala	Thr	Lys	Val	Arg	Trp	Ile	Leu	Asp	
145			150				155							160		
His	Val	Glu	Gly	Ala	Gln	Glu	Arg	Ala	Glu	Lys	Gly	Glu	Leu	Leu	Phe	
			165				170						175			
Gly	Thr	Ile	Asp	Thr	Trp	Leu	Val	Trp	Lys	Leu	Thr	Asp	Gly	Ala	Ala	
		180				185						190				
His	Val	Thr	Asp	Tyr	Ser	Asn	Ala	Ala	Arg	Thr	Met	Leu	Tyr	Asn	Ile	
	195				200						205					
Lys	Glu	Leu	Lys	Trp	Asp	Asp	Glu	Ile	Leu	Glu	Ile	Leu	Asn	Ile	Pro	
	210				215					220						
Lys	Ala	Ile	Leu	Pro	Glu	Val	Arg	Ser	Asn	Ser	Glu	Ile	Tyr	Gly	Lys	
225			230				235							240		
Thr	Ala	Pro	Phe	His	Phe	Tyr	Gly	Gly	Glu	Val	Pro	Ile	Ser	Gly	Met	
			245				250						255			
Ala	Gly	Asp	Gln	Gln	Ala	Ala	Leu	Phe	Gly	Gln	Leu	Ala	Phe	Glu	Pro	
		260					265					270				
Gly	Met	Val	Lys	Asn	Thr	Tyr	Gly	Thr	Gly	Ser	Phe	Ile	Ile	Met	Asn	
		275					280					285				

Thr Gly Glu Glu Met Gln Leu Ser Glu Asn Asn Leu Leu Thr Thr Ile
 290 295 300
 Gly Tyr Gly Ile Asn Gly Lys Val Tyr Tyr Ala Leu Glu Gly Ser Ile
 305 310 315 320
 Phe Ile Ala Gly Ser Ala Ile Gln Trp Leu Arg Asp Gly Leu Arg Met
 325 330 335
 Val Glu Asn Ser Pro Glu Ser Glu Lys Tyr Ala Arg Asp Ser His Asn
 340 345 350
 Asn Asp Glu Val Tyr Val Val Pro Ala Phe Thr Gly Leu Gly Ala Pro
 355 360 365
 Tyr Trp Asn Gln Asn Ala Arg Gly Ser Val Phe Gly Leu Thr Arg Gly
 370 375 380
 Thr Ser Lys Glu Asp Phe Ile Lys Ala Thr Leu Gln Ser Ile Ala Tyr
 385 390 395 400
 Gln Val Arg Asp Ile Ile Asp Thr Met Gln Val Asp Thr Gln Thr Ala
 405 410 415
 Ile Gln Val Leu Lys Val Asp Gly Gly Ala Ala Met Asn Asn Phe Leu
 420 425 430
 Met Gln Phe Gln Ala Asp Ile Leu Gly Ile Asp Ile Ala Arg Ala Lys
 435 440 445
 Asn Leu Glu Thr Thr Ala Leu Gly Ala Ala Phe Leu Ala Gly Leu Ser
 450 455 460
 Val Gly Tyr Trp Lys Asn Leu Asp Glu Leu Lys Leu Leu Asn Glu Thr
 465 470 475 480
 Gly Glu Leu Phe Glu Pro Ser Met Asn Glu Ser Arg Lys Glu Gln Leu
 485 490 495
 Tyr Lys Gly Trp Lys Lys Ala Val Lys Ala Thr Gln Val Phe Ala Glu
 500 505 510
 Val Asp Asp
 515

(2) INFORMATION FOR SEQ ID NO:2913:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 68 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...68
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2913:

Lys Met Asn Thr Glu Gln Leu Asn Gln Ala Leu Gln Met Thr Ile Ser
 1 5 10 15
 Glu Met Ser Thr Thr Ser Thr Asn Ser Met Ile Thr Ser Asn Ile Leu
 20 25 30
 Ser Ile Gln Leu Asn Glu Gln Arg Glu Glu Asn Gln Arg Leu Gln Ala

	35		40		45
Arg	Val	Asp	Glu	Leu	Glu
	50		55		60
Asp	Lys	Gly	Glu		
65					

(2) INFORMATION FOR SEQ ID NO:2914:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 89 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...89
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2914:

Leu	Asn	Cys	Thr	Pro	Lys	Val	Arg	Gln	Lys	Lys	Ser	Asn	Phe	Trp	Gly
1				5				10						15	
Val	Phe	Ile	Met	Lys	Leu	Thr	Tyr	Asp	Asp	Lys	Val	Gln	Ile	Tyr	Glu
			20					25						30	
Leu	Arg	Lys	Gln	Gly	Tyr	Ser	Leu	Glu	Lys	Leu	Ser	Asn	Lys	Phe	Gly
			35					40						45	
Ile	Asn	Asn	Ser	Asn	Ile	Arg	Tyr	Met	Ile	Lys	Leu	Ile	Asp	Arg	Tyr
			50					55						60	
Gly	Ile	Glu	Phe	Val	Lys	Lys	Gly	Lys	Asn	Arg	Tyr	Tyr	Ser	Pro	Asp
65					70					75					80
Leu	Lys	Gln	Glu	Met	Ile	Asn	Lys	Val							
					85										

(2) INFORMATION FOR SEQ ID NO:2915:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 190 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...190

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2915:

Met	Asn	Cys	Thr	Pro	Lys	Val	Arg	Gln	Lys	Lys	Ser	Asn	Phe	Trp	Gly
1				5					10					15	
Val	Phe	Ile	Met	Lys	Leu	Thr	Tyr	Asp	Asp	Lys	Val	Gln	Ile	Tyr	Glu
			20					25					30		
Leu	Arg	Lys	Gln	Gly	Tyr	Ser	Leu	Glu	Lys	Leu	Ser	Asn	Lys	Phe	Gly
			35				40					45			
Ile	Asn	Asn	Ser	Asn	Ile	Arg	Tyr	Met	Ile	Lys	Leu	Ile	Asp	Arg	Tyr
	50					55					60				
Gly	Ile	Glu	Phe	Val	Lys	Lys	Gly	Lys	Asn	Arg	Tyr	Tyr	Ser	Pro	Asp
65					70					75					80
Leu	Lys	Gln	Glu	Met	Ile	His	Lys	Val	Leu	His	Glu	Gly	Trp	Thr	Lys
				85					90					95	
Asp	Arg	Val	Ser	Leu	Glu	Tyr	Gly	Leu	Pro	Ser	Arg	Thr	Ile	Leu	Leu
			100					105					110		
Asn	Trp	Leu	Ala	Gln	Tyr	Arg	Lys	Asn	Gly	Tyr	Thr	Ile	Val	Glu	Lys
		115					120					125			
Thr	Arg	Gly	Arg	Val	Pro	Lys	Met	Gly	Arg	Lys	Pro	Lys	Thr	Arg	Pro
	130					135					140				
Glu	Glu	Arg	Thr	Glu	Leu	Glu	Arg	Leu	Gln	Ala	Glu	Asn	Glu	Tyr	Leu
145					150					155					160
Arg	Ala	Glu	Lys	Ala	Ile	Leu	Lys	Lys	Leu	Arg	Glu	Leu	Arg	Leu	Lys
				165					170					175	
Glu	Glu	Lys	Glu	Lys	Glu	Glu	Arg	Gln	Lys	Leu	Phe	Lys	Asn		
			180					185					190		

(2) INFORMATION FOR SEQ ID NO:2916:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...63

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2916:

Met	Asn	Cys	Thr	Pro	Lys	Val	Arg	Gln	Lys	Lys	Ser	Asn	Phe	Trp	Ser
1				5					10					15	
Val	Phe	Ile	Met	Lys	Leu	Thr	Tyr	Asp	Asp	Lys	Val	Gln	Ile	Tyr	Glu
			20					25					30		
Leu	Arg	Lys	Gln	Gly	Tyr	Ser	Leu	Glu	Lys	Leu	Ser	Asn	Lys	Phe	Glu
			35				40					45			
Ile	Asn	Asn	Ser	Asn	Leu	Arg	Tyr	Met	Ile	Lys	Leu	Ile	Asp	Arg	
	50					55					60				

(2) INFORMATION FOR SEQ ID NO:2917:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 928 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...928
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2917:

Phe	Ile	Cys	Thr	Met	Pro	Val	Ser	Arg	Met	Trp	Cys	Ser	Thr	Ser	Ile	1	5	10	15
Leu	Arg	Ile	Leu	Thr	Val	Trp	Ser	Thr	Ser	Met	Ile	Lys	Arg	Lys	Thr	20	25	30	
Tyr	Trp	Lys	Asp	Leu	Ile	Gln	Ser	Phe	Thr	Gly	Ser	Lys	Gly	Arg	Phe	35	40	45	
Leu	Ser	Ile	Leu	Ile	Leu	Met	Met	Leu	Gly	Ser	Leu	Ala	Leu	Val	Gly	50	55	60	
Leu	Lys	Val	Thr	Ser	Pro	Asn	Met	Glu	Ala	Thr	Ala	Asn	Ala	Tyr	Leu	65	70	75	80
Thr	Thr	Ala	Gln	Thr	Leu	Asp	Leu	Ala	Val	Met	Ser	Asn	Tyr	Gly	Leu	85	90	95	
Asp	Gln	Ala	Asp	Gln	Glu	Glu	Leu	Lys	Gln	Thr	Glu	Gly	Ala	Glu	Val	100	105	110	
Glu	Phe	Gly	Tyr	Leu	Thr	Asp	Val	Thr	Met	Asp	Asn	Gly	Gln	Asp	Ala	115	120	125	
Ile	Arg	Leu	Tyr	Ser	Lys	Pro	Glu	Arg	Ile	Ser	Thr	Phe	Gln	Leu	Arg	130	135	140	
Lys	Gly	Arg	Leu	Pro	Gln	Ser	Asp	Lys	Glu	Ile	Ala	Leu	Ala	Thr	His	145	150	155	160
Leu	Gln	Asp	Gln	Tyr	Ser	Val	Gly	Gln	Glu	Ile	Ser	Phe	Lys	Glu	Lys	165	170	175	
Glu	Glu	Gly	His	Ser	Ser	Leu	Lys	Asp	His	Thr	Tyr	Thr	Ile	Thr	Gly	180	185	190	
Phe	Val	Asp	Ser	Ala	Glu	Ile	Leu	Ser	Gln	Arg	Asp	Met	Gly	Tyr	Ala	195	200	205	
Gly	Ser	Gly	Ser	Gly	Thr	Leu	Ala	Ala	Tyr	Gly	Val	Ile	Leu	Pro	Ser	210	215	220	
Gln	Phe	Asp	Gln	Lys	Val	Tyr	Asn	Ile	Ala	Arg	Leu	Lys	Tyr	Gln	Asp	225	230	235	240
Leu	Ala	Gly	Leu	Asn	Ala	Phe	Ser	Ser	Ala	Tyr	Glu	Glu	Lys	Ser	Lys	245	250	255	
Gln	His	Gln	Glu	Glu	Leu	Glu	Gln	Ile	Leu	Ser	Asp	Asn	Gly	Lys	Val	260	265	270	
Arg	Leu	Gln	Leu	Leu	Lys	Lys	Glu	Gly	Gln	Glu	Ser	Leu	Asp	Lys	Gly	275	280	285	
Gln	Glu	Thr	Leu	Asp	Lys	Ala	Gln	Thr	Asn	Leu	Gln	Glu	Gly	Lys	Arg	290	295	300	

Arg	Leu	Ala	Ala	Ala	Gln	Ala	Arg	Ile	Gln	Ala	Gln	Glu	Ser	Gln	Leu	305	310	315	320
Ala	Leu	Phe	Pro	Gln	Val	Gln	Arg	Glu	Gln	Ala	Ser	Ala	Gln	Leu	Thr	325	330	335	335
Gln	Ala	Lys	Gln	Glu	Leu	Gly	Lys	Glu	Glu	Ala	Lys	Leu	Lys	Gln	Ala	340	345	350	350
Glu	Gln	Asn	Leu	Ala	Gln	Glu	Lys	Glu	Lys	Leu	Glu	Lys	His	Gln	Gln	355	360	365	365
Val	Leu	Asp	Asp	Leu	Ala	Glu	Pro	Arg	Tyr	Gln	Val	Tyr	Asn	Arg	Gln	370	375	380	380
Thr	Met	Pro	Gly	Gly	Gln	Gly	Tyr	Leu	Met	Tyr	Ser	Asn	Ala	Ser	Ser	385	390	395	400
Ser	Ile	Arg	Ala	Val	Gly	Asn	Ile	Phe	Pro	Val	Val	Leu	Tyr	Ala	Val	405	410	415	415
Ala	Ala	Met	Val	Thr	Phe	Thr	Thr	Met	Thr	Arg	Phe	Val	Asp	Glu	Glu	420	425	430	430
Arg	Thr	His	Ala	Gly	Ile	Phe	Lys	Ala	Leu	Gly	Tyr	Arg	Ser	Lys	Asp	435	440	445	445
Ile	Ile	Ala	Lys	Phe	Leu	Leu	Tyr	Gly	Leu	Val	Ala	Gly	Thr	Val	Gly	450	455	460	460
Thr	Ala	Leu	Gly	Ser	Ile	Leu	Gly	His	Tyr	Leu	Leu	Ala	Ser	Val	Ile	465	470	475	480
Ser	Ser	Val	Ile	Thr	Lys	Gly	Met	Val	Val	Gly	Glu	Thr	Gln	Ile	Gln	485	490	495	495
Phe	Tyr	Trp	Thr	Tyr	Ser	Leu	Leu	Ala	Phe	Val	Leu	Ser	Leu	Leu	Ala	500	505	510	510
Ser	Val	Leu	Ser	Ala	Tyr	Leu	Val	Ala	Trp	Arg	Glu	Leu	His	Asp	Glu	515	520	525	525
Ala	Ala	Gln	Leu	Leu	Leu	Pro	Lys	Pro	Pro	Val	Lys	Gly	Ala	Lys	Ile	530	535	540	540
Leu	Leu	Glu	Arg	Ile	Gly	Phe	Ile	Trp	Arg	Arg	Leu	Ser	Phe	Thr	His	545	550	555	560
Lys	Val	Thr	Ala	Arg	Asn	Ile	Phe	Arg	Tyr	Lys	Gln	Arg	Met	Leu	Met	565	570	575	575
Thr	Ile	Phe	Gly	Val	Ala	Gly	Ser	Val	Ala	Leu	Leu	Phe	Ala	Gly	Leu	580	585	590	590
Gly	Ile	Gln	Ser	Ser	Val	Ala	Gly	Val	Pro	Ser	Lys	Gln	Phe	Gln	Gln	595	600	605	605
Ile	Gln	Gln	Tyr	Gln	Met	Leu	Val	Ser	Glu	Asn	Pro	Ser	Ala	Thr	Asn	610	615	620	620
Gln	Asp	Lys	Val	Glu	Leu	Ala	Glu	Val	Leu	Lys	Gly	Gln	Glu	Ile	Leu	625	630	635	640
Ala	Tyr	Gln	Lys	Ile	Tyr	Ser	Lys	Thr	Leu	Asp	Lys	Asp	Phe	Lys	Gly	645	650	655	655
Lys	Ala	Gly	Leu	Gln	Asn	Ile	Thr	Leu	Met	Met	Ile	Glu	Lys	Glu	Asp	660	665	670	670
Leu	Thr	Pro	Phe	Ile	His	Leu	Gln	His	His	Gln	Gln	Glu	Leu	Thr	Leu	675	680	685	685
Lys	Asp	Gly	Ile	Val	Ile	Thr	Ala	Lys	Leu	Ala	Gln	Leu	Ala	Gly	Val	690	695	700	700
Lys	Val	Gly	Gln	Thr	Leu	Glu	Ile	Glu	Gly	Lys	Glu	Leu	Lys	Val	Ala	705	710	715	720
Ala	Ile	Thr	Glu	Asn	Tyr	Val	Gly	His	Phe	Ile	Tyr	Met	Ser	Gln	Ala	725	730	735	735
Ser	Tyr	Glu	Gln	Leu	Tyr	Gly	Gln	Leu	Pro	Gln	Ala	Asn	Thr	Tyr	Leu	740	745	750	750
Val	Ser	Leu	Arg	Asp	Thr	Ser	Ala	Thr	Ser	Ile	Glu	Ser	Gln	Ala	Gly	745	750	755	755

Phe	His	Arg	Val	Ile	Asp	Gly	Phe	Met	Val	Gln	Thr	Gly	Asp	Pro	Lys
		115					120					125			
Gly	Asp	Gly	Thr	Gly	Gly	Gln	Ser	Ile	Trp	His	Asp	Lys	Asp	Lys	Thr
	130					135					140				
Lys	Asp	Lys	Gly	Thr	Gly	Phe	Lys	Asn	Glu	Ile	Thr	Pro	Tyr	Leu	Tyr
145					150					155					160
Asn	Ile	Arg	Gly	Ala	Leu	Ala	Met	Ala	Asn	Thr	Gly	Gln	Pro	Asn	Thr
			165						170					175	
Asn	Gly	Ser	Gln	Phe	Phe	Ile	Asn	Gln	Asn	Ser	Thr	Asp	Thr	Ser	Ser
			180					185					190		
Lys	Leu	Pro	Thr	Ser	Lys	Tyr	Pro	Gln	Lys	Ile	Ile	Glu	Ala	Tyr	Lys
		195					200					205			
Glu	Gly	Gly	Asn	Pro	Ser	Leu	Asp	Gly	Lys	His	Pro	Val	Phe	Gly	Gln
	210					215					220				
Val	Ile	Gly	Gly	Met	Asp	Val	Val	Asp	Lys	Ile	Ala	Lys	Ala	Glu	Lys
225					230					235					240
Asp	Glu	Lys	Asp	Lys	Pro	Thr	Thr	Ala	Ile	Thr	Ile	Asp	Ser	Ile	Glu
				245					250					255	
Val	Val	Lys	Asp	Tyr	Asp	Phe	Lys	Ser							
			260					265							

(2) INFORMATION FOR SEQ ID NO:2919:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 167 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...167

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2919:

Lys	Asn	Ser	Thr	Thr	Leu	Thr	Ile	Ser	Ser	Asn	Arg	Leu	Ser	Phe	Asn
1				5					10					15	
Ile	Ser	Tyr	Phe	Pro	Ile	Asp	Phe	Leu	Arg	Asn	Lys	Ile	Trp	Tyr	Ser
			20					25					30		
Ser	Ser	Met	Asn	Asp	Glu	Ala	Ser	Lys	Gln	Leu	Thr	Asp	Ala	Arg	Phe
		35					40					45			
Lys	Arg	Leu	Val	Gly	Val	Gln	Arg	Thr	Thr	Phe	Glu	Glu	Ile	Leu	Ala
	50				55					60					
Val	Leu	Lys	Thr	Ala	Tyr	Gln	Leu	Lys	His	Ala	Lys	Gly	Gly	Arg	Lys
65					70				75					80	
Pro	Lys	Leu	Ser	Leu	Glu	Asp	Leu	Leu	Met	Ala	Thr	Leu	Gln	Tyr	Val
			85					90					95		
Arg	Glu	Tyr	Arg	Thr	Tyr	Glu	Gln	Ile	Ala	Ala	Asp	Phe	Gly	Ile	His
			100					105					110		
Glu	Ser	Asn	Leu	Ile	Arg	Arg	Ser	Gln	Trp	Val	Glu	Val	Thr	Leu	Val
		115					120					125			

Gln	Ser	Gly	Val	Thr	Ile	Ser	Arg	Thr	Pro	Leu	Ser	Ser	Glu	Asp	Thr
130						135					140				
Val	Met	Ile	Ile	Asp	Ala	Thr	Glu	Val	Lys	Ile	Asn	Arg	Pro	Lys	Lys
145					150					155					160
Arg	Ile	Ser	Glu	Leu	Phe	Trp									
				165											

(2) INFORMATION FOR SEQ ID NO:2920:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 155 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...155
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2920:

Glu	Gln	Gly	Thr	Leu	Ser	Leu	Val	Asn	Cys	Glu	Pro	Leu	Glu	Ala	Tyr
1				5				10						15	
Arg	Gln	Leu	Glu	Glu	Ala	Ala	Leu	Val	Gly	Cys	Trp	Ala	His	Val	Arg
		20					25					30			
Arg	Lys	Phe	Phe	Glu	Ala	Thr	Pro	Lys	Gln	Ala	Asp	Lys	Ser	Ser	Leu
		35				40					45				
Gly	Ala	Lys	Gly	Leu	Ala	Tyr	Cys	Asp	Gln	Leu	Phe	Ser	Leu	Glu	Arg
	50				55					60					
Asp	Trp	Glu	Ala	Leu	Pro	Ala	Asp	Glu	Arg	Leu	Gln	Lys	Arg	Gln	Glu
65				70				75						80	
Glu	Leu	Gln	Pro	Leu	Ile	Glu	Asp	Phe	Phe	Ala	Trp	Cys	Arg	Arg	Gln
			85					90					95		
Ser	Val	Leu	Ala	Gly	Ser	Lys	Leu	Gly	Arg	Ala	Ile	Glu	Tyr	Ser	Leu
		100					105					110			
Lys	Tyr	Glu	Thr	Phe	Lys	Thr	Ile	Leu	Lys	Asp	Gly	His	Leu	Val	
		115				120					125				
Leu	Ser	Asn	Asn	Leu	Ala	Glu	Cys	Ala	Ile	Lys	Ser	Leu	Val	Met	Gly
	130					135				140					
Arg	Ser	Lys	Arg	Val	Gln	Trp	Thr	Leu	Leu	Ala					
145					150					155					

(2) INFORMATION FOR SEQ ID NO:2921:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 111 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...111

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2921:

Ile	Leu	Gly	Thr	Ser	Gln	Asp	Ile	Phe	Ile	Ser	Leu	Ala	Ser	Asp	Asn
1				5				10						15	
Leu	Val	Leu	Phe	Phe	Val	Asp	Phe	Leu	Asp	Ile	Gln	Lys	Asn	Gln	Val
			20					25					30		
Ser	Asp	Ser	His	Glu	Phe	Val	Lys	Leu	Leu	Lys	Val	Thr	Trp	Phe	Ile
			35				40					45			
Thr	Glu	Arg	Lys	Ser	Thr	Gly	Ile	Gln	Gly	Thr	Val	Asp	Ser	Leu	Phe
			50			55				60					
Leu	Ser	Leu	Gly	Glu	Glu	Ser	Asn	Gln	Glu	Ile	Asn	Leu	Gln	Glu	Ser
65					70					75				80	
Phe	Ser	Ser	Thr	Asp	Cys	Asn	Pro	Thr	Leu	Ile	Ser	Pro	Glu	Thr	Thr
				85					90					95	
Val	Ala	Gln	Gly	Leu	Cys	Gln	Asp	Ile	Ile	Tyr	Arg	Pro	Phe	Thr	
			100					105					110		

(2) INFORMATION FOR SEQ ID NO:2922:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2922:

Lys	Asn	Arg	Leu	Lys	Ile	Lys	Thr	Met	Ile	Ser	Met	Val	Ala	Asn	Leu
1				5				10						15	
Ile	Thr	Lys	Ser	Arg	Ile	Pro	Lys	Pro	Leu	Ala	Phe	Gln	Leu	Arg	Val
			20					25					30		
Asn	Ser	Leu	Glu	Ile	Met	Ile	Ser	Asn	Ser	Leu	Ala	Thr	Ser	Thr	Lys
			35				40					45			
Lys	Met	Gln	Leu	Leu	Leu	Asp	Leu	Leu	Val	Ser	Val	Ser	Glu	Gln	Val
			50			55				60					
Leu	Arg	Thr	Ser	Lys	Lys	Ala	Ser	Leu	Gln	Pro	Ala	Phe	Leu	Val	Val
65					70					75				80	
Trp	Lys	Ser	Ser	Leu	Arg	Lys	Met	Glu	Pro	Arg	Ser	Ser	Ser	Thr	Met

85
Pro Thr Met Gly Ile Val
100

90

95

(2) INFORMATION FOR SEQ ID NO:2923:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 403 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2923:

Gly	Gly	Leu	Thr	Asp	Ser	Gln	Arg	Arg	Asn	His	Met	Thr	Gln	His	Leu
1				5					10					15	
Thr	Ala	Glu	Thr	Leu	Arg	Lys	Asp	Phe	Leu	Ala	Val	Phe	Gly	Gln	Glu
			20					25					30		
Ala	Asp	Gln	Ile	Phe	Phe	Ser	Pro	Gly	Arg	Ile	Asn	Leu	Ile	Gly	Glu
		35					40					45			
His	Thr	Asp	Tyr	Asn	Gly	Gly	His	Val	Phe	Pro	Ala	Ala	Ile	Ser	Leu
	50				55					60					
Gly	Thr	Tyr	Gly	Ala	Ala	Arg	Lys	Arg	Asp	Asp	Gln	Val	Leu	Arg	Phe
65				70					75					80	
Tyr	Ser	Ala	Asn	Phe	Glu	Asp	Lys	Gly	Ile	Ile	Glu	Val	Pro	Leu	Ala
			85					90					95		
Asp	Leu	Lys	Phe	Glu	Lys	Glu	His	Asn	Trp	Thr	Asn	Tyr	Pro	Lys	Gly
		100						105					110		
Val	Leu	His	Phe	Leu	Gln	Glu	Ala	Gly	His	Val	Ile	Asp	Lys	Gly	Phe
		115					120					125			
Asp	Phe	Tyr	Val	Tyr	Gly	Asn	Ile	Pro	Asn	Gly	Ala	Gly	Leu	Ser	Ser
	130					135					140				
Ser	Ala	Ser	Leu	Glu	Leu	Leu	Thr	Gly	Val	Val	Ala	Glu	His	Leu	Phe
145					150					155				160	
Asp	Leu	Lys	Leu	Glu	Arg	Leu	Asp	Leu	Val	Lys	Ile	Gly	Lys	Gln	Thr
			165						170					175	
Glu	Asn	Asn	Phe	Ile	Gly	Val	Asn	Ser	Gly	Ile	Met	Asp	Gln	Phe	Ala
			180				185						190		
Ile	Gly	Met	Gly	Ala	Asp	Gln	Arg	Ala	Ile	Tyr	Leu	Asp	Thr	Asn	Thr
		195					200						205		
Leu	Glu	Tyr	Asp	Leu	Val	Pro	Leu	Asp	Leu	Lys	Asp	Asn	Val	Val	Val
	210					215					220				
Ile	Met	Asn	Thr	Asn	Lys	Arg	Arg	Glu	Leu	Ala	Asp	Ser	Lys	Tyr	Asn
225					230					235				240	
Glu	Arg	Arg	Ala	Glu	Cys	Glu	Lys	Ala	Val	Glu	Glu	Leu	Gln	Val	Ala

(A) LENGTH: 266 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...266

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2925:

Trp	Lys	Leu	Thr	Thr	Val	Ala	Leu	His	Leu	Ser	Lys	Arg	Leu	Phe	Arg
1			5						10					15	
Thr	Cys	Trp	Arg	Ala	Asp	Glu	Met	Ile	Asp	Ile	His	Ser	His	Ile	Val
		20						25					30		
Phe	Asp	Val	Asp	Asp	Gly	Pro	Lys	Ser	Arg	Glu	Glu	Ser	Lys	Ala	Leu
		35					40					45			
Leu	Thr	Glu	Ala	Tyr	Arg	Gln	Gly	Val	Arg	Thr	Ile	Val	Ser	Thr	Ser
		50				55				60					
His	Arg	Arg	Lys	Gly	Met	Phe	Glu	Thr	Pro	Glu	Glu	Lys	Ile	Ala	Glu
65				70					75					80	
Asn	Phe	Leu	Gln	Val	Arg	Glu	Ile	Ala	Lys	Glu	Val	Ala	Ser	Asp	Leu
			85					90					95		
Val	Ile	Ala	Tyr	Gly	Ala	Glu	Ile	Tyr	Tyr	Thr	Pro	Asp	Val	Leu	Asp
		100						105					110		
Lys	Leu	Glu	Asn	Asn	Arg	Ile	Pro	Thr	Leu	Asn	Asn	Ser	Arg	Tyr	Ala
		115					120					125			
Leu	Ile	Glu	Phe	Ser	Met	Asn	Thr	Pro	Tyr	Arg	Asp	Ile	His	Ser	Ala
		130				135				140					
Leu	Asn	Lys	Ile	Leu	Met	Leu	Gly	Ile	Thr	Pro	Val	Ile	Ala	His	Ile
145					150				155					160	
Glu	Arg	Tyr	Asp	Val	Leu	Glu	Asn	Asn	Glu	Lys	Arg	Val	Arg	Glu	Leu
			165						170					175	
Ile	Asp	Met	Gly	Cys	Tyr	Thr	Gln	Ile	Asn	Ser	Ser	His	Val	Leu	Lys
		180					185						190		
Ser	Lys	Leu	Phe	Gly	Glu	Pro	Tyr	Lys	Phe	Met	Lys	Lys	Arg	Ala	Gln
		195					200					205			
Tyr	Phe	Leu	Glu	Arg	Asp	Leu	Val	His	Ile	Ile	Ala	Ser	Asp	Met	His
		210				215					220				
Asn	Val	Asp	Gly	Arg	Pro	Pro	His	Met	Ala	Glu	Ala	Tyr	Asp	Leu	Val
225					230					235				240	
Ser	Gln	Lys	Tyr	Gly	Glu	Ala	Lys	Ala	Gln	Glu	Leu	Phe	Ile	Asp	Asn
			245						250					255	
Pro	Arg	Lys	Ile	Val	Met	Asp	Gln	Leu	Ile						
			260					265							

(2) INFORMATION FOR SEQ ID NO:2926:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 315 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2926:

Thr	Ser	Leu	Thr	Leu	Lys	Phe	Leu	Ser	Gln	Leu	Leu	Leu	Asn	Ala	Ile
1				5					10					15	
Thr	Thr	Ile	Ser	Val	Ser	Val	Leu	Asn	Lys	Val	Ser	Thr	Ser	Ser	Gln
			20					25					30		
Phe	His	Ser	Tyr	Val	Leu	Gln	Lys	Asn	Val	Asn	Glu	Val	Arg	Ala	Ile
		35				40						45			
Cys	Glu	Glu	Thr	Gly	Asn	Gly	His	Val	Gln	Leu	Phe	Ala	Lys	Ile	Glu
	50				55						60				
Asn	Gln	Gln	Gly	Ile	Asp	Asn	Leu	Asp	Glu	Ile	Ile	Glu	Ala	Ala	Asp
65					70					75					80
Gly	Ile	Met	Ile	Ala	Arg	Gly	Asp	Met	Gly	Ile	Glu	Val	Pro	Phe	Glu
				85					90					95	
Met	Val	Pro	Val	Tyr	Gln	Lys	Met	Ile	Ile	Lys	Lys	Val	Asn	Ala	Ala
			100					105					110		
Gly	Lys	Val	Val	Ile	Thr	Ala	Thr	Asn	Met	Leu	Glu	Thr	Met	Thr	Glu
		115				120						125			
Lys	Pro	Arg	Ala	Thr	Arg	Ser	Glu	Val	Ser	Asp	Val	Phe	Asn	Ala	Val
	130				135						140				
Ile	Asp	Gly	Thr	Asp	Ala	Thr	Met	Leu	Ser	Gly	Glu	Ser	Ala	Asn	Gly
145					150					155					160
Lys	Tyr	Pro	Leu	Glu	Ser	Val	Thr	Thr	Met	Ala	Thr	Ile	Asp	Lys	Asn
			165					170						175	
Ala	Gln	Ala	Leu	Leu	Asn	Glu	Tyr	Gly	Arg	Leu	Asp	Ser	Asp	Ser	Phe
		180					185					190			
Glu	Arg	Asn	Ser	Lys	Thr	Glu	Val	Met	Ala	Ser	Ala	Val	Lys	Asp	Ala
	195					200						205			
Thr	Ser	Ser	Met	Asp	Ile	Lys	Leu	Val	Val	Thr	Leu	Thr	Lys	Thr	Gly
	210				215						220				
His	Thr	Ala	Arg	Leu	Ile	Ser	Lys	Tyr	Arg	Pro	Asn	Ala	Asp	Ile	Leu
225				230						235					240
Ala	Leu	Thr	Phe	Asp	Glu	Leu	Thr	Glu	Arg	Gly	Leu	Met	Leu	Asn	Trp
			245					250						255	
Gly	Val	Ile	Pro	Met	Leu	Thr	Asp	Ala	Pro	Ser	Ser	Thr	Asp	Asp	Met
		260					265						270		
Phe	Glu	Ile	Ala	Glu	Arg	Lys	Ala	Val	Glu	Ala	Gly	Leu	Val	Glu	Ser
	275					280						285			
Gly	Asp	Asp	Ile	Val	Ile	Val	Ala	Gly	Val	Pro	Val	Gly	Glu	Ala	Val
	290				295						300				
Arg	Thr	Asn	Thr	Met	Arg	Ile	Arg	Thr	Val	Arg					
305				310						315					

(2) INFORMATION FOR SEQ ID NO:2927:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 80 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...80
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2927:

```

Lys Thr Arg Leu Glu Glu Met Ile Phe Asp Thr His Thr His Leu Asn
1          5          10          15
Val Glu Glu Phe Ala Gly Arg Glu Ala Glu Glu Ile Ala Leu Ala Asp
20          25          30
Glu Met Gly Val Thr Gln Met Asn Ile Val Gly Phe Asp Ile Pro Thr
35          40          45
Ile Glu Arg Ala Leu Glu Leu Val Asp Glu Tyr Glu Gln Leu Tyr Ala
50          55          60
Thr Ile Gly Trp His Pro Thr Glu Ala Gly Ile Tyr Thr Val Gly Ser
65          70          75          80

```

(2) INFORMATION FOR SEQ ID NO:2928:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 421 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...421
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2928:

```

Lys Lys Arg Phe Tyr Met Leu Ser Ser Lys Asp Ile Ile Lys Ala His
1          5          10          15
Lys Val Leu Asn Gly Val Val Val Asn Thr Pro Leu Asp Tyr Asp His
20          25          30
Tyr Leu Ser Glu Lys Tyr Gly Ala Lys Ile Tyr Leu Lys Lys Glu Asn
35          40          45
Ala Gln Arg Val Arg Ser Phe Lys Ile Arg Gly Ala Tyr Tyr Ala Ile

```

50					55					60					
Ser	Gln	Leu	Ser	Lys	Glu	Glu	Arg	Glu	Arg	Gly	Val	Val	Cys	Ala	Ser
65					70					75					80
Ala	Gly	Asn	His	Ala	Gln	Gly	Val	Ala	Tyr	Thr	Cys	Asn	Glu	Met	Lys
				85					90					95	
Ile	Pro	Ala	Thr	Ile	Phe	Met	Pro	Ile	Thr	Thr	Pro	Gln	Gln	Lys	Ile
			100					105				110			
Gly	Gln	Val	Arg	Phe	Phe	Gly	Gly	Asp	Phe	Val	Thr	Ile	Lys	Leu	Val
	115					120						125			
Gly	Asp	Thr	Phe	Asp	Ala	Ser	Ala	Lys	Ala	Ala	Gln	Glu	Phe	Thr	Val
	130					135					140				
Ser	Glu	Asn	Arg	Thr	Phe	Ile	Asp	Pro	Phe	Asp	Asp	Ala	His	Val	Gln
145					150					155					160
Ala	Gly	Gln	Gly	Thr	Val	Ala	Tyr	Glu	Ile	Leu	Glu	Glu	Ala	Arg	Lys
				165				170						175	
Glu	Ser	Ile	Asp	Phe	Asp	Ala	Val	Leu	Val	Pro	Val	Gly	Gly	Gly	Gly
			180					185				190			
Leu	Ile	Ala	Gly	Val	Ser	Thr	Tyr	Ile	Lys	Glu	Thr	Ser	Pro	Glu	Ile
	195						200					205			
Glu	Val	Ile	Gly	Val	Glu	Ala	Asn	Gly	Ala	Arg	Ser	Met	Lys	Ala	Ala
	210					215					220				
Phe	Glu	Ala	Gly	Gly	Pro	Val	Lys	Leu	Lys	Glu	Ile	Asp	Lys	Phe	Ala
225					230					235					240
Asp	Gly	Ile	Ala	Val	Gln	Lys	Val	Gly	Gln	Leu	Thr	Tyr	Glu	Ala	Thr
			245					250						255	
Arg	Gln	His	Ile	Lys	Thr	Leu	Val	Gly	Val	Asp	Glu	Gly	Leu	Ile	Ser
			260					265					270		
Glu	Thr	Leu	Ile	Asp	Leu	Tyr	Ser	Lys	Gln	Gly	Ile	Val	Ala	Glu	Pro
	275						280					285			
Ala	Gly	Ala	Ala	Ser	Ile	Ala	Ser	Leu	Glu	Val	Leu	Ala	Glu	Tyr	Ile
	290					295					300				
Lys	Gly	Lys	Thr	Ile	Cys	Cys	Ile	Ile	Ser	Gly	Gly	Asn	Asn	Asp	Ile
305					310					315					320
Asn	Arg	Met	Pro	Glu	Met	Glu	Glu	Arg	Ala	Leu	Ile	Tyr	Asp	Gly	Ile
			325					330						335	
Lys	His	Tyr	Phe	Val	Val	Asn	Phe	Pro	Gln	Arg	Pro	Gly	Ala	Leu	Arg
			340					345					350		
Glu	Phe	Val	Asn	Asp	Ile	Leu	Gly	Pro	Asn	Asp	Asp	Ile	Thr	Arg	Phe
	355						360					365			
Glu	Tyr	Ile	Lys	Arg	Ala	Ser	Lys	Gly	Thr	Gly	Pro	Val	Leu	Ile	Gly
	370					375					380				
Ile	Ala	Leu	Ala	Asp	Lys	His	Asp	Tyr	Ala	Gly	Leu	Ile	Arg	Arg	Met
385					390					395					400
Glu	Gly	Phe	Asp	Pro	Ala	Tyr	Ile	Asn	Leu	Asn	Gly	Asn	Glu	Thr	Leu
			405					410						415	
Tyr	Asn	Met	Leu	Val											
			420												

(2) INFORMATION FOR SEQ ID NO:2929:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...66

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2929:

```
His Ser Ile Thr Ile Tyr Tyr Leu Ile Lys Lys Glu Asn His Asn Met
1           5           10           15
Asp Lys Lys Gln Asn Leu Thr Ser Phe Gln Glu Leu Thr Thr Thr Glu
          20           25           30
Leu Asn Gln Ile Ile Gly Gly Gly Trp Trp Glu Asp Phe Leu Tyr Arg
          35           40           45
Phe Asn Ile Ile Glu Gln Lys Asn Thr Lys Gly Phe Tyr Gln Pro Ile
          50           55           60
Gln Leu
65
```

(2) INFORMATION FOR SEQ ID NO:2930:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...114

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2930:

```
Ala Asn Ile Thr Lys Lys Arg Arg Asn Thr Met Ala Lys Ala Ile Thr
1           5           10           15
Asp Ala Thr Phe Glu Gln Glu Thr Lys Asp Gly Leu Val Leu Val Asp
          20           25           30
Phe Trp Ala Thr Trp Cys Gly Pro Cys Arg Met Gln Gly Pro Ile Leu
          35           40           45
Asp Lys Leu Ser Glu Glu Leu Ser Glu Asp Val Leu Lys Ile Val Lys
          50           55           60
Met Asp Val Asp Glu Asn Pro Asn Thr Ala Arg Ala Phe Gly Ile Met
          65           70           75           80
Ser Ile Pro Thr Leu Leu Phe Lys Lys Asp Gly Gln Val Val Lys Gln
          85           90           95
Val Ala Gly Val His Thr Ala Glu Gln Ile Lys Ala Ile Ile Ala Glu
          100          105          110
Leu Ser
```

(2) INFORMATION FOR SEQ ID NO:2931:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...178

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2931:

Lys	Arg	Ile	Thr	Ser	Pro	Lys	Asp	Val	Ser	Ala	Gln	Ile	Thr	Ile	Asn
1				5				10						15	
His	Lys	Lys	Ala	Arg	Tyr	Val	Arg	Ile	Glu	Leu	Glu	Gly	Tyr	Asn	Ala
			20				25						30		
Leu	Ser	Leu	Ala	Glu	Val	Glu	Val	Phe	Arg	Phe	Ile	Ala	Thr	Asn	Gly
		35					40				45				
Glu	Thr	Ala	Ile	Gln	Val	Ser	Lys	Pro	Val	Gln	Pro	Ile	Ser	Gln	Thr
	50					55				60					
Pro	Val	Lys	Asp	Lys	Thr	Leu	Thr	Ile	Gln	His	Ser	Gly	Ala	Tyr	Ile
65				70					75					80	
Ala	Arg	Tyr	Ser	Ile	Thr	Trp	Glu	Glu	Val	Pro	Val	Asp	Lys	Asp	Gly
			85						90					95	
Asn	Gln	Val	Val	Arg	Ser	His	Ser	Trp	Glu	Gly	Asn	Gly	Arg	Asn	Gln
		100						105					110		
Thr	Ala	Gly	Phe	Val	Leu	Asn	Leu	Pro	Ile	Lys	Glu	Asn	Met	Arg	Asn
	115						120					125			
Leu	Arg	Val	Lys	Ile	Glu	Lys	Lys	Thr	Gly	Leu	Leu	Trp	Asn	Arg	Trp
	130					135					140				
Gln	Thr	Ile	Tyr	Glu	Asn	Arg	Pro	Ile	Leu	Ala	Gln	Pro	His	Arg	Lys
145					150					155				160	
Ile	Thr	His	Trp	Gly	Thr	Ile	Leu	Asn	Ser	Lys	Val	Ser	Asp	Asp	Asp
			165					170						175	
Val	Leu														

(2) INFORMATION FOR SEQ ID NO:2932:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2932:

```

Glu Arg Arg Leu Glu Glu Met Ile Ile Thr Lys Ile Ser Arg Leu Gly
1          5          10          15
Thr Tyr Val Gly Val Asn Pro His Phe Ala Thr Leu Ile Asp Phe Leu
20          25          30
Glu Lys Thr Gly Leu Glu Asn Leu Thr Glu Gly Ser Ile Ala Ile Asp
35          40          45
Gly Asn Arg Leu Phe Gly Asn Cys Phe Thr Tyr Leu Ala Asp Gly Gln
50          55          60
Ala Gly Ala Phe Phe Glu Thr His Gln Lys Tyr Leu Asp Ile His Leu
65          70          75          80
Val Leu Glu Asn Glu Glu Ala Met Ala Val Thr Ser Pro Glu Asn Val
85          90          95
Ser Val Thr Gln Glu Tyr Asp Glu Glu Lys Asp Ile Glu Leu Tyr Thr
100         105         110
Gly Lys Val Glu Gln Leu Val His Leu Arg Ala Gly Glu Cys Leu Ile
115         120         125
Thr Phe Pro Glu Asp Leu His Gln Pro Lys Val Arg Ile Asn Asp Glu
130         135         140
Pro Val Lys Lys Val Val Phe Lys Val Ala Ile Ser
145         150         155

```

(2) INFORMATION FOR SEQ ID NO:2933:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 79 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...79

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2933:

```

Ser His Ser Thr Thr Cys Lys Cys Pro Cys Leu Gly Cys Leu Gly Thr
1          5          10          15
Thr Trp Arg Cys Cys Asp Leu Ser Arg Ser Gly Arg Lys Ser Ile Cys
20          25          30
Thr Arg Asp Cys Cys Gly Asn Cys Gln Trp Cys Ile Cys Ser Tyr Cys
35          40          45

```

Arg	Asn	Ser	Ser	Leu	Thr	Cys	Leu	Cys	Arg	Asn	Pro	Asn	Ser	Cys	Arg
50						55					60				
Lys	Phe	Glu	Lys	Gly	Leu	Ile	Leu	Asn	Glu	Asn	Gln	Arg	Ala	Asn	
65					70				75						

(2) INFORMATION FOR SEQ ID NO:2934:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 222 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...222

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2934:

Glu	Asn	Ser	Thr	Arg	Arg	Thr	Trp	Asn	Pro	Leu	Leu	Ser	Lys	Leu	Ser
1				5					10					15	
Lys	Gly	Gly	Leu	Met	Gly	Lys	Ile	Ile	Gly	Ile	Thr	Gly	Gly	Ile	Ala
			20					25					30		
Ser	Gly	Lys	Ser	Thr	Val	Thr	Asn	Phe	Leu	Lys	His	Gln	Gly	Leu	Ser
		35					40					45			
Ser	Ser	Gly	Leu	Pro	Thr	Gln	Cys	Ser	Thr	Asn	Tyr	Arg	Lys	Pro	Gly
		50				55					60				
Gly	Arg	Leu	Phe	Glu	Ala	Leu	Val	Gln	His	Phe	Gly	Gln	Glu	Ile	Ile
65					70				75					80	
Leu	Glu	Asn	Gly	Glu	Leu	Asn	Arg	Pro	Leu	Ile	Ala	Ser	Leu	Ile	Phe
			85					90						95	
Ser	Asn	Pro	Glu	Glu	Gln	Lys	Trp	Ser	Asn	Gln	Ile	Gln	Gly	Glu	Ile
		100						105					110		
Ile	Arg	Glu	Glu	Leu	Ala	Thr	Leu	Arg	Glu	Gln	Leu	Ala	Gln	Thr	Glu
		115					120					125			
Glu	Ile	Phe	Phe	Met	Asp	Ile	Pro	Leu	Leu	Phe	Glu	Gln	Asp	Tyr	Ser
		130				135					140				
Asp	Trp	Phe	Ala	Glu	Thr	Trp	Leu	Val	Tyr	Val	Asp	Arg	Asp	Ala	Gln
145					150				155						160
Val	Glu	Arg	Leu	Met	Lys	Arg	Asp	Gln	Leu	Ser	Lys	Asp	Glu	Ala	Glu
			165					170						175	
Ser	Arg	Met	Ala	Ala	Gln	Trp	Pro	Leu	Glu	Lys	Lys	Lys	Asp	Leu	Ala
		180					185						190		
Ser	Gln	Val	Leu	Asp	Asn	Asn	Gly	Asn	Gln	Asn	Gln	Leu	Leu	Asn	Gln
		195				200						205			
Val	His	Ile	Leu	Leu	Glu	Gly	Gly	Arg	Gln	Asp	Asp	Arg	Asp		
	210					215					220				

(2) INFORMATION FOR SEQ ID NO:2935:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 137 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...137

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2935:

Thr	Leu	Ser	Thr	Asp	Ser	Arg	Arg	Arg	Lys	Asn	Ala	Gly	Arg	Asn	Gln
1				5					10					15	
Arg	Lys	Gln	Arg	Ile	Lys	Glu	Lys	Pro	Met	Gln	Val	Ile	Lys	Arg	Asn
			20					25					30		
Gly	Glu	Ile	Ala	Glu	Phe	Asn	Pro	Asp	Lys	Ile	Tyr	Gln	Ala	Ile	Leu
		35				40						45			
Lys	Ala	Ala	Gln	Thr	Val	Tyr	Val	Leu	Thr	Asp	Asp	Leu	Arg	Gln	Asn
	50				55					60					
Leu	Ala	Gln	Val	Thr	Lys	Lys	Val	Val	Leu	Asp	Leu	Gln	Glu	Ala	Lys
65					70					75					80
Val	Glu	Arg	Ala	Thr	Ile	Ser	Met	Ile	Gln	Ser	Met	Val	Glu	His	Arg
				85					90					95	
Leu	Leu	Gly	Ala	Gly	Tyr	Ile	Thr	Ile	Ala	Glu	His	Tyr	Ile	Ser	Tyr
		100						105					110		
Arg	Leu	Gln	Arg	Asp	Leu	Glu	Arg	Ser	Gly	Tyr	Gly	Asp	His	Ile	Ala
		115					120					125			
Val	His	Leu	His	Phe	Glu	Gln	Ile	Arg							
		130					135								

(2) INFORMATION FOR SEQ ID NO:2936:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 212 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2936:

Lys Glu Ser Thr Met Glu Cys Lys Lys Leu Asn Ile Trp Thr Ala Ser

1				5				10					15			
Ser	Phe	Phe	Ile	Phe	Leu	Thr	Tyr	Leu	Val	Phe	Leu	Val	Tyr	Pro	Ile	
			20					25					30			
Val	Thr	Val	Leu	Lys	Gln	Ala	Leu	Ile	His	Glu	Gly	Gln	Phe	Ser	Leu	
		35					40					45				
Ala	Asn	Phe	Val	Thr	Phe	Phe	Ser	Lys	Val	Tyr	Tyr	Ser	Glu	Thr	Leu	
	50					55				60						
Val	Asn	Ser	Phe	Lys	Val	Ser	Ile	Thr	Ala	Thr	Val	Thr	Ser	Leu	Val	
65				70					75					80		
Val	Gly	Thr	Leu	Leu	Ala	Tyr	Leu	Phe	Ser	Met	Tyr	Asp	Phe	Lys	Gly	
			85					90					95			
Lys	Lys	Phe	Leu	Gln	Ile	Leu	Ile	Ile	Ile	Ala	Ser	Met	Ser	Ala	Pro	
		100					105						110			
Phe	Val	Gly	Ala	Tyr	Ser	Trp	Val	Leu	Leu	Leu	Gly	Arg	Asn	Gly	Val	
	115					120						125				
Ile	Thr	Lys	Phe	Leu	Thr	Asn	Ala	Leu	His	Leu	Pro	Ala	Ile	Asp	Ile	
	130				135						140					
Tyr	Gly	Phe	Lys	Gly	Ile	Val	Leu	Val	Phe	Thr	Leu	Gln	Leu	Phe	Pro	
145				150					155					160		
Leu	Val	Phe	Leu	Tyr	Val	Ala	Glu	Thr	Met	Asn	Ser	Ile	Asp	Asn	Ser	
			165					170						175		
Leu	Leu	Glu	Ala	Glu	Ser	Met	Gly	Ser	Phe	Gly	Phe	Lys	Pro	Ile		
		180					185					190				
Val	Thr	Val	Val	Leu	Pro	Leu	Leu	Val	Pro	Thr	Leu	Leu	Ala	Ala	Pro	
	195					200						205				
Cys	Leu	Tyr	Leu													
	210															

(2) INFORMATION FOR SEQ ID NO:2937:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2937:

Lys	Lys	Pro	Thr	Phe	Ile	Ile	Val	Met	Ile	Gly	Ile	Ser	Leu	Ile	Pro	
1				5				10					15			
Asp	Leu	Tyr	Asn	Ile	Ile	Phe	Leu	Ser	Ser	Met	Trp	Asp	Pro	Tyr	Gly	
		20					25					30				
Gln	Leu	Ser	Asp	Leu	Pro	Val	Ala	Val	Val	Asn	Asn	Asp	Lys	Glu	Ala	
	35					40						45				
Ser	Tyr	Asn	Gly	Asn	Thr	Met	Ala	Ile	Gly	Lys	Asp	Met	Val	Ser	Asn	
	50			55							60					
Leu	Lys	Glu	Asn	Lys	Thr	Leu	Asp	Phe	His	Phe	Val	Asp	Glu	Glu	Glu	

65					70					75					80
Gly	Lys	Lys	Gly	Leu	Glu	Asp	Gly	Asp	Tyr	Tyr	Met	Val	Val	Thr	Leu
				85					90					95	
Pro	Ser	Asp	Leu	Ser	Asp	Lys	Thr	Thr	Leu	Ser	Asn	Ile	Gln	Ser	
			100					105				110			
Thr	Ala	Ala	Tyr	Gln	Ser	Leu	Thr	Ser	Glu	Gln	Gln	Thr	Glu	Ile	Ser
		115					120					125			
Asp	Ser	Val	Ser	Gln	Asn	Ser	Thr	Asp	Ser	Ile	Gln	Ser	Ala	Gln	Ser
		130				135					140				
Ile	Val	Ala	Leu	Val	Gln	Asp	Leu	Gln	Gly	Ser	Leu	Glu	Asn	Leu	Gln
145					150				155					160	
Asn	Gln	Ser	Ser	Asn	Leu	Ser	Thr	Leu	Lys	Asn	Gln	Ala	Asn	Gln	Val
				165					170					175	
Ser	Pro	Ile	Thr	Ser	Thr	Ser	Leu	Ile	Gly	Leu	Ser	Ser	Gly	Leu	Thr
			180					185					190		
Glu	Ile	Gln	Gly	Asp	Val	Thr	Ser	Lys	Leu	Val	Pro	Ala	Ser	Gln	Ser
		195					200				205				
Ile	Ala	Ser	Gly	Val	Asn	Ala	Tyr	Thr	Thr	Gly	Val	Asp	Lys	Val	Ser
	210				215					220					
Gln	Gly	Ala	Ser	Gln	Leu	Ser	Glu	Lys	Asn	Ala	Thr	Leu	Thr	Gly	Ser
225					230				235					240	
Leu	Asp	Lys	Leu	Val	Ser	Gly	Ser	Asn	Thr	Leu	Thr	Gln	Lys	Ser	Ser
			245					250						255	
Arg	Leu	Thr	Ala	Gly	Val	Gly									
			260												

(2) INFORMATION FOR SEQ ID NO:2938:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 72 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...72
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2938:

Ser	Ile	Gly	Phe	Tyr	Ser	Thr	Arg	Lys	Gln	Gly	Gln	Glu	Asn	Phe	Gln
1				5				10						15	
Glu	Glu	Asn	Asp	Ser	Arg	Gln	Val	Ile	Leu	Thr	Val	Thr	Gln	Ile	Ile
			20					25					30		
Glu	Arg	Leu	Tyr	Pro	Met	Phe	Leu	Asp	Ile	Glu	Gly	Lys	Pro	Leu	Asp
		35				40					45				
Phe	Trp	Asp	Leu	Thr	Val	Leu	Glu	Ile	Arg	Glu	Met	Ile	Glu	Ser	Tyr
	50				55					60					
Asn	Arg	Val	Lys	Ile	Gln	Glu	Arg								
65					70										

(2) INFORMATION FOR SEQ ID NO:2939:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...458

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2939:

Arg	Gly	Ala	Thr	Ser	Tyr	Gly	Asp	Ser	Pro	Tyr	Gln	Ser	Phe	Ser	Ala
1				5					10					15	
Phe	Ala	Gly	Asn	Thr	His	Phe	Ile	Asp	Leu	Asp	Ile	Leu	Val	Glu	Gln
			20					25					30		
Gly	Leu	Leu	Glu	Ala	Ser	Asp	Leu	Glu	Gly	Val	Asp	Phe	Gly	Ser	Asp
		35					40					45			
Ala	Ser	Glu	Val	Asp	Tyr	Ala	Lys	Ile	Tyr	Tyr	Ala	Arg	Arg	Pro	Leu
	50					55					60				
Leu	Glu	Lys	Ala	Val	Lys	Arg	Phe	Phe	Glu	Val	Gly	Asp	Val	Lys	Asp
65					70				75					80	
Phe	Glu	Lys	Phe	Ala	Gln	Asp	Asn	Gln	Ser	Trp	Leu	Glu	Leu	Phe	Ala
			85					90						95	
Glu	Tyr	Met	Ala	Ile	Lys	Glu	His	Phe	Asp	Asn	Leu	Ala	Trp	Thr	Glu
			100					105					110		
Trp	Pro	Asp	Ala	Asp	Ala	Arg	Ala	Arg	Lys	Ala	Ser	Ala	Leu	Glu	Ser
		115				120						125			
Tyr	Arg	Glu	Gln	Leu	Ala	Asp	Lys	Leu	Val	Tyr	His	Arg	Val	Thr	Gln
	130					135					140				
Tyr	Phe	Phe	Phe	Gln	Gln	Trp	Leu	Lys	Leu	Lys	Ala	Tyr	Ala	Asn	Asp
145				150					155					160	
Asn	His	Ile	Glu	Ile	Val	Gly	Asp	Met	Pro	Ile	Tyr	Val	Ala	Glu	Asp
			165					170						175	
Ser	Ser	Asp	Met	Trp	Ala	Asn	Pro	His	Leu	Phe	Lys	Thr	Asp	Val	Asn
			180					185					190		
Gly	Lys	Ala	Thr	Cys	Ile	Ala	Gly	Cys	Pro	Pro	Asp	Glu	Phe	Ser	Val
		195					200					205			
Thr	Gly	Gln	Leu	Trp	Gly	Asn	Pro	Ile	Tyr	Asp	Trp	Glu	Ala	Met	Asp
	210					215					220				
Lys	Asp	Gly	Tyr	Lys	Trp	Trp	Ile	Glu	Arg	Leu	Arg	Glu	Ser	Phe	Lys
225				230					235					240	
Ile	Tyr	Asp	Ile	Val	Arg	Ile	Asp	His	Phe	Arg	Gly	Phe	Glu	Ser	Tyr
			245					250						255	
Trp	Glu	Ile	Pro	Ala	Gly	Ser	Asp	Thr	Ala	Ala	Pro	Gly	Glu	Trp	Val
		260						265					270		
Lys	Gly	Pro	Gly	Tyr	Lys	Leu	Phe	Ala	Ala	Val	Lys	Glu	Glu	Leu	Gly
	275					280						285			
Glu	Leu	Asn	Ile	Ile	Ala	Glu	Asp	Leu	Gly	Phe	Met	Thr	Asp	Glu	Val

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...159

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2941:

```
Val Val Gln Thr Arg Gly Thr Gly Leu Lys Phe Val Lys Glu Val Ile
1           5           10           15
Asn Trp Asn Tyr Glu Ser Tyr Asn Ser Gly His Gly Arg Lys Phe Ile
          20          25          30
Phe Lys Arg Ile Ile Glu Ala Arg Leu Thr Ile Ser Asn Ser Pro Phe
          35          40          45
Val Gln Arg Arg Tyr Gln Ile Lys Pro Glu Ala Phe Tyr Val Leu Phe
          50          55          60
Lys Glu Leu Thr Ala Pro Ile Pro Leu Asn Thr Asp Phe Pro Ile Phe
65          70          75          80
Ala Ala Asp Gly Ser Asp Ile Ser Ile Pro Arg Asn Pro Met Asp Thr
          85          90          95
Glu Thr Tyr Ile Gln Thr Gln Thr Asp Val Lys Ser Tyr Asn Leu Ile
          100         105         110
His Ile Asn Ala Leu Tyr Asp Leu Thr Thr Gly Val Tyr Arg Asp Val
          115         120         125
Ser Ile Gln Asp Lys His Ala Gln His Glu Arg Leu Ala Leu Ile Gln
          130         135         140
Met Met Glu Ala Ser Pro Phe Arg Glu Ser Ser Cys Tyr His Gly
145          150          155
```

(2) INFORMATION FOR SEQ ID NO:2942:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 118 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...118

(xi) SEQUENCE DESCRIPTION: SEO ID NO:2942:

[illegible]

(2) INFORMATION FOR SEQ ID NO:2943:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 124 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...124

(xi) SEQUENCE DESCRIPTION: SEO ID NO:2943:

Val	Trp	Gln	Thr	Tyr	Arg	Arg	Thr	Leu	Leu	Ser	Ser	Ser	Lys	Pro	Glu
1				5					10					15	
Leu	Ser	Gln	Lys	Thr	Asn	Thr	Glu	Glu	Asn	Ile	Met	Leu	Lys	Met	Thr
			20					25					30		
Leu	Asn	Asn	Leu	Gln	Leu	Phe	Ala	His	Lys	Lys	Gly	Gly	Gly	Ser	Thr
			35				40					45			
Ser	Asn	Gly	Arg	Asp	Ser	Gln	Ala	Lys	Arg	Leu	Gly	Ala	Lys	Ala	Ala
			50			55				60					
Asp	Gly	Gln	Thr	Val	Thr	Gly	Gly	Ser	Ile	Leu	Tyr	Arg	Gln	Arg	Gly
65					70				75					80	
Thr	His	Ile	Tyr	Pro	Gly	Val	Asn	Val	Gly	Arg	Gly	Gly	Asp	Asp	Thr
				85					90				95		
Leu	Phe	Ala	Lys	Val	Glu	Gly	Val	Val	Arg	Phe	Glu	Arg	Lys	Gly	Arg
			100					105					110		
Asp	Lys	Lys	Gln	Val	Ser	Val	Tyr	Pro	Ile	Ala	Lys				
			115				120								

(2) INFORMATION FOR SEQ ID NO:2944:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 806 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...806
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2944:

Ser	Tyr	Lys	Thr	Ser	Tyr	Thr	Lys	Asp	Leu	Arg	Arg	Leu	Leu	Gln	Val
1				5					10					15	
Phe	Phe	Phe	Cys	Pro	Lys	Gln	Ile	Tyr	Ser	Phe	Lys	Leu	Tyr	Gln	Thr
			20					25					30		
Leu	Ile	Phe	Tyr	Asn	Tyr	Thr	Asp	Ala	Phe	Phe	Ser	Val	Lys	Ile	Val
			35				40					45			
Ser	Thr	Thr	Asn	Phe	Gly	Gly	His	Ile	Met	Ser	Thr	Thr	Ile	Val	Gly
			50				55				60				
Phe	Pro	Arg	Leu	Gly	Glu	Phe	Arg	Glu	Leu	Lys	Phe	Thr	Thr	Glu	Lys
65					70					75					80
Tyr	Phe	Arg	Lys	Glu	Ile	Ser	Glu	Glu	Glu	Leu	Leu	Ala	Ala	Ala	Lys
				85					90					95	
Asp	Leu	Arg	Ala	Lys	His	Trp	Asn	Ile	Val	Lys	Glu	Lys	Gly	Ile	Thr
			100				105						110		
Glu	Ile	Pro	Ser	Asn	Asp	Phe	Ser	His	Tyr	Asp	Asn	Phe	Leu	Asp	Ala
			115				120					125			
Ala	Phe	Leu	Phe	Asn	Val	Val	Pro	Ala	Ser	Val	Gln	Asn	Leu	Asp	Leu
			130			135					140				
Ser	Asp	Leu	Glu	Arg	Tyr	Phe	Ala	Leu	Gly	Arg	Gly	Tyr	Gln	Gly	Glu
145					150					155					160
Lys	Gly	Asp	Val	Arg	Ala	Leu	Pro	Met	Lys	Lys	Trp	Phe	Asn	Thr	Asn
				165					170					175	
Tyr	His	Tyr	Ile	Val	Pro	Lys	Phe	Glu	Lys	Asp	Thr	Gln	Val	Lys	Leu
			180					185					190		
Ala	Gly	His	Lys	Ile	Phe	Asp	Glu	Phe	Gln	Glu	Ala	Lys	Glu	Ile	Gly
			195			200						205			
Leu	Asn	Thr	Arg	Pro	Val	Leu	Val	Gly	Pro	Phe	Thr	Phe	Leu	Gln	Leu
			210			215					220				
Ser	Asp	Phe	Glu	Glu	Gly	Val	Lys	Ala	Asp	Asp	Phe	Val	Asp	Ser	Leu
225					230					235					240
Val	Ala	Ala	Tyr	Gln	Glu	Val	Phe	Ala	Lys	Leu	Ala	Glu	Leu	Gly	Ala
				245					250					255	
Thr	Cys	Ile	Gln	Leu	Asp	Glu	Ala	Ala	Leu	Val	Lys	Asp	Leu	Thr	Ala
			260				265						270		
Glu	Glu	Lys	Ala	Leu	Phe	Leu	Asn	Leu	Tyr	Asn	Lys	Leu	Leu	Ala	Asp
			275				280					285			
Lys	Lys	Gly	Leu	Glu	Val	Leu	Leu	Gln	Thr	Tyr	Phe	Gly	Asp	Val	Arg
			290			295					300				

Asp	Val	Tyr	Ala	Asp	Leu	Val	Asn	Leu	Pro	Val	Asp	Ala	Ile	Gly	Phe
305					310					315					320
Asp	Phe	Val	Glu	Gly	Lys	Lys	Thr	Leu	Glu	Leu	Val	Lys	Gly	Gly	Phe
				325					330						335
Pro	Ala	Asp	Lys	Thr	Leu	Tyr	Ala	Gly	Ile	Val	Asn	Gly	Lys	Asn	Ile
			340					345						350	
Trp	Arg	Asn	Asn	Tyr	Glu	Lys	Ser	Leu	Ala	Val	Leu	Glu	Gln	Ile	Pro
		355					360						365		
Ala	Glu	Asn	Ile	Val	Leu	Thr	Ser	Ser	Cys	Ser	Leu	Leu	His	Val	Pro
	370					375						380			
Phe	Thr	Thr	Ala	Asn	Glu	Glu	Phe	Glu	Pro	Ala	Leu	Leu	Asn	His	Phe
385					390					395					400
Ala	Phe	Ala	Val	Glu	Lys	Leu	Asp	Glu	Ile	Arg	Asp	Leu	Asp	Ala	Ile
				405					410					415	
Arg	Asn	Gly	Gln	Gly	Ser	Glu	Ala	Leu	Ala	Ala	Asn	Lys	Glu	Leu	Phe
		420						425					430		
Ala	Thr	Glu	Arg	Val	Gly	Glu	Asn	Ala	Glu	Leu	Arg	Ala	Arg	Ile	Ala
	435						440					445			
Gly	Leu	Thr	Asp	Thr	Asp	Tyr	Thr	Arg	Leu	Pro	Ala	Phe	Ala	Glu	Arg
	450				455						460				
Glu	Ala	Ile	Gln	Glu	Glu	Ala	Phe	Lys	Leu	Pro	Ala	Leu	Pro	Thr	Thr
465					470					475					480
Thr	Ile	Gly	Ser	Phe	Pro	Gln	Thr	Lys	Glu	Val	Arg	Ala	Lys	Arg	Leu
			485						490					495	
Ala	Tyr	Arg	Lys	Gly	Glu	Leu	Ser	Gln	Lys	Glu	Tyr	Asp	Ala	Phe	Leu
			500					505					510		
Ala	Glu	Thr	Ile	Asp	Glu	Trp	Ile	Lys	Trp	Gln	Glu	Asp	Ile	Asp	Phe
	515						520					525			
Asp	Val	Leu	Val	His	Gly	Glu	Phe	Glu	Arg	Asn	Asp	Met	Val	Glu	Tyr
530					535						540				
Phe	Gly	Gln	Asn	Leu	Ser	Gly	Tyr	Leu	Phe	Ser	Lys	Asn	Gly	Trp	Val
545					550					555					560
Gln	Ser	Tyr	Gly	Met	Arg	Gly	Val	Lys	Pro	Pro	Ile	Ile	Trp	Gly	Asp
			565						570					575	
Val	Thr	Arg	Leu	Asn	Pro	Ile	Thr	Val	Lys	Trp	Ser	Ser	Tyr	Ala	Gln
			580					585					590		
Ser	Arg	Thr	Asn	Lys	Pro	Val	Lys	Gly	Met	Leu	Thr	Gly	Pro	Val	Thr
	595						600					605			
Ile	Leu	Asn	Trp	Ser	Phe	Pro	Arg	Glu	Asp	Ile	Ser	Ile	Lys	Asp	Ser
610					615						620				
Thr	Leu	Gln	Ile	Ala	Leu	Ala	Ile	Lys	Asp	Glu	Val	Leu	Asp	Leu	Glu
625					630					635					640
Ala	Ala	Gly	Val	Lys	Ile	Ile	Gln	Ile	Asp	Glu	Ala	Ala	Leu	Arg	Glu
			645						650					655	
Lys	Leu	Pro	Leu	Arg	Arg	Ser	Asp	Trp	Tyr	Glu	Asp	Tyr	Leu	Asp	Trp
			660				665						670		
Ala	Ile	Pro	Ala	Phe	Arg	Leu	Val	His	Ser	Thr	Val	Ala	Pro	Asp	Thr
	675						680					685			
Gln	Ile	His	Thr	His	Met	Cys	Tyr	Ser	Glu	Phe	Thr	Asp	Ile	Ile	Pro
690					695						700				
Ala	Ile	Asp	Asn	Met	Asp	Ala	Asp	Val	Ile	Ser	Phe	Glu	Ala	Ser	Arg
705					710				715						720
Ser	Asn	Leu	Glu	Ile	Leu	Asp	Glu	Leu	Lys	Ala	Lys	Asn	Phe	Gln	Thr
			725						730					735	
Glu	Val	Gly	Pro	Gly	Val	Tyr	Asp	Ile	His	Ser	Pro	Arg	Val	Pro	Asn
			740				745					750			
Glu	Gly	Glu	Ile	Asp	Asn	Thr	Ile	Glu	Ala	Ile	Leu	Ala	Lys	Val	Pro

	755					760						765							
Ser	Lys	Lys	Val	Trp	Ile	Asn	Pro	Asp	Cys	Gly	Leu	Lys	Thr	Arg	Gly				
	770					775					780								
Ile	Pro	Glu	Thr	Lys	Glu	Ser	Leu	Ile	Arg	Leu	Val	Glu	Ala	Ala	Lys				
	785				790					795					800				
Ala	Ala	Arg	Glu	Lys	Leu														
					805														

(2) INFORMATION FOR SEQ ID NO:2945:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...536

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2945:

Tyr	Gly	Lys	Thr	Asn	Ile	Asn	Arg	Lys	Arg	Phe	Leu	Glu	Cys	Leu	Phe				
1				5				10						15					
Lys	Lys	Val	Val	Gly	Phe	Leu	His	Phe	Val	Arg	His	Gln	Glu	Glu	Lys				
		20					25					30							
Gln	Met	Ser	Glu	Lys	Ala	Lys	Lys	Gly	Phe	Lys	Met	Pro	Ser	Ser	Tyr				
		35				40					45								
Thr	Val	Leu	Leu	Ile	Ile	Ile	Ala	Ile	Met	Ala	Val	Leu	Thr	Trp	Phe				
	50				55				60										
Ile	Pro	Ala	Gly	Ala	Phe	Ile	Glu	Gly	Ile	Tyr	Glu	Thr	Gln	Pro	Gln				
65				70				75						80					
Asn	Pro	Gln	Gly	Ile	Trp	Asp	Val	Leu	Met	Ala	Pro	Ile	Arg	Ala	Met				
		85				90							95						
Leu	Gly	Thr	His	Pro	Glu	Glu	Gly	Ser	Leu	Ile	Lys	Glu	Thr	Ser	Ala				
		100				105						110							
Ala	Ile	Asp	Val	Ala	Phe	Phe	Ile	Leu	Met	Val	Gly	Gly	Phe	Leu	Gly				
	115				120					125									
Ile	Val	Asn	Lys	Thr	Gly	Ala	Leu	Asp	Val	Gly	Ile	Ala	Ser	Ile	Val				
	130				135					140									
Lys	Lys	Tyr	Lys	Gly	Arg	Glu	Lys	Met	Leu	Ile	Leu	Val	Leu	Met	Pro				
145				150				155						160					
Leu	Phe	Ala	Leu	Gly	Gly	Thr	Thr	Tyr	Gly	Met	Gly	Glu	Glu	Thr	Met				
		165			170									175					
Ala	Phe	Tyr	Pro	Leu	Leu	Val	Pro	Val	Met	Met	Ala	Val	Gly	Phe	Asp				
		180			185								190						
Ser	Leu	Thr	Gly	Val	Ala	Ile	Ile	Leu	Leu	Gly	Ser	Gln	Ile	Gly	Cys				
	195				200							205							
Leu	Ala	Ser	Thr	Leu	Asn	Pro	Phe	Ala	Thr	Gly	Ile	Ala	Ser	Ala	Thr				
	210				215					220									
Ala	Gly	Val	Gly	Thr	Gly	Asp	Gly	Ile	Val	Leu	Arg	Leu	Ile	Phe	Trp				

225		230		235		240									
Val	Thr	Leu	Thr	Ala	Leu	Ser	Thr	Trp	Phe	Val	Tyr	Arg	Tyr	Ala	Asp
				245					250					255	
Lys	Ile	Gln	Lys	Asp	Pro	Thr	Lys	Ser	Leu	Val	Tyr	Ser	Thr	Arg	Lys
				260					265					270	
Glu	Asp	Leu	Lys	His	Phe	Asn	Val	Glu	Glu	Ser	Ser	Ser	Val	Glu	Ser
				275					280					285	
Thr	Leu	Ser	Ser	Lys	Gln	Lys	Ser	Val	Leu	Phe	Leu	Phe	Val	Leu	Thr
				290					295					300	
Phe	Ile	Leu	Met	Val	Leu	Ser	Phe	Ile	Pro	Trp	Thr	Asp	Leu	Gly	Val
305					310					315				320	
Thr	Ile	Phe	Asp	Asp	Phe	Asn	Ala	Trp	Leu	Thr	Gly	Leu	Pro	Val	Ile
				325					330					335	
Gly	Asn	Ile	Val	Gly	Ser	Ser	Thr	Ser	Ala	Leu	Gly	Thr	Trp	Tyr	Phe
			340						345					350	
Pro	Glu	Gly	Ala	Met	Leu	Phe	Ala	Phe	Met	Gly	Ile	Leu	Ile	Gly	Val
			355				360							365	
Ile	Tyr	Gly	Leu	Lys	Glu	Asp	Lys	Ile	Ile	Ser	Ser	Phe	Met	Asn	Gly
370					375					380					
Ala	Ala	Asp	Leu	Leu	Ser	Val	Ala	Leu	Ile	Val	Ala	Ile	Ala	Arg	Gly
385					390					395				400	
Ile	Gln	Val	Ile	Met	Asn	Asp	Gly	Met	Ile	Thr	Asp	Thr	Ile	Leu	Asn
				405					410					415	
Trp	Gly	Lys	Glu	Gly	Leu	Ser	Gly	Leu	Ser	Ser	Gln	Val	Phe	Ile	Val
			420						425					430	
Val	Thr	Tyr	Ile	Phe	Tyr	Leu	Pro	Met	Ser	Phe	Leu	Ile	Pro	Ser	Ser
			435				440							445	
Ser	Gly	Leu	Ala	Ser	Ala	Thr	Met	Gly	Ile	Met	Ala	Pro	Leu	Gly	Glu
			450				455				460				
Phe	Val	Asn	Val	Arg	Pro	Ser	Leu	Ile	Ile	Thr	Ala	Tyr	Gln	Ser	Ala
465					470					475				480	
Ser	Gly	Val	Leu	Asn	Leu	Ile	Ala	Pro	Thr	Ser	Gly	Ile	Val	Met	Gly
				485					490					495	
Ala	Leu	Ala	Leu	Gly	Arg	Ile	Asn	Ile	Gly	Thr	Trp	Trp	Lys	Phe	Met
			500				505						510		
Gly	Lys	Leu	Val	Val	Ala	Ile	Ile	Val	Val	Thr	Ile	Ala	Leu	Leu	Leu
			515				520					525			
Leu	Gly	Thr	Phe	Leu	Pro	Phe	Leu								
			530				535								

(2) INFORMATION FOR SEQ ID NO:2946:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 74 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...74

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2946:

Lys	Ser	Lys	Thr	Gln	Gly	Met	Lys	Phe	Ile	Lys	Lys	Leu	His	Lys	Ile
1				5					10					15	
Ile	Leu	Leu	Asn	Lys	Gln	Thr	Ser	Tyr	Thr	Ser	Phe	Phe	Ser	Ser	Ser
			20					25					30		
Leu	Ser	Lys	Thr	Asn	His	Phe	Ile	Leu	Phe	Glu	Asn	Gln	Ile	Gln	Thr
		35					40					45			
Thr	Ser	Thr	Ser	Pro	Cys	Arg	Thr	Gln	Val	Gln	Pro	Ala	Ala	Ser	Phe
	50				55						60				
Leu	Val	Cys	Ser	Leu	Ile	Phe	Ile	Glu	Tyr						
65					70										

(2) INFORMATION FOR SEQ ID NO:2947:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2947:

Ile	Pro	Lys	Thr	Lys	Thr	Leu	Ala	Glu	Leu	Ala	Asp	Val	Ile	Leu	Trp
1				5					10					15	
Ser	Phe	Asp	Phe	Val	Asn	Ala	His	Ala	His	Ala	Phe	Phe	Met	Asp	Asn
			20					25					30		
Val	Glu	Trp	Ser	His	Ala	Asp	Ser	Tyr	Phe	Leu	Ser	Phe	Val	Ser	Asp
		35					40					45			
Asp	Val	Glu	Glu	Arg	Tyr	Thr	Glu	Asn	Val	Tyr	Leu	Asp	Ser	Leu	Ser
	50				55						60				
Val	Lys	Gln	Lys	Phe	Lys	Phe	Leu	Phe	Asp	Phe	Gly	Asp	Glu	Trp	Arg
65					70					75				80	
Phe	Glu	Cys	Gln	Val	Leu	Arg	Glu	Ile	Glu	Thr	Glu	Asp	Glu	Glu	Ala
			85						90					95	
Tyr	Leu	Val	Arg	Ser	Val	Gly	Thr	Ser	Pro	Glu	Gln	Tyr	Pro	Asp	Tyr
		100						105					110		
Asp	Gly	Phe	Asp	Tyr	Glu	Glu	Trp								
		115					120								

(2) INFORMATION FOR SEQ ID NO:2948:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 641 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...641

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2948:

```

Met Lys Lys Thr Thr Ile Leu Ser Leu Thr Thr Ala Ala Val Ile Leu
1      5      10      15
Ala Ala Tyr Val Pro Asn Glu Pro Ile Leu Ala Asp Thr Pro Ser Ser
20      25      30
Glu Val Ile Lys Glu Thr Lys Val Gly Ser Ile Ile Gln Gln Asn Asn
35      40      45
Ile Lys Tyr Lys Val Leu Thr Val Glu Gly Asn Ile Arg Thr Val Gln
50      55      60
Val Gly Asn Gly Val Thr Pro Val Glu Phe Glu Ala Gly Gln Asp Gly
65      70      75      80
Lys Pro Phe Thr Ile Pro Thr Lys Ile Thr Val Gly Asp Lys Val Phe
85      90      95
Thr Val Thr Glu Val Ala Ser Gln Ala Phe Ser Tyr Tyr Pro Asp Glu
100     105     110
Thr Gly Arg Ile Val Tyr Tyr Pro Ser Ser Ile Thr Ile Pro Ser Ser
115     120     125
Ile Lys Lys Ile Gln Lys Lys Gly Phe His Gly Ser Lys Ala Lys Thr
130     135     140
Ile Ile Phe Asp Lys Gly Ser Gln Leu Glu Lys Ile Glu Asp Arg Ala
145     150     155     160
Phe Asp Phe Ser Glu Leu Glu Glu Ile Glu Leu Pro Ala Ser Leu Glu
165     170     175
Tyr Ile Gly Thr Ser Ala Phe Ser Phe Ser Gln Lys Leu Lys Lys Leu
180     185     190
Thr Phe Ser Ser Ser Lys Leu Glu Leu Ile Ser His Glu Ala Phe
195     200     205
Ala Asn Leu Ser Asn Leu Glu Lys Leu Thr Leu Pro Lys Ser Val Lys
210     215     220
Thr Leu Gly Ser Asn Leu Phe Arg Leu Thr Thr Ser Leu Lys His Val
225     230     235     240
Asp Val Glu Glu Gly Asn Glu Ser Phe Ala Ser Val Asp Gly Val Leu
245     250     255
Phe Ser Lys Asp Lys Thr Gln Leu Ile Tyr Tyr Pro Ser Gln Lys Asn
260     265     270
Asp Glu Ser Tyr Lys Thr Pro Lys Glu Thr Lys Glu Leu Ala Ser Tyr
275     280     285
Ser Phe Asn Lys Asn Ser Tyr Leu Lys Lys Leu Glu Leu Asn Glu Gly
290     295     300
Leu Glu Lys Ile Gly Thr Phe Ala Phe Ala Asp Ala Ile Lys Leu Glu
305     310     315     320
Glu Ile Ser Leu Pro Asn Ser Leu Glu Thr Ile Glu Arg Leu Ala Phe
325     330     335
Tyr Gly Asn Leu Glu Leu Lys Glu Leu Ile Leu Pro Asp Asn Val Lys

```

			340					345				350					
Asn	Phe	Gly	Lys	His	Val	Met	Asn	Gly	Leu	Pro	Lys	Leu	Lys	Ser	Leu		
		355					360					365					
Thr	Ile	Gly	Asn	Asn	Ile	Asn	Ser	Leu	Pro	Ser	Phe	Phe	Leu	Ser	Gly		
		370					375					380					
Val	Leu	Asp	Ser	Leu	Lys	Glu	Ile	His	Ile	Lys	Asn	Lys	Ser	Thr	Glu		
385					390					395					400		
Phe	Ser	Val	Lys	Lys	Asp	Thr	Phe	Ala	Ile	Pro	Glu	Thr	Val	Lys	Phe		
				405					410					415			
Tyr	Val	Thr	Ser	Glu	His	Ile	Lys	Asp	Val	Leu	Lys	Ser	Asn	Leu	Ser		
			420					425					430				
Thr	Ser	Asn	Asp	Ile	Ile	Val	Glu	Lys	Val	Asp	Asn	Ile	Lys	Gln	Glu		
		435						440				445					
Thr	Asp	Val	Ala	Lys	Pro	Lys	Lys	Asn	Ser	Asn	Gln	Gly	Val	Val	Gly		
		450					455				460						
Trp	Val	Lys	Asp	Lys	Gly	Leu	Trp	Tyr	Tyr	Leu	Asn	Glu	Ser	Gly	Ser		
465					470					475					480		
Met	Ala	Thr	Gly	Trp	Val	Lys	Asp	Lys	Gly	Leu	Trp	Tyr	Tyr	Leu	Asn		
				485					490					495			
Glu	Ser	Gly	Ser	Met	Ala	Thr	Gly	Trp	Val	Lys	Asp	Lys	Gly	Leu	Trp		
			500					505					510				
Tyr	Tyr	Leu	Asn	Glu	Ser	Gly	Ser	Met	Ala	Thr	Gly	Trp	Val	Lys	Asp		
		515						520				525					
Lys	Gly	Leu	Trp	Tyr	Tyr	Leu	Asn	Glu	Ser	Gly	Ser	Met	Ala	Thr	Gly		
		530				535					540						
Trp	Val	Lys	Asp	Lys	Gly	Leu	Trp	Tyr	Tyr	Leu	Asn	Glu	Ser	Gly	Ser		
545					550					555					560		
Met	Ala	Thr	Gly	Trp	Val	Lys	Asp	Lys	Gly	Leu	Trp	Tyr	Tyr	Leu	Asn		
				565					570					575			
Glu	Ser	Gly	Ser	Met	Ala	Thr	Gly	Trp	Val	Lys	Asp	Lys	Gly	Leu	Trp		
			580					585					590				
Tyr	Tyr	Leu	Asn	Glu	Ser	Gly	Ser	Met	Ala	Thr	Gly	Trp	Phe	Thr	Val		
		595					600					605					
Ser	Gly	Lys	Trp	Tyr	Tyr	Thr	Tyr	Asn	Ser	Gly	Asp	Leu	Leu	Val	Asn		
		610				615				620							
Thr	Thr	Thr	Pro	Asp	Gly	Tyr	Arg	Val	Asn	Ala	Asn	Gly	Glu	Trp	Val		
625					630				635					640			
Gly																	

(2) INFORMATION FOR SEQ ID NO:2949:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...160

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2949:

Cys	Arg	Lys	Thr	Ala	Lys	Gly	Lys	Thr	Met	Lys	Pro	Leu	Leu	Glu	Thr
1				5					10					15	
Ile	Asp	Thr	Arg	Phe	Gly	Thr	Thr	Asn	Lys	His	Ala	Phe	Ser	Arg	Gly
			20					25					30		
Asn	Thr	Leu	Pro	Tyr	Thr	Gly	Val	Pro	Phe	Gly	Met	Asn	Tyr	Phe	Val
		35					40					45			
Pro	Gln	Thr	Ser	Asp	Gln	Asp	Gly	Ala	Trp	Phe	Phe	Asp	Pro	His	Leu
	50					55					60				
Pro	Ile	Phe	Gln	Gly	Ile	Arg	Leu	Thr	His	Gln	Pro	Ser	Pro	Trp	Ile
65					70					75				80	
Gly	Asp	Tyr	Ser	Trp	Leu	Leu	Leu	Thr	Pro	Val	Thr	Ser	Gln	Leu	Gly
			85						90					95	
Glu	Asp	Ser	Leu	Phe	His	Arg	Gln	Ser	Ser	Tyr	Asn	Arg	Asp	Lys	Ala
			100					105					110		
Ser	Phe	Gln	Pro	His	Tyr	Leu	Lys	Ile	Phe	Ser	Leu	Arg	Tyr	Gln	Ile
		115					120					125			
Glu	Thr	Gln	Leu	Thr	Pro	Thr	Cys	Tyr	Gly	Ala	Ser	Ile	Arg	Leu	Lys
	130					135					140				
Gln	Lys	Gln	Gly	Lys	Ala	Ser	Pro	Ser	Ile	Phe	Thr	Gln	Gln	Met	Asn
145					150					155					160

(2) INFORMATION FOR SEQ ID NO:2950:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 654 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...654

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2950:

Gly	Arg	Lys	Thr	Met	Lys	Ile	Gln	Asp	Leu	Leu	Arg	Lys	Asp	Val	Met
1				5					10					15	
Leu	Leu	Asp	Leu	Gln	Ala	Thr	Glu	Lys	Thr	Ala	Val	Ile	Glu	Glu	Met
			20					25					30		
Ile	Lys	Ser	Leu	Thr	Gly	His	Gly	Tyr	Val	Thr	Asp	Phe	Glu	Thr	Phe
		35				40						45			
Lys	Glu	Gly	Ile	Leu	Ala	Arg	Glu	Ala	Leu	Thr	Ser	Thr	Gly	Leu	Gly
	50				55						60				
Asp	Gly	Ile	Ala	Met	Pro	His	Ser	Lys	Asn	Ala	Ala	Val	Lys	Glu	Ala
65				70						75				80	
Thr	Val	Leu	Phe	Ala	Lys	Ser	Asn	Lys	Gly	Val	Asp	Tyr	Glu	Ser	Leu
			85						90					95	
Asp	Gly	Gln	Ala	Thr	Asp	Leu	Phe	Phe	Met	Ile	Ala	Ala	Pro	Glu	Gly

Arg	Asn	Ser	Gly	Leu	Thr	Asn	Ile	Ile	Met	Gly	Leu	Ser	Phe	Ile	Thr
				565					570					575	
Glu	Gly	Ala	Ile	Pro	Phe	Gly	Ala	Ala	Asp	Pro	Ala	Arg	Ala	Ile	Pro
				580					585					590	
Ser	Phe	Ile	Leu	Gly	Ser	Ala	Val	Ala	Gly	Gly	Leu	Val	Gly	Leu	Thr
				595				600					605		
Gly	Ile	Lys	Leu	Met	Ala	Pro	His	Gly	Gly	Ile	Phe	Val	Ile	Ala	Leu
				610			615				620				
Thr	Ser	Asn	Ala	Leu	Leu	Tyr	Leu	Val	Ser	Val	Leu	Val	Gly	Ala	Ile
				625			630				635				640
Val	Ser	Gly	Val	Val	Tyr	Gly	Tyr	Leu	Arg	Lys	Pro	Gln	Ala		
				645					650						

(2) INFORMATION FOR SEQ ID NO:2951:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...82

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2951:

Lys	Arg	Lys	Thr	Trp	Gly	Leu	Val	Leu	Phe	Glu	Asn	Leu	Phe	Lys	Pro
1				5					10					15	
Arg	Gln	Arg	Arg	Leu	Ala	Val	Cys	Arg	Leu	Leu	Thr	Ser	Ser	Val	Leu
				20				25					30		
Ser	Thr	Thr	Ser	Lys	Gln	Cys	Phe	Glu	Gln	Pro	Ala	Ala	Ser	Phe	Leu
				35			40					45			
Val	Cys	Ser	Leu	Ile	Phe	Ile	Glu	Tyr	Trp	Pro	Gln	Val	Ser	Ile	Cys
				50		55					60				
Asn	Gln	Lys	Gly	Ile	Leu	Cys	Pro	Leu	Phe	Lys	Asn	Phe	Gly	Gly	Phe
				65		70				75				80	
Ser	Ser														

(2) INFORMATION FOR SEQ ID NO:2952:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2952:

```

Lys Met Lys Thr Lys Lys Leu Leu Lys Met Val Ile Pro Val Leu Met
1           5           10           15
Ile Ser Ala Val Gly Thr Thr Phe Val Glu Ala Asn Gln Ile Gly Ala
          20           25           30
Phe Ser Asn Phe Val Ile Thr Thr Ser Tyr Lys Arg Thr Gly Tyr Leu
          35           40           45
Thr Lys Glu Asn Glu Gly Ala Glu Tyr Ile Met Asn Leu Asn Pro Cys
          50           55           60
Arg Asn Leu His Pro Met Thr Val Lys His Arg Ile Val Asn Ser Asn
65           70           75           80
Gly Glu Ala Arg Ser Gly Glu Ser Leu Thr Thr Cys Gly Thr Arg Ser
          85           90           95
Thr His Gly Asn Trp Ala Thr Val Gly Tyr Val Tyr Ala Ala Asp Met
          100          105          110
Ala Arg Gln Asn Trp Trp Asp Leu Ser Ala Ala Ile Ser Gly Ser Trp
          115          120          125
Ser Pro Asn
          130
  
```

(2) INFORMATION FOR SEQ ID NO:2953:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 127 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...127

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2953:

```

Lys Glu Lys Thr Glu Met Ile Gln Thr Glu Thr Arg Leu Lys Val Ala
1           5           10           15
Asp Asn Ser Gly Ala Arg Glu Ile Leu Thr Ile Lys Val Leu Gly Gly
          20           25           30
Ser Gly Arg Lys Phe Ala Asn Ile Gly Asp Val Ile Val Ala Ser Val
          35           40           45
Lys Gln Ala Thr Pro Gly Gly Ala Val Lys Lys Gly Asp Val Val Lys
          50           55           60
Ala Val Ile Val Arg Thr Lys Ser Gly Ala Arg Arg Ala Asp Gly Ser
  
```

65		70		75		80									
Tyr	Ile	Lys	Phe	Asp	Glu	Asn	Ala	Ala	Val	Ile	Ile	Arg	Glu	Asp	Lys
			85						90					95	
Thr	Pro	Arg	Gly	Thr	Arg	Ile	Phe	Gly	Pro	Val	Ala	Arg	Glu	Leu	Arg
			100					105					110		
Glu	Gly	Gly	Phe	Met	Lys	Ile	Val	Ser	Leu	Ala	Pro	Glu	Val	Leu	
		115					120					125			

(2) INFORMATION FOR SEQ ID NO:2954:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 70 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...70
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2954:

Met	Ser	Glu	Thr	Ile	Leu	Glu	Ile	Lys	Glu	Leu	Lys	Lys	Ser	Phe	Gly
1				5				10						15	
Asp	Asn	Pro	Ile	Leu	Gln	Gly	Leu	Ser	Leu	Glu	Ile	Lys	Lys	Gly	Gly
			20					25					30		
Ser	Cys	Cys	His	Pro	Arg	Gly	Ile	Trp	Leu	Trp	Glu	Lys	Tyr	Pro	Pro
		35				40					45				
Ser	Leu	Pro	Gln	Arg	Leu	Arg	Lys	Tyr	Ser	Arg	Trp	Arg	Tyr	Ser	Ser
	50				55					60					
Gly	Trp	Ser	Val	Tyr	Arg										
65					70										

(2) INFORMATION FOR SEQ ID NO:2955:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 148 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...148

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2955:

Ile	Asp	Glu	Thr	Gly	Phe	Asp	Thr	Tyr	Phe	Tyr	Arg	Glu	Tyr	Gly	Arg	
1				5					10					15		
Ser	Leu	Lys	Gly	Gln	Leu	Arg	Arg	Gly	Lys	Val	Ser	Gly	Arg	Arg	Tyr	
			20					25					30			
Gln	Arg	Ile	Ser	Leu	Val	Ala	Gly	Leu	Thr	Asn	Gly	Glu	Leu	Ile	Ala	
		35					40					45				
Pro	Met	Thr	Tyr	Glu	Glu	Met	Met	Thr	Ser	Asp	Phe	Phe	Glu	Ala	Trp	
	50					55					60					
Phe	Gln	Lys	Phe	Leu	Leu	Pro	Thr	Leu	Thr	Thr	Pro	Ser	Val	Ile	Ile	
65				70					75					80		
Met	Asp	Asn	Ala	Arg	Phe	His	Arg	Met	Gly	Lys	Leu	Glu	Leu	Leu	Cys	
			85						90				95			
Glu	Glu	Phe	Gly	His	Lys	Leu	Leu	Ser	Leu	Pro	Pro	Tyr	Ser	Pro	Glu	
			100					105					110			
Tyr	Asn	Pro	Ile	Glu	Lys	Thr	Trp	Ala	His	Ile	Lys	Lys	His	Leu	Lys	
		115					120					125				
Lys	Val	Leu	Pro	Ser	Cys	Asn	Thr	Phe	Tyr	Glu	Ala	Leu	Leu	Ser	Cys	
	130					135					140					
Ser	Cys	Phe	Asn													
145																

(2) INFORMATION FOR SEQ ID NO:2956:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 82 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...82

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2956:

Ile	Asp	Glu	Thr	Gly	Phe	Asp	Thr	Tyr	Phe	Tyr	Arg	Glu	Tyr	Gly	Arg	
1				5					10					15		
Ser	Leu	Lys	Gly	Gln	Leu	Arg	Arg	Gly	Lys	Val	Ser	Gly	Arg	Arg	Tyr	
			20					25					30			
Gln	Arg	Ile	Ser	Leu	Val	Ala	Gly	Leu	Thr	Asn	Gly	Glu	Leu	Ile	Ala	
		35					40					45				
Pro	Met	Thr	Tyr	Glu	Glu	Met	Met	Thr	Ser	Asp	Phe	Phe	Glu	Val	Trp	
	50					55					60					
Phe	Gln	Lys	Phe	Phe	Leu	Pro	Thr	Leu	Thr	Thr	Pro	Ser	Val	Ile	Ile	
65				70					75					80		
Val	Lys															

(2) INFORMATION FOR SEQ ID NO:2957:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 148 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...148
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2957:

```

Ile Asp Glu Thr Gly Phe Asp Thr Tyr Phe Tyr Arg Glu Tyr Gly Arg
1      5      10      15
Ser Leu Lys Asp Gln Leu Ile Arg Gly Lys Val Ser Gly Arg Arg Tyr
20     25     30
Gln Arg Ile Ser Leu Val Ala Gly Leu Thr Asn Gly Glu Leu Ile Ala
35     40     45
Pro Met Thr Tyr Glu Glu Thr Met Thr Ser Asp Phe Phe Glu Ala Trp
50     55     60
Phe Gln Lys Phe Leu Leu Pro Thr Leu Asn Thr Pro Ser Val Ile Ile
65     70     75     80
Met Asp Asn Ala Arg Phe His Arg Met Gly Lys Leu Glu Leu Leu Cys
85     90     95
Glu Glu Phe Gly Tyr Lys Leu Leu Pro Leu Pro Pro Tyr Ser Pro Glu
100    105    110
Tyr Asn Pro Ile Glu Lys Thr Trp Ala His Ile Lys Lys His Leu Lys
115    120    125
Arg Val Leu Pro Ser Cys Asn Thr Phe Tyr Glu Ala Leu Leu Ser Cys
130    135    140
Ser Cys Phe Asn
145

```

(2) INFORMATION FOR SEQ ID NO:2958:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 149 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...149

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2958:

```
Ile Asp Glu Thr Gly Phe Asp Thr Tyr Phe Tyr Arg Glu Tyr Gly Arg
1          5          10          15
Ser Leu Lys Gly Gln Leu Arg Arg Gly Lys Val Ser Gly Arg Arg Tyr
20          25          30
Gln Arg Ile Ser Leu Val Ala Gly Leu Thr Asn Gly Glu Leu Ile Ala
35          40          45
Pro Ile Thr Tyr Glu Glu Met Met Thr Ser Asp Phe Phe Glu Ala Trp
50          55          60
Phe Gln Lys Phe Leu Leu Pro Thr Leu Thr Thr Pro Ser Val Ile Ile
65          70          75          80
Met Asp Asn Ala Arg Phe His Arg Met Gly Lys Leu Glu Leu Leu Cys
85          90          95
Glu Glu Phe Gly His Lys Leu Leu Pro Leu Pro Pro Tyr Ser Pro Glu
100         105         110
Tyr Asn Pro Ile Glu Lys Thr Trp Ala His Ile Lys Lys His Leu Lys
115         120         125
Lys Val Leu Pro Ser Cys Cys Asn Thr Phe Tyr Glu Ala Leu Leu Ser
130         135         140
Cys Ser Cys Phe Asn
145
```

(2) INFORMATION FOR SEQ ID NO:2959:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...235

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2959:

```
Tyr Glu Glu Thr Ser Gly Glu Ser Arg Glu Phe Asn Met Lys Lys Arg
1          5          10          15
Ala Ile Gln Ile Leu Leu Ala Leu Ser Leu Ile Phe Tyr Lys Ser Thr
20          25          30
Trp Phe Trp Arg Val Phe Asn His Leu Ala Lys Pro Tyr Leu Pro Ala
35          40          45
Ser Arg Glu Phe Phe Gln Ile Leu Leu Leu Met Glu Ser Gly Val Leu
50          55          60
Phe Leu Ala Val Ile Tyr Leu Leu Val Phe Ala Gly Lys Lys Ile Phe
65          70          75          80
His Phe Lys Trp Gln Leu Arg Tyr Phe Ile Tyr Leu Leu Leu Gly Tyr
85          90          95
Ile Ile Ser Tyr Met Ser Asp Phe Leu Phe Ser Tyr Phe Ile Ser Leu
```

			100				105				110				
Ser	Ser	Asn	Gln	Ile	Ser	Leu	Asn	Glu	Thr	Val	Glu	Met	Met	Gly	Arg
		115					120					125			
Gln	Glu	Phe	Pro	Tyr	Phe	Leu	Leu	Ile	Val	Cys	Phe	Ile	Ala	Pro	Ile
		130					135					140			
Ala	Glu	Glu	Leu	Ile	Tyr	Arg	Gly	Val	Leu	Met	Thr	Thr	Phe	Phe	Lys
145					150					155					160
Asn	Ser	Pro	Trp	Tyr	Gly	Asp	Val	Leu	Leu	Ser	Ala	Ile	Ile	Phe	Gly
				165						170				175	
Tyr	Ile	His	Ile	Asn	Phe	Ala	Leu	Thr	Pro	Leu	Ala	Phe	Phe	Ile	Tyr
			180					185					190		
Ala	Ser	Gly	Gly	Leu	Ile	Leu	Ala	Leu	Leu	Tyr	Arg	Met	Thr	Lys	Asn
		195					200					205			
Leu	Tyr	Tyr	Pro	Ile	Leu	Val	His	Ile	Leu	Ile	Asn	Ile	Thr	Ala	Phe
		210				215					220				
Trp	Asp	Val	Trp	Leu	Leu	Leu	Phe	Ser	Gly	Ser					
225					230					235					

(2) INFORMATION FOR SEQ ID NO:2960:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 358 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...358

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2960:

Asp	Arg	Glu	Thr	Glu	Arg	Thr	Asn	Met	Lys	Leu	Lys	Ser	Tyr	Ile	Leu
1				5					10					15	
Val	Gly	Tyr	Ile	Ile	Ser	Thr	Leu	Leu	Thr	Ile	Leu	Val	Val	Phe	Trp
			20					25					30		
Ala	Val	Gln	Lys	Met	Leu	Ile	Ala	Lys	Gly	Glu	Ile	Tyr	Phe	Leu	Leu
		35					40					45			
Gly	Met	Thr	Ile	Val	Ala	Ser	Leu	Val	Gly	Ala	Gly	Ile	Ser	Leu	Phe
	50					55					60				
Leu	Leu	Leu	Pro	Val	Phe	Thr	Ser	Leu	Gly	Lys	Leu	Lys	Glu	His	Ala
65					70					75				80	
Lys	Arg	Val	Ser	Ala	Lys	Asp	Phe	Pro	Ser	Asn	Leu	Glu	Val	Gln	Gly
			85					90						95	
Pro	Val	Lys	Phe	Gln	Gln	Leu	Gly	Gln	Thr	Phe	Asn	Glu	Met	Ser	His
			100					105					110		
Asp	Leu	Gln	Val	Ser	Phe	Asp	Ser	Leu	Glu	Glu	Ser	Glu	Arg	Glu	Lys
		115					120					125			
Gly	Leu	Met	Ile	Ala	Gln	Leu	Ser	His	Asp	Ile	Lys	Thr	Pro	Ile	Thr
		130					135					140			
Ser	Ile	Gln	Ala	Thr	Val	Glu	Gly	Ile	Leu	Asp	Gly	Ile	Ile	Lys	Glu

145		150		155		160									
Ser	Glu	Gln	Ala	His	Tyr	Leu	Ala	Thr	Ile	Gly	Arg	Gln	Thr	Glu	Arg
			165						170					175	
Leu	Asn	Lys	Leu	Val	Glu	Glu	Leu	Asn	Phe	Leu	Thr	Leu	Asn	Thr	Ala
			180						185					190	
Arg	Asn	Gln	Val	Glu	Thr	Thr	Ser	Lys	Asp	Ser	Ile	Phe	Leu	Asp	Lys
			195					200					205		
Leu	Leu	Ile	Glu	Cys	Met	Ser	Glu	Phe	Gln	Phe	Leu	Ile	Glu	Gln	Glu
		210				215					220				
Arg	Arg	Asp	Val	His	Leu	Gln	Val	Ile	Pro	Glu	Ser	Ala	Arg	Ile	Glu
225					230					235				240	
Gly	Asp	Tyr	Ala	Lys	Leu	Ser	Arg	Ile	Leu	Val	Asn	Leu	Val	Asp	Asn
			245						250					255	
Ala	Phe	Lys	Tyr	Ser	Ala	Pro	Gly	Thr	Lys	Leu	Glu	Val	Val	Thr	Lys
			260					265					270		
Leu	Glu	Lys	Gly	Gln	Leu	Ser	Ile	Ser	Val	Thr	Asp	Glu	Gly	Gln	Gly
		275					280					285			
Ile	Ala	Pro	Glu	Asp	Leu	Glu	Asn	Ile	Phe	Lys	Arg	Leu	Tyr	Arg	Val
		290				295					300				
Glu	Thr	Ser	Arg	Asn	Met	Lys	Thr	Gly	Gly	His	Gly	Leu	Gly	Leu	Ala
305				310						315				320	
Ile	Ala	Arg	Glu	Leu	Ala	His	Gln	Leu	Gly	Gly	Glu	Ile	Thr	Val	Ser
			325						330					335	
Ser	Gln	Tyr	Gly	Leu	Gly	Ser	Thr	Phe	Thr	Leu	Val	Leu	Asn	Leu	Ser
			340					345					350		
Gly	Ser	Glu	Asn	Lys	Ala										
			355												

(2) INFORMATION FOR SEQ ID NO:2961:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...99

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2961:

Asn	Met	Glu	Thr	Ser	Ile	Ser	Met	Ala	Asp	Phe	Tyr	Gly	Lys	Tyr	Gln
1				5				10						15	
Asn	Glu	Asn	Leu	Glu	Leu	Ile	Asp	Val	Arg	Glu	Ala	His	Glu	Phe	Gln
			20					25					30		
Ala	Gly	His	Ala	Leu	Gly	Ala	Lys	Asn	Leu	Pro	Leu	Ser	Thr	Leu	Glu
		35				40					45				
Ala	Ser	Tyr	Lys	Glu	Leu	Lys	Pro	Asp	His	Glu	Tyr	Val	Ile	Cys	
50						55				60					

Gln	Gly	Gly	Val	Arg	Ser	Ala	Ser	Thr	Cys	Gln	Phe	Leu	Ser	Ser	Gln
65					70				75						80
Gly	Leu	Thr	Val	Thr	Asn	Val	Glu	Gly	Gly	Met	Asn	Ala	Trp	Pro	Gly
				85					90					95	
Gln	Val	Lys													

(2) INFORMATION FOR SEQ ID NO:2962:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 339 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2962:

Ser	Glu	Glu	Thr	Arg	Met	Lys	Glu	Ile	Ile	Glu	Lys	Leu	Ala	Lys	Phe
1				5				10						15	
Glu	Asn	Leu	Ser	Gly	Val	Glu	Met	Thr	Asp	Val	Ile	Glu	Arg	Ile	Val
			20					25					30		
Thr	Gly	Arg	Val	Thr	Glu	Ala	Gln	Ile	Ala	Ser	Leu	Leu	Leu	Ala	Leu
		35					40					45			
Lys	Met	Lys	Gly	Glu	Thr	Pro	Glu	Glu	Arg	Thr	Ala	Ile	Ala	Gln	Val
	50					55				60					
Met	Arg	Gly	His	Ala	Gln	His	Ile	Pro	Thr	Glu	Ile	His	Asp	Ala	Met
65				70						75					80
Asp	Asn	Cys	Gly	Thr	Gly	Gly	Asp	Lys	Ser	Phe	Ser	Phe	Asn	Ile	Ser
			85					90					95		
Thr	Thr	Ala	Ala	Phe	Val	Leu	Ala	Gly	Gly	Gly	Ile	His	Met	Ala	Lys
			100					105					110		
His	Gly	Asn	Arg	Ser	Ile	Ser	Ser	Lys	Ser	Gly	Ser	Ala	Asp	Val	Leu
		115					120					125			
Glu	Ala	Leu	Gly	Ile	Asn	Leu	Asp	Leu	Lys	Pro	Ala	Glu	Leu	Gly	Lys
		130				135					140				
Val	Phe	Asp	Lys	Thr	Gly	Ile	Val	Phe	Leu	Phe	Ala	Lys	Asn	Met	His
145				150						155					160
Pro	Ala	Met	Lys	Tyr	Ile	Met	Pro	Ala	Arg	Leu	Glu	Leu	Gly	Ile	Pro
				165					170					175	
Thr	Ile	Met	Asn	Leu	Thr	Gly	Pro	Leu	Ile	His	Pro	Met	Ala	Leu	Glu
			180					185					190		
Thr	Gln	Leu	Leu	Gly	Ile	Ser	Arg	Pro	Glu	Leu	Leu	Glu	Ser	Thr	Ala
			195				200					205			
Gln	Val	Leu	Lys	Asn	Met	Gly	Arg	Lys	Arg	Ala	Ile	Val	Val	Ala	Gly
	210					215					220				
Pro	Glu	Gly	Leu	Asp	Glu	Ala	Gly	Leu	Asn	Gly	Thr	Thr	Lys	Ile	Ala
225					230					235					240

Leu	Leu	Glu	Asn	Gly	Glu	Ile	Ser	Leu	Ser	Ser	Phe	Thr	Pro	Glu	Asp
				245					250					255	
Leu	Gly	Met	Glu	Gly	Tyr	Ala	Met	Glu	Asp	Ile	Arg	Gly	Gly	Asn	Ala
			260					265					270		
Gln	Glu	Asn	Ala	Glu	Ile	Leu	Leu	Ser	Val	Leu	Lys	Asn	Glu	Ala	Ser
		275					280					285			
Pro	Phe	Leu	Glu	Thr	Thr	Val	Leu	Asn	Ala	Gly	Leu	Gly	Phe	Tyr	Ala
	290					295					300				
Asn	Gly	Lys	Ile	Asp	Ser	Ile	Lys	Glu	Gly	Val	Ala	Leu	Ala	Arg	Gln
305				310					315					320	
Val	Ile	Ala	Arg	Gly	Lys	Ala	Leu	Glu	Lys	Leu	Arg	Leu	Leu	Gln	Glu
			325					330						335	
Tyr	Gln	Lys													

(2) INFORMATION FOR SEQ ID NO:2963:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 194 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...194
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2963:

Asn	Trp	Arg	Thr	Lys	Thr	Met	Ile	Leu	Leu	Ile	Asp	Asn	Tyr	Asp	Ser
1				5					10					15	
Phe	Thr	Tyr	Asn	Leu	Ala	Gln	Tyr	Ile	Gly	Asn	Phe	Ala	Glu	Val	Gln
			20					25				30			
Val	Leu	Arg	Asn	Asp	Asp	Ser	Lys	Leu	Tyr	Glu	Glu	Ala	Glu	Lys	Ala
	35					40					45				
Asp	Gly	Leu	Val	Phe	Ser	Pro	Gly	Pro	Gly	Trp	Pro	Val	Asp	Ala	Gly
	50				55					60					
Lys	Met	Glu	Asp	Met	Ile	Arg	Asp	Phe	Ala	Gly	Lys	Lys	Pro	Ile	Leu
65				70					75					80	
Gly	Ile	Cys	Leu	Gly	His	Gln	Ala	Ile	Ala	Glu	Val	Phe	Gly	Gly	Lys
			85					90					95		
Leu	Gly	Leu	Ala	Pro	Lys	Val	Met	His	Gly	Lys	Gln	Ser	Asn	Ile	Asn
		100					105					110			
Phe	Glu	Ala	Pro	Ser	Val	Leu	Tyr	Gln	Gly	Ile	Glu	Asp	Gly	Arg	Ala
	115					120					125				
Val	Met	Arg	Tyr	His	Ser	Ile	Leu	Ile	Glu	Glu	Met	Pro	Glu	Asp	Phe
	130				135					140					
Glu	Val	Thr	Ala	Arg	Ser	Thr	Asp	Asp	Gln	Ala	Ile	Met	Gly	Ile	Gln
145				150					155					160	
His	Lys	Asn	Leu	Pro	Ile	Tyr	Gly	Phe	Gln	Tyr	His	Pro	Glu	Ser	Ile
			165					170						175	

Gly Thr Pro Asp Gly Leu Ser Ser Ile Arg Asn Phe Ile Glu Lys Val
180 185 190
Val Lys

(2) INFORMATION FOR SEQ ID NO:2964:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 888 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...888

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2964:

Leu	Arg	Arg	Thr	His	Met	Ser	Lys	Glu	Leu	Ser	Ser	Lys	Tyr	Asn	Pro	1	5	10	15
Ala	Glu	Val	Glu	Ala	Gly	Arg	Tyr	Gln	Lys	Trp	Leu	Asp	Ala	Asp	Val	20	25	30	
Phe	Lys	Pro	Ser	Gly	Asp	Gln	Lys	Ala	Lys	Pro	Tyr	Ser	Ile	Val	Ile	35	40	45	
Pro	Pro	Pro	Asn	Val	Thr	Gly	Lys	Leu	His	Leu	Gly	His	Ala	Trp	Asp	50	55	60	
Thr	Thr	Leu	Gln	Asp	Ile	Ile	Ile	Arg	Gln	Lys	Arg	Met	Gln	Gly	Phe	65	70	75	80
Asp	Thr	Leu	Trp	Leu	Pro	Gly	Met	Asp	His	Ala	Gly	Ile	Ala	Thr	Gln	85	90	95	
Ala	Lys	Val	Glu	Glu	Arg	Leu	Arg	Gly	Glu	Gly	Ile	Ser	Arg	Tyr	Asp	100	105	110	
Leu	Gly	Arg	Glu	Ser	Phe	Leu	Thr	Lys	Val	Trp	Glu	Trp	Lys	Asp	Glu	115	120	125	
Tyr	Ala	Thr	Thr	Ile	Lys	Glu	Gln	Trp	Gly	Lys	Met	Gly	Leu	Ser	Val	130	135	140	
Asp	Tyr	Ser	Arg	Glu	Arg	Phe	Thr	Leu	Asp	Glu	Gly	Leu	Ser	Lys	Ala	145	150	155	160
Val	Arg	Lys	Val	Phe	Val	Asp	Leu	Tyr	Lys	Lys	Gly	Trp	Ile	Tyr	Arg	165	170	175	
Gly	Glu	Phe	Ile	Ile	Asn	Trp	Asp	Pro	Ala	Ala	Arg	Thr	Ala	Leu	Ser	180	185	190	
Asp	Ile	Glu	Val	Ile	His	Lys	Asp	Val	Glu	Gly	Ala	Phe	Tyr	His	Met	195	200	205	
Asn	Tyr	Met	Leu	Glu	Asp	Gly	Ser	Arg	Ala	Leu	Glu	Val	Ala	Thr	Thr	210	215	220	
Arg	Pro	Glu	Thr	Met	Phe	Gly	Asp	Val	Ala	Val	Ala	Val	Asn	Pro	Glu	225	230	235	240
Asp	Pro	Arg	Tyr	Lys	Asp	Leu	Ile	Gly	Lys	Asn	Val	Ile	Leu	Pro	Ile				

Gln	Tyr	Ala	Glu	Gly	Ser	Ile	Val	Thr	Ala	Ala	Tyr	Pro	Thr	Val	Asn
705					710				715						720
Pro	Ala	Phe	Glu	Asp	Leu	Ala	Ala	His	Thr	Gly	Val	Glu	Ser	Leu	Lys
			725						730						735
Asn	Leu	Ile	Arg	Ala	Val	Arg	Asn	Ala	Arg	Ala	Glu	Val	Asn	Val	Ala
			740					745					750		
Pro	Ser	Lys	Pro	Ile	Thr	Ile	Leu	Val	Lys	Thr	Ser	Asp	Ser	Asp	Leu
		755					760					765			
Glu	Ala	Phe	Phe	Asn	Ser	Asn	Val	Asn	Tyr	Ile	Lys	Arg	Phe	Thr	Asn
	770					775					780				
Pro	Glu	His	Leu	Glu	Ile	Ala	Ser	Thr	Ile	Pro	Ala	Pro	Glu	Leu	Ala
785					790					795					800
Met	Ser	Ser	Val	Ile	Thr	Gly	Ala	Glu	Ile	Tyr	Leu	Pro	Leu	Ala	Asp
			805					810						815	
Leu	Leu	Asn	Val	Glu	Glu	Glu	Leu	Ala	Arg	Leu	Asp	Lys	Glu	Leu	Ala
			820					825					830		
Lys	Trp	Gln	Lys	Glu	Leu	Asp	Met	Val	Gly	Lys	Lys	Leu	Ser	Asn	Glu
	835						840					845			
Arg	Phe	Val	Ala	Asn	Ala	Lys	Pro	Glu	Val	Val	Gln	Lys	Glu	Arg	Asp
	850					855					860				
Lys	Gln	Ala	Asp	Tyr	Gln	Ala	Lys	Tyr	Asp	Ala	Thr	Val	Ala	Arg	Ile
865					870					875					880
Asp	Glu	Met	Lys	Lys	Leu	Val	Lys								
				885											

(2) INFORMATION FOR SEQ ID NO:2965:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 312 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...312
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2965:

Gly	Arg	Arg	Thr	Lys	Met	Thr	Glu	Leu	Ala	Lys	Gln	Leu	Leu	Glu	Leu
1				5					10					15	
Thr	Tyr	Ile	Val	Ile	Gly	Cys	Gln	Phe	Leu	His	Thr	Ala	Tyr	Cys	Ser
			20					25					30		
Tyr	Lys	Asp	Lys	Thr	Asn	Pro	Val	Arg	Leu	Gly	Thr	Ser	Ala	Phe	Trp
		35				40						45			
Thr	Leu	Leu	Ser	Ile	Thr	Phe	Ile	Gly	Gly	Ser	Tyr	Met	Pro	Asn	Met
	50					55					60				
Ser	Ile	Gly	Ile	Ile	Val	Ile	Leu	Leu	Ser	Leu	Leu	Thr	Leu	Phe	Lys
65					70					75					80
Gln	Val	Arg	Ile	Gly	Thr	Leu	Pro	Ser	Leu	Asp	Glu	Met	Lys	Ala	Asn
				85					90					95	

Ile	Glu	Ser	Asn	Arg	Leu	Lys	Asn	Lys	Ile	Phe	Ile	Pro	Val	Met	Leu
			100					105					110		
Met	Ala	Ile	Leu	Ala	Leu	Val	Leu	Ala	Gln	Met	Ile	Pro	Glu	Phe	Ser
		115					120					125			
Lys	Ile	Ser	Ile	Ser	Leu	Ala	Ala	Leu	Phe	Ala	Thr	Ile	Ser	Val	Leu
	130				135						140				
Val	Ile	Thr	Asn	Ser	His	Pro	Lys	Ser	Leu	Leu	Ser	Glu	Asn	Asn	Arg
145				150					155						160
Met	Thr	Gln	Gln	Val	Ser	Thr	Ser	Gly	Ile	Val	Pro	Gln	Leu	Leu	Gly
			165					170					175		
Ala	Leu	Gly	Ala	Ile	Phe	Thr	Val	Ala	Gly	Val	Gly	Asp	Val	Ile	Ser
		180					185				190				
His	Leu	Ile	Ser	Gly	Ile	Val	Pro	Ser	Asp	Ser	Arg	Phe	Ile	Gly	Val
	195					200					205				
Leu	Ala	Tyr	Val	Leu	Gly	Met	Val	Leu	Phe	Thr	Met	Ile	Met	Gly	Asn
	210				215						220				
Ala	Phe	Ala	Ala	Phe	Thr	Val	Ile	Thr	Ala	Gly	Val	Gly	Val	Pro	Phe
225				230				235						240	
Val	Phe	Ala	Leu	Gly	Ala	Asn	Pro	Ile	Val	Ala	Gly	Ala	Leu	Ala	Met
			245					250					255		
Thr	Ala	Gly	Tyr	Cys	Gly	Thr	Leu	Leu	Thr	Pro	Met	Ala	Ala	Asn	Phe
		260					265						270		
Asn	Ala	Leu	Pro	Ala	Ala	Leu	Met	Asp	Met	Lys	Asp	Gln	Asn	Gly	Val
	275					280						285			
Ile	Lys	Ala	Gln	Ala	Gly	Val	Ala	Leu	Val	Met	Ile	Val	Ile	His	Ile
	290				295						300				
Phe	Leu	Met	Tyr	Phe	Leu	Ala	Phe								
305					310										

(2) INFORMATION FOR SEQ ID NO:2966:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...348

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2966:

Ile	Leu	Gly	Thr	Gln	Glu	Gly	Lys	Asp	Met	Asn	Ile	Thr	Tyr	Ile	Val
1			5				10						15		
Gly	Asn	Gly	Leu	Asp	Leu	Gln	Tyr	Gly	Leu	Lys	Thr	Arg	Tyr	Arg	Asp
	20						25					30			
Phe	Tyr	Glu	Phe	Gln	Asn	Lys	Val	Tyr	Ile	Ser	Arg	Thr	Glu	Asn	Glu
	35				40						45				
Glu	Lys	Tyr	Ser	Asn	Phe	Ile	Tyr	Glu	Ser	Leu	Phe	Ser	Asp	Lys	Val

50					55					60					
Asn	Asp	Tyr	Glu	Asn	Trp	Ser	Asp	Phe	Glu	Leu	Ser	Ile	Gly	Lys	Leu
65					70					75					80
Thr	Lys	Asp	Asn	Asp	Leu	Ile	Ser	Ser	Ser	Ile	Glu	Ile	Lys	Glu	Lys
				85					90					95	
Phe	Ile	Asp	Asp	Phe	Ser	Glu	Val	Val	Asp	Asp	Leu	Arg	Glu	Tyr	Leu
			100					105					110		
Arg	Ile	Gln	Gln	Glu	Lys	Asn	Leu	Glu	Lys	Gly	Asn	Ala	Ile	Asp	Phe
		115					120					125			
Ile	Ser	Thr	Leu	Asp	Asn	Met	Arg	Thr	Ser	Leu	Pro	Val	Ile	Asn	Gln
	130					135					140				
Pro	Ala	Ile	Asp	Lys	Lys	Tyr	Asn	Glu	Asn	Leu	Tyr	Gln	His	Asp	Ile
145				150					155					160	
Val	Asn	Ile	Leu	Thr	Leu	Asn	Tyr	Thr	Asn	Val	Ile	Asp	Lys	Leu	Tyr
			165						170					175	
Asn	Glu	Ser	Ala	Lys	Ser	Phe	Ser	Asn	Gln	Leu	Arg	Thr	Asn	Asn	Tyr
			180					185					190		
Lys	Phe	His	Ile	Ala	Pro	Pro	Ile	His	Ala	His	Gly	Thr	Val	Asp	Ile
		195					200					205			
Cys	Thr	Val	Leu	Gly	Val	Ser	Asp	Glu	Thr	Gln	Ile	Ser	Asn	Ser	Phe
210						215					220				
Asp	Glu	Glu	Gln	Lys	Glu	Ser	Leu	Ile	Lys	Asn	Leu	Val	Leu	Lys	Asn
225				230						235				240	
Tyr	Arg	Glu	Asn	Met	Asp	Val	Lys	Asn	Ser	Asp	Ile	Ile	Lys	Asn	Ser
			245						250				255		
Asp	Ile	Ile	Ile	Leu	Tyr	Gly	Val	Ser	Leu	Gly	Glu	Thr	Asp	Gly	Tyr
			260				265						270		
Ile	Trp	Asn	Gln	Ile	Ala	Glu	Gln	Ser	Ile	Arg	Ser	Ser	Val	Pro	Val
	275						280					285			
Ile	Ile	Tyr	His	Tyr	Val	Pro	His	Phe	Asp	Ala	Gly	Asn	Pro	Thr	Arg
	290					295					300				
Val	Lys	Arg	Leu	Tyr	Arg	Asn	Val	Glu	Asp	Lys	Phe	Ile	Gln	Asn	Ser
305				310						315				320	
Gly	Ile	Asp	Leu	Glu	Leu	Glu	Lys	Lys	Leu	Arg	Asp	Asn	Leu	Ile	Val
			325						330				335		
Val	Ile	Gly	Lys	Thr	Ile	Phe	Asn	Leu	Met	Glu	Arg				
			340					345							

(2) INFORMATION FOR SEQ ID NO:2967:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 260 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2967:

Glu	Gly	Gly	Thr	Lys	Leu	Met	Ala	Leu	Leu	Glu	Val	Lys	Gln	Leu	Thr
1				5					10					15	
Lys	His	Phe	Gly	Gly	Leu	Thr	Ala	Val	Gly	Asp	Val	Thr	Leu	Glu	Leu
			20					25					30		
Asn	Glu	Gly	Glu	Leu	Val	Gly	Leu	Ile	Gly	Pro	Asn	Gly	Ala	Gly	Lys
		35					40					45			
Thr	Thr	Leu	Phe	Asn	Leu	Leu	Thr	Gly	Val	Tyr	Glu	Pro	Ser	Glu	Gly
	50				55					60					
Thr	Val	Thr	Leu	Asp	Gly	His	Leu	Leu	Asn	Gly	Lys	Ser	Pro	Tyr	Lys
65				70					75					80	
Ile	Ala	Ser	Leu	Gly	Leu	Gly	Arg	Thr	Phe	Gln	Asn	Ile	Arg	Leu	Phe
			85					90					95		
Lys	Asp	Leu	Thr	Val	Leu	Asp	Asn	Val	Leu	Ile	Ala	Phe	Gly	Asn	His
		100					105					110			
His	Lys	Gln	His	Val	Phe	Thr	Ser	Phe	Leu	Arg	Leu	Pro	Ala	Phe	Tyr
	115					120					125				
Lys	Ser	Glu	Lys	Glu	Leu	Lys	Ala	Lys	Ala	Leu	Glu	Leu	Leu	Lys	Ile
	130				135					140					
Phe	Asp	Leu	Asp	Gly	Asp	Ala	Glu	Thr	Leu	Ala	Lys	Asn	Leu	Ser	Tyr
145				150					155					160	
Gly	Gln	Gln	Arg	Arg	Leu	Glu	Ile	Val	Arg	Ala	Leu	Ala	Thr	Glu	Pro
			165					170					175		
Lys	Ile	Leu	Phe	Leu	Asp	Glu	Pro	Ala	Ala	Gly	Met	Asn	Pro	Gln	Glu
		180					185					190			
Thr	Ala	Glu	Leu	Thr	Glu	Leu	Ile	Arg	Arg	Ile	Lys	Asp	Glu	Phe	Lys
	195					200					205				
Ile	Thr	Ile	Met	Leu	Ile	Glu	His	Asp	Met	Asn	Leu	Val	Met	Glu	Val
	210				215					220					
Thr	Glu	Arg	Ile	Tyr	Val	Leu	Glu	Tyr	Gly	Arg	Leu	Ile	Ala	Gln	Gly
225				230					235					240	
Thr	Pro	Asp	Glu	Ile	Lys	Thr	Asn	Lys	Arg	Val	Ile	Glu	Ala	Tyr	Leu
			245					250					255		
Gly	Gly	Glu	Ala												
		260													

(2) INFORMATION FOR SEQ ID NO:2968:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2968:

Arg	Gly	Gly	Thr	Leu	Met	Glu	Ile	Ser	Lys	Gly	Ile	Ile	Phe	Asn	Ile
1				5					10					15	
Gln	His	Phe	Ser	Ile	His	Asp	Gly	Pro	Gly	Ile	Arg	Thr	Thr	Val	Phe
			20					25					30		
Leu	Lys	Gly	Cys	Pro	Leu	Arg	Cys	Pro	Trp	Cys	Ser	Asn	Pro	Glu	Ser
		35					40					45			
Gln	Arg	Met	Lys	Pro	Glu	Lys	Met	Lys	Asp	Ala	Gln	Arg	Glu	Lys	Phe
		50				55					60				
Thr	Leu	Val	Gly	Glu	Glu	Lys	Thr	Val	Glu	Glu	Ile	Ile	Thr	Glu	Val
65					70					75				80	
Leu	Lys	Asp	Lys	Glu	Phe	Tyr	Glu	Glu	Ser	Gly	Gly	Gly	Leu	Thr	Leu
				85					90					95	
Ser	Gly	Gly	Glu	Ile	Phe	Ala	Gln	Phe	Glu	Phe	Ala	Lys	Ala	Ile	Leu
			100					105					110		
Lys	Ser	Ala	Lys	Glu	His	His	Ile	His	Thr	Ala	Ile	Glu	Thr	Thr	Ala
		115					120					125			
Phe	Val	Asp	His	Glu	Lys	Phe	Ile	Asp	Leu	Ile	Gln	Tyr	Val	Asp	Phe
		130				135					140				
Ile	Tyr	Thr	Asp	Leu	Lys	His	Tyr	Asn	Ser	Ile	Lys	His	Lys	Lys	Val
145					150					155				160	
Thr	Gly	Val	Phe	Asn	Gln	Met	Ile	Ile	Lys	Asn	Ile	His	Tyr	Ala	Phe
				165					170					175	
Ser	Gln	Asn	Lys	Thr	Ile	Val	Leu	Arg	Ile	Pro	Val	Ile	Pro	Asn	Phe
			180					185					190		
Asn	Asn	Ser	Leu	Glu	Asp	Ala	Glu	Lys	Phe	Ala	Thr	Leu	Phe	Asn	Ser
		195					200					205			
Leu	Asn	Ile	Asp	Gln	Val	Gln	Leu	Leu	Pro	Phe	His	Gln	Phe	Gly	Glu
		210				215					220				
Asn	Lys	Tyr	Arg	Leu	Leu	Asn	Arg	Lys	Tyr	Glu	Met	Asp	Gly	Ile	Asn
225					230					235				240	
Ala	Leu	His	Pro	Glu	Asp	Leu	Ile	Asp	Tyr	Gln	Lys	Val	Phe	Leu	Asn
				245					250					255	
His	His	Ile	Asn	Cys	Tyr	Phe									
				260											

(2) INFORMATION FOR SEQ ID NO:2969:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 275 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...275

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2969:

Ala	Val	Glu	Thr	Lys	Leu	Lys	Arg	Thr	Tyr	Glu	Glu	Lys	Leu	Lys	Ile
1				5					10					15	

Leu	Leu	Leu	Pro	Lys	Asp	Pro	Asn	Asp	Asp	Lys	Asn	Ile	Ile	Leu	Glu
			20					25				30			
Ile	Arg	Gly	Ala	Ala	Gly	Gly	Asp	Glu	Ala	Ala	Leu	Phe	Ala	Gly	Asp
		35					40					45			
Leu	Leu	Thr	Met	Tyr	Gln	Lys	Tyr	Ala	Glu	Ala	Gln	Gly	Trp	Arg	Phe
		50				55					60				
Glu	Val	Met	Glu	Ala	Ser	Met	Asn	Gly	Val	Gly	Gly	Phe	Lys	Glu	Val
65					70					75					80
Val	Ala	Met	Val	Ser	Gly	Gln	Ser	Val	Tyr	Ser	Lys	Leu	Lys	Tyr	Glu
				85					90					95	
Ser	Gly	Ala	His	Arg	Val	Gln	Arg	Val	Pro	Val	Thr	Glu	Ser	Gln	Gly
			100					105						110	
Arg	Val	His	Thr	Ser	Thr	Ala	Thr	Val	Leu	Val	Met	Pro	Glu	Val	Glu
		115					120					125			
Glu	Val	Glu	Tyr	Asp	Ile	Asp	Pro	Lys	Asp	Leu	Arg	Val	Asp	Ile	Tyr
		130				135					140				
His	Ala	Ser	Gly	Ala	Gly	Gly	Gln	Asn	Val	Asn	Lys	Val	Ala	Thr	Ala
145					150					155					160
Val	Arg	Ile	Val	His	Leu	Pro	Thr	Asn	Ile	Lys	Val	Glu	Met	Gln	Glu
			165					170						175	
Glu	Arg	Thr	Gln	Gln	Lys	Asn	Arg	Glu	Lys	Ala	Met	Lys	Ile	Ile	Arg
		180						185					190		
Ala	Arg	Val	Ala	Asp	His	Phe	Ala	Gln	Ile	Ala	Gln	Asp	Glu	Gln	Asp
		195					200					205			
Ala	Glu	Arg	Lys	Ser	Thr	Ile	Gly	Thr	Gly	Asp	Arg	Ser	Glu	Arg	Ile
		210				215					220				
Arg	Thr	Tyr	Asn	Phe	Pro	Gln	Asn	Arg	Val	Thr	Asp	His	Arg	Ile	Gly
225					230					235					240
Leu	Thr	Leu	Gln	Lys	Leu	Asp	Thr	Ile	Leu	Ser	Gly	Lys	Leu	Asp	Glu
			245						250					255	
Val	Val	Asp	Ala	Leu	Val	Leu	Tyr	Asp	Gln	Thr	Gln	Lys	Leu	Glu	Glu
			260					265					270		
Leu	Asn	Lys													
		275													

(2) INFORMATION FOR SEQ ID NO:2970:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2970:

Arg Val Leu Thr Thr Tyr Leu Tyr Asp Ile Glu Ser Trp Thr Trp Phe

1		5		10		15									
Glu	Leu	Tyr	Leu	Phe	Cys	Asn	Thr	Met	Pro	Phe	Leu	Ser	His	Gln	Asp
		20						25					30		
Leu	Ile	Phe	Leu	Ser	Thr	Ser	Leu	Glu	Lys	Ser	Lys	Glu	Phe	Lys	
		35					40				45				
Glu	Leu	Val	His	Asn	Arg	Leu	Tyr	Met	Lys	Gln	Gly	Leu	Leu	Asn	Ile
	50					55				60					
Leu	Ser	Glu	Leu	Met	Glu	Arg	Lys	Leu	Phe	Ser	Tyr	Ile	Pro	Ile	Phe
65					70					75					80
Glu	Ala	Glu	Leu	Glu	Arg	Met	Leu	Arg	Pro	Tyr	Asp	Val	Phe	Glu	Lys
				85					90					95	
Val	Ser	Trp	Gln	Phe	Leu	Lys	Lys	Met	Ser	Val	Phe	Leu	Gln	Thr	Lys
		100						105					110		
Gly	Ser	Asn	Gln	Lys	Glu	Ile	Glu	Arg	Phe	Ile	Gln	Ser	Leu	Gln	Val
	115						120				125				
Leu	Glu	Asn	Pro	Gln	Leu	Thr	Ser	Leu	Phe	Glu	Leu	Arg	Phe	Gln	Gln
	130					135					140				
Tyr	Lys	Glu	Leu	Ile	Asp										
145					150										

(2) INFORMATION FOR SEQ ID NO:2971:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...247

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2971:

Ile	Ser	Leu	Thr	Phe	Phe	Trp	Glu	Glu	Leu	Gly	Ile	Leu	Leu	Val	Lys
1				5					10					15	
Asn	Leu	Gly	Ala	Leu	Pro	Met	Ile	Leu	Gly	Ser	Phe	Ile	Val	Thr	Ile
		20						25					30		
Leu	Ser	Ala	Leu	Ile	Ala	Thr	Pro	Phe	Ala	Ile	Gly	Ala	Ala	Val	Phe
		35				40					45				
Met	Thr	Glu	Val	Ser	Pro	Lys	Gly	Ala	Lys	Ile	Leu	Gln	Pro	Ala	Ile
	50					55				60					
Glu	Leu	Leu	Val	Gly	Ile	Pro	Ser	Val	Val	Tyr	Gly	Phe	Ile	Gly	Leu
65				70						75					80
Gln	Val	Val	Val	Pro	Phe	Val	Arg	Ser	Val	Phe	Gly	Gly	Thr	Gly	Phe
				85					90					95	
Gly	Ile	Leu	Ser	Gly	Ile	Ser	Val	Leu	Phe	Val	Met	Ile	Leu	Pro	Thr
		100						105					110		
Val	Thr	Phe	Met	Thr	Thr	Asp	Ser	Leu	Arg	Ala	Val	Pro	Arg	Tyr	Tyr
	115						120					125			
Arg	Glu	Ala	Ser	Phe	Ala	Met	Gly	Ala	Thr	Arg	Trp	Gln	Thr	Ile	Trp

130	135	140
Arg Val Ile Leu Lys	Ala Ala Arg Ser Gly	Ile Phe Thr Ala Val Val
145	150	155
Phe Gly Met Ala Arg	Ala Phe Gly Glu Ala	Leu Ala Ile Gln Met Val
165	170	175
Val Gly Asn Ser Ala	Val Ile Pro Thr Ser	Leu Thr Thr Pro Ala Ala
180	185	190
Thr Leu Thr Ser Ile	Leu Thr Met Gly	Ile Gly Asn Thr Val Met Gly
195	200	205
Thr Val Asn Asn Asn	Val Leu Trp Ser	Leu Ala Leu Val Leu Leu Leu
210	215	220
Met Ser Leu Val Phe	Asn Ser Val Ile	Lys Leu Ile Thr Lys Glu Arg
225	230	235
Gly Lys Lys Asn Tyr	Ala Arg	
245		

(2) INFORMATION FOR SEQ ID NO:2972:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2972:

Ile Asn Leu Thr Phe Leu Ile Glu Leu Phe Thr Ser Tyr Phe Asn Ser	
1	5 10 15
Leu Tyr Phe Pro Leu Tyr Ser Met Lys Ile Lys Ala Gln Thr Arg Lys	
	20 25 30
Leu Ala Thr Gly Cys Ser Lys His Cys Phe Glu Val Val Asp Lys Thr	
	35 40 45
Asp Glu Val Ser Ser Lys Tyr Cys Phe Glu Val Ala Asp Lys Thr Asp	
	50 55 60
Glu Val Ser Ser Lys Tyr Cys Phe Glu Val Ala Asp Lys Thr Asp Glu	
65	70 75 80
Val Ser Ser Lys Tyr Cys Phe Glu Val Ala Asp Lys Thr Asp Glu Val	
	85 90 95
Ser Ser Lys Tyr Cys Phe Glu Val Ala Asp Lys Thr Asp Glu Val Ser	
	100 105 110
Ser Lys Tyr Cys Phe Glu Val Ala Asp Lys Thr Asp Glu Val Ser Ser	
	115 120 125
Lys Tyr Cys Phe Glu Val Ala Asp Lys Thr Asp Glu Val Ser Ser Lys	
	130 135 140
Tyr Cys Phe Glu Val Ala Asp Gly Ser	
145	150

(2) INFORMATION FOR SEQ ID NO:2973:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...85

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2973:

Ile	Asn	Leu	Thr	Phe	Leu	Ile	Glu	Leu	Phe	Thr	Ser	Tyr	Phe	Lys	Ser
1				5					10					15	
Leu	Tyr	Phe	Lys	Lys	Val	Leu	Ala	Met	Thr	Gly	Thr	Glu	Thr	Phe	Thr
			20					25					30		
Val	Ile	Ser	Thr	Glu	Asp	Leu	Glu	Gln	Thr	Ser	Gly	Gly	Leu	Ala	Val
			35				40					45			
Trp	Glu	Asp	Gly	Tyr	Ser	Arg	Trp	Leu	Tyr	Tyr	Arg	Glu	Phe	Ala	Pro
			50			55					60				
Tyr	Met	Arg	Gln	Gly	Ala	Leu	Asn	Ser	Tyr	Ile	Asp	Ala	Trp	Lys	Tyr
65					70				75					80	
Gly	Phe	Arg	Thr	Gly											
				85											

(2) INFORMATION FOR SEQ ID NO:2974:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...97

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2974:

Gly	Ser	Leu	Thr	Ala	Arg	Ala	Thr	Thr	Arg	Ala	Gly	Thr	Lys	Val	Gly
1				5				10					15		
Leu	Ser	Asp	Pro	Val	Val	Pro	Tyr	Gly	Arg	Ala	Ile	Ala	Gln	Arg	Ile
			20					25					30		

Lys	Ala	Thr	Leu	Gly	Ile	Thr	Gly	Leu	Ser	Pro	Pro	Arg	Val	His	Ile
	35						40					45			
Asp	Gly	Glu	Val	Trp	His	Leu	Asp	Val	Gly	Ser	Ser	His	Pro	Gly	Ala
	50					55				60					
Val	Val	Gly	Pro	Lys	Gly	Trp	Ala	Val	Arg	Pro	Leu	Lys	Arg	His	Ala
65				70					75					80	
Ser	Trp	Val	Gln	Asn	Val	Val	Arg	Gln	Phe	Gly	Pro	Tyr	Pro	Ser	Arg
			85					90						95	
Ala															

(2) INFORMATION FOR SEQ ID NO:2975:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...97

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2975:

Gly	Ser	Leu	Thr	Ala	Arg	Ala	Thr	Thr	Arg	Ala	Gly	Thr	Lys	Val	Gly
1				5					10				15		
Leu	Ser	Asp	Pro	Val	Val	Pro	Tyr	Gly	Arg	Ala	Ile	Ala	Gln	Arg	Ile
		20						25				30			
Lys	Ala	Thr	Leu	Gly	Ile	Thr	Gly	Leu	Ser	Pro	Pro	Arg	Val	His	Ile
	35					40					45				
Asp	Gly	Glu	Val	Trp	His	Leu	Asp	Val	Gly	Ser	Ser	His	Pro	Gly	Ala
	50					55				60					
Val	Val	Gly	Pro	Lys	Gly	Trp	Ala	Val	Arg	Pro	Leu	Lys	Arg	His	Ala
65				70					75					80	
Ser	Trp	Val	Gln	Asn	Val	Val	Arg	Gln	Phe	Gly	Pro	Tyr	Pro	Ser	Arg
			85					90						95	
Ala															

(2) INFORMATION FOR SEQ ID NO:2976:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...97

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2976:

Gly	Ser	Leu	Thr	Ala	Arg	Ala	Thr	Thr	Arg	Ala	Gly	Thr	Lys	Val	Gly
1				5					10					15	
Leu	Ser	Asp	Pro	Val	Val	Pro	Tyr	Gly	Arg	Ala	Ile	Ala	Gln	Arg	Ile
			20					25					30		
Lys	Ala	Thr	Leu	Gly	Ile	Thr	Gly	Leu	Ser	Pro	Pro	Arg	Val	His	Ile
			35				40					45			
Asp	Gly	Glu	Val	Trp	His	Leu	Asp	Val	Gly	Ser	Ser	His	Pro	Gly	Ala
			50			55					60				
Val	Val	Gly	Pro	Lys	Gly	Trp	Ala	Val	Arg	Pro	Leu	Lys	Arg	His	Ala
65					70					75					80
Ser	Trp	Val	Gln	Asn	Val	Val	Arg	Gln	Phe	Gly	Pro	Tyr	Pro	Ser	Arg
				85				90						95	
Ala															

(2) INFORMATION FOR SEQ ID NO:2977:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 97 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...97

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2977:

Gly	Ser	Leu	Thr	Ala	Arg	Ala	Thr	Thr	Arg	Ala	Gly	Thr	Lys	Val	Gly
1				5					10					15	
Leu	Ser	Asp	Pro	Val	Val	Pro	Tyr	Gly	Arg	Ala	Ile	Ala	Gln	Arg	Ile
			20					25					30		
Lys	Ala	Thr	Leu	Gly	Ile	Thr	Gly	Leu	Ser	Pro	Pro	Arg	Val	His	Ile
			35				40					45			
Asp	Gly	Glu	Val	Trp	His	Leu	Asp	Val	Gly	Ser	Ser	His	Pro	Gly	Ala
			50			55					60				
Val	Val	Gly	Pro	Lys	Gly	Trp	Ala	Val	Arg	Pro	Leu	Lys	Arg	His	Ala
65					70					75					80
Ser	Trp	Val	Gln	Asn	Val	Val	Arg	Gln	Phe	Gly	Pro	Tyr	Pro	Ser	Arg
				85				90						95	

Ala

(2) INFORMATION FOR SEQ ID NO:2978:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...78

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2978:

Ala	Ser	Leu	Thr	Cys	Ser	Pro	Ser	Leu	Asp	Ser	Ile	Tyr	Ile	Cys	Arg
1				5					10					15	
Ala	Arg	Glu	Arg	Pro	Glu	Asp	Met	Arg	Leu	Leu	Gly	Val	Leu	Val	Glu
			20				25						30		
Val	Pro	Asn	Val	Tyr	Met	Arg	Ala	Ala	Val	Ser	Pro	Thr	Ile	Arg	Pro
		35				40						45			
Ile	Ala	Ser	Ile	Thr	Pro	Ala	Lys	Ile	Pro	Gly	Met	Ala	Thr	Gly	Arg
	50					55				60					
Thr	Ile	Leu	Lys	Thr	Val	Arg	Asn	Leu	Pro	Ala	Pro	Ser	Pro		
65					70				75						

(2) INFORMATION FOR SEQ ID NO:2979:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...245

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2979:

Lys	Met	Leu	Thr	Asn	Ser	Ile	Ile	Lys	Thr	Lys	Glu	Asn	Ser	Met	Leu
1				5					10					15	
Lys	Trp	Glu	Asp	Leu	Pro	Val	Glu	Met	Lys	Ser	Ser	Glu	Val	Glu	Ser

		20					25				30				
Tyr	Tyr	Gln	Leu	Val	Ser	Lys	Arg	Lys	Gly	Ser	Leu	Ile	Phe	Lys	Arg
		35					40					45			
Cys	Leu	Asp	Trp	Val	Leu	Ala	Leu	Val	Leu	Thr	Trp	Val	Leu	Thr	Ser
		50				55					60				
Pro	Ile	Phe	Leu	Ile	Leu	Ser	Ile	Trp	Ile	Lys	Leu	Asp	Ser	Lys	Gly
65					70					75					80
Pro	Val	Ile	Tyr	Lys	Gln	Glu	Arg	Val	Thr	Gln	Tyr	Asn	Arg	Arg	Phe
				85					90					95	
Lys	Ile	Trp	Lys	Phe	Arg	Thr	Met	Val	Thr	Asp	Ala	Asp	Lys	Lys	Gly
			100					105					110		
Ser	Leu	Val	Thr	Ser	Ala	Asn	Asp	Ser	Arg	Ile	Thr	Lys	Val	Gly	Asn
		115				120						125			
Phe	Ile	Arg	Arg	Val	Arg	Leu	Asp	Glu	Leu	Pro	Gln	Leu	Val	Asn	Val
		130				135					140				
Leu	Lys	Gly	Glu	Met	Ser	Phe	Val	Gly	Thr	Arg	Pro	Glu	Val	Pro	Arg
145					150					155					160
Tyr	Thr	Glu	Gln	Tyr	Ser	Pro	Glu	Met	Met	Ala	Thr	Leu	Leu	Leu	Gln
				165					170					175	
Ala	Gly	Ile	Thr	Ser	Pro	Ala	Ser	Ile	Asn	Tyr	Lys	Asp	Glu	Asp	Thr
			180					185					190		
Ile	Ile	Ser	Gln	Met	Thr	Glu	Lys	Gly	Leu	Ser	Val	Asp	Gln	Ala	Tyr
		195					200					205			
Val	Glu	His	Val	Leu	Pro	Glu	Lys	Met	Arg	Tyr	Asn	Leu	Ala	Tyr	Leu
		210				215					220				
Arg	Glu	Phe	Ser	Phe	Phe	Gly	Asp	Ile	Lys	Ile	Met	Phe	Gln	Thr	Val
225					230					235					240
Phe	Glu	Val	Leu	Lys											
				245											

(2) INFORMATION FOR SEQ ID NO:2980:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...61

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2980:

Met	Leu	Leu	Thr	Ser	Ser	Val	Leu	Ser	Ala	Thr	Ser	Lys	Gln	Cys	Phe
1				5					10					15	
Glu	Leu	Thr	Ser	Ser	Val	Leu	Ser	Thr	Thr	Ser	Lys	Gln	Cys	Phe	Glu
			20					25					30		
Gln	Pro	Val	Thr	Ser	Phe	Leu	Ser	Asp	Ala	Leu	Val	Leu	Ile	Ala	Tyr
		35				40						45			
Asn	Gln	Lys	Glu	Lys	Phe	Ser	Pro	Glu	Lys	His	Ile	Glu			

(2) INFORMATION FOR SEQ ID NO:2981:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 333 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2981:

```

Asn Lys Leu Thr Arg Lys Asn Lys Gly Glu Thr Met Ser Gln Leu Tyr
1      5      10      15
Asp Ile Thr Ile Val Gly Gly Gly Pro Val Gly Leu Phe Ala Ala Phe
      20      25      30
Tyr Ala His Leu Arg Gln Ala Lys Val Gln Ile Ile Asp Ser Leu Pro
      35      40      45
Gln Leu Gly Gly Gln Pro Ala Ile Leu Tyr Pro Glu Lys Glu Ile Leu
      50      55      60
Asp Val Pro Gly Phe Pro Asn Leu Thr Gly Glu Glu Leu Thr Asn Arg
65      70      75      80
Leu Ile Glu Gln Leu Asn Gly Phe Asp Thr Pro Ile His Leu Asn Glu
      85      90      95
Thr Val Leu Glu Ile Asp Lys Gln Glu Glu Glu Phe Ala Ile Thr Thr
      100     105     110
Ser Lys Gly Ser His Leu Thr Lys Thr Val Ile Ile Ala Met Gly Gly
      115     120     125
Gly Ala Phe Lys Pro Arg Pro Leu Glu Leu Glu Gly Val Glu Gly Tyr
      130     135     140
Glu Asn Ile His Tyr His Val Ser Asn Ile Gln Gln Tyr Ala Gly Lys
145     150     155     160
Lys Val Thr Ile Leu Gly Gly Gly Asp Ser Ala Val Asp Trp Ala Leu
      165     170     175
Ala Phe Glu Lys Ile Ala Pro Thr Thr Leu Val His Arg Arg Asp Asn
      180     185     190
Phe Arg Ala Leu Glu His Ser Val Gln Ala Leu Gln Glu Ser Ser Val
      195     200     205
Thr Ile Lys Thr Pro Phe Ala Pro Ser Gln Leu Leu Gly Asn Gly Lys
      210     215     220
Thr Leu Asp Lys Leu Glu Ile Thr Lys Val Lys Ser Asp Glu Thr Glu
225     230     235     240
Thr Ile Asp Leu Asp His Leu Phe Val Asn Tyr Gly Phe Lys Ser Ser
      245     250     255
Val Gly Asn Leu Lys Asn Trp Gly Leu Asp Leu Asn Arg His Lys Ile
      260     265     270
Ile Val Asn Ser Lys Gln Glu Ser Ser Gln Ala Gly Ile Tyr Ala Ile

```

	275		280		285										
Gly	Asp	Cys	Cys	Tyr	Tyr	Asp	Gly	Lys	Ile	Asp	Leu	Ile	Ala	Thr	Gly
	290					295					300				
Leu	Gly	Glu	Ala	Pro	Thr	Ala	Val	Asn	Asn	Ala	Ile	Asn	Tyr	Ile	Asp
305						310					315				320
Pro	Glu	Gln	Lys	Val	Gln	Pro	Lys	His	Ser	Thr	Ser	Leu			
				325					330						

(2) INFORMATION FOR SEQ ID NO:2982:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 89 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...89
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2982:

Asn	Glu	Leu	Thr	Pro	Lys	Val	Arg	Gln	Lys	Lys	Ser	Asn	Phe	Trp	Gly
1				5					10					15	
Val	Phe	Ile	Met	Lys	Leu	Thr	Tyr	Asp	Asp	Lys	Val	Gln	Ile	Tyr	Glu
			20					25					30		
Leu	Arg	Lys	Gln	Gly	Tyr	Ser	Leu	Glu	Lys	Leu	Ser	Asn	Lys	Phe	Gly
		35					40					45			
Ile	Asn	Asn	Ser	Asn	Leu	Arg	Tyr	Met	Ile	Lys	Leu	Ile	Asp	Arg	Tyr
	50					55					60				
Gly	Ile	Glu	Phe	Gly	Lys	Lys	Gly	Lys	Asn	Arg	Tyr	Tyr	Ser	Pro	Asp
65					70				75						80
Leu	Lys	Gln	Glu	Met	Ile	Tyr	Lys	Val							
				85											

(2) INFORMATION FOR SEQ ID NO:2983:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 97 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature

(B) LOCATION 1...97

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2983:

```
Ile Glu Leu Thr Lys Ser Ala Gln Ser Thr Ala Leu Arg Leu Gln Met
1      5      10      15
Lys Leu Thr Lys Ser Ala Gln Asn Met Phe Leu Arg Leu Trp Met Lys
      20      25      30
Leu Thr Lys Ser Ala Gln Asn Met Phe Leu Arg Leu Trp Met Lys Leu
      35      40      45
Thr Lys Ser Ala Gln Asn Met Phe Leu Arg Leu Trp Met Lys Leu Thr
      50      55      60
Lys Ser Val Thr Ile His Thr Val Arg Arg Arg Asp Val Val Cys Arg
65      70      75      80
Asp Phe Arg Arg Val Leu Ala Phe His Ile Val Phe Gln Ser Leu Ser
      85      90      95
Cys
```

(2) INFORMATION FOR SEQ ID NO:2984:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...127

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2984:

```
Ile Arg Leu Thr Lys Ser Ala Gln Asn Thr Val Leu Arg Leu Gln Ile
1      5      10      15
Arg Leu Thr Lys Ser Ala Gln Asn Thr Val Leu Arg Leu Gln Ile Arg
      20      25      30
Leu Thr Lys Ser Ala Gln Asn Thr Val Leu Arg Leu Gln Ile Arg Leu
      35      40      45
Thr Lys Ser Ala Gln Asn Thr Val Leu Arg Leu Gln Ile Arg Leu Thr
      50      55      60
Lys Ser Ala Gln Asn Thr Val Leu Arg Leu Gln Ile Arg Leu Thr Lys
65      70      75      80
Ser Ala Gln Asn Thr Val Leu Lys Leu Gln Ile Arg Leu Thr Lys Ser
      85      90      95
Ala Gln Asn Thr Val Leu Arg Leu Gln Met Glu Ala Asp Val Val Cys
      100      105      110
Arg Asp Phe Arg Arg Val Leu Tyr Glu Lys Asn Pro Leu Leu Tyr
      115      120      125
```

(2) INFORMATION FOR SEQ ID NO:2985:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 136 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...136
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2985:

Phe	Leu	Met	Thr	Lys	Ser	Leu	Ile	Leu	Val	Ser	His	Gly	Arg	Phe	Cys
1				5					10					15	
Glu	Glu	Leu	Arg	Gly	Ser	Thr	Glu	Met	Ile	Met	Gly	Leu	Gln	Asp	Asn
			20					25					30		
Ile	Tyr	Thr	Val	Ala	Leu	Leu	Pro	Glu	Asp	Gly	Pro	Glu	Glu	Phe	Thr
		35					40					45			
Ala	Lys	Phe	Glu	Ala	Val	Ile	Glu	Gly	Leu	Asp	Asp	Phe	Leu	Val	Phe
		50				55					60				
Ala	Asp	Leu	Leu	Gly	Gly	Thr	Pro	Cys	Asn	Val	Val	Ser	Arg	Leu	Ile
65					70					75					80
Met	Glu	Gly	Arg	Asp	Ile	Asp	Leu	Tyr	Ala	Gly	Met	Asn	Leu	Pro	Met
				85					90					95	
Val	Ile	Glu	Phe	Ile	Asn	Ala	Ser	Leu	Thr	Gly	Ala	Asp	Ala	Asp	Tyr
			100					105					110		
Lys	Ser	Arg	Ala	Ala	Glu	Ser	Ile	Val	Lys	Val	Asn	Asp	Leu	Leu	Ala
			115				120					125			
Gly	Phe	Asp	Asp	Asp	Glu	Asp	Glu								
		130				135									

(2) INFORMATION FOR SEQ ID NO:2986:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 151 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...151
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2986:

Thr	Asn	Met	Thr	Leu	Thr	Thr	Phe	Leu	Leu	Gln	Ala	Val	Ala	Ser	Phe
1				5				10						15	
Leu	Ala	Ile	Ile	Thr	Phe	Leu	Ile	Val	Leu	Asn	Val	Gln	Arg	Ser	Met
			20					25					30		
Leu	Leu	Pro	Gly	Gly	Ile	Leu	Gly	Met	Thr	Val	Trp	Leu	Ile	Tyr	Leu
		35					40					45			
Leu	Leu	Lys	Glu	Pro	Thr	Asn	Val	Ile	Val	Ala	Thr	Phe	Ile	Ala	Ala
	50					55					60				
Ile	Ile	Gly	Ser	Cys	Val	Ser	Gln	Ile	Leu	Ser	Ile	Leu	Tyr	Lys	Thr
65				70				75						80	
Pro	Ala	Val	Val	Phe	Ile	Leu	Ala	Ile	Leu	Ala	Pro	Leu	Val	Pro	Gly
				85				90						95	
Tyr	Leu	Ser	Tyr	Arg	Thr	Thr	Ala	Phe	Phe	Val	Thr	Gly	Asp	Tyr	Asn
			100					105					110		
Lys	Ala	Leu	Ala	Ser	Gly	Leu	Leu	Val	Val	Met	Leu	Ala	Leu	Val	Ile
		115				120						125			
Ser	Ile	Gly	Met	Ala	Ser	Gly	Ser	Val	Ile	Leu	Arg	Leu	Tyr	His	Tyr
	130					135					140				
Ile	Lys	Thr	His	Arg	Val	Ser									
145					150										

(2) INFORMATION FOR SEQ ID NO:2987:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 916 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...916

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2987:

Lys	Asp	Met	Thr	Glu	Arg	Glu	Ser	Val	Leu	His	Thr	Met	Ser	Arg	Arg
1				5				10						15	
Arg	His	Met	Ser	Lys	Glu	Gln	Lys	Arg	Gln	Ala	Phe	Tyr	Thr	Gln	Ser
			20					25					30		
Pro	Glu	Glu	Val	Leu	Gln	Ala	Val	Asp	Ala	Thr	Glu	Gln	Gly	Leu	Ser
		35					40					45			
Ser	Ser	Glu	Ala	Glu	Lys	Arg	Leu	Ala	Glu	Phe	Gly	His	Asn	Glu	Leu
	50				55					60					
Glu	Glu	Gly	Glu	Lys	Arg	Ser	Ile	Leu	Val	Lys	Phe	Ile	Glu	Gln	Phe
65				70				75						80	
Lys	Asp	Leu	Met	Ile	Ile	Ile	Leu	Val	Ala	Ala	Ala	Ile	Leu	Ser	Val
			85					90					95		
Val	Thr	Ser	Gly	Gly	Glu	Asp	Ile	Ala	Asp	Ala	Ile	Ile	Ile	Leu	Ala
			100					105					110		
Val	Val	Ile	Ile	Asn	Ala	Ala	Phe	Gly	Val	Tyr	Gln	Glu	Gly	Lys	Ala

Ala	Ile	Ala	Lys	Arg	Leu	Gly	Ile	Ile	Asp	Ala	Asn	Asp	Thr	Glu	Asp		
			580					585					590				
His	Val	Leu	Thr	Gly	Ala	Glu	Leu	Asn	Glu	Leu	Ser	Asp	Glu	Asp	Phe		
		595					600					605					
Glu	Lys	Val	Val	Gly	Gln	Tyr	Ser	Val	Tyr	Ala	Arg	Val	Ser	Pro	Glu		
	610				615						620						
His	Lys	Val	Arg	Ile	Val	Lys	Ala	Trp	Gln	Lys	Gln	Gly	Lys	Val	Val		
	625				630				635						640		
Ala	Met	Thr	Gly	Asp	Gly	Val	Asn	Asp	Ala	Pro	Ala	Leu	Lys	Thr	Ala		
			645						650						655		
Asp	Ile	Gly	Ile	Gly	Met	Gly	Ile	Thr	Gly	Thr	Glu	Val	Ser	Lys	Gly		
		660					665						670				
Ala	Ser	Asp	Met	Ile	Leu	Ala	Asp	Asp	Asn	Phe	Ala	Thr	Ile	Ile	Val		
	675						680					685					
Ala	Val	Glu	Glu	Gly	Arg	Lys	Val	Phe	Ser	Asn	Ile	Gln	Lys	Thr	Ile		
	690					695					700						
Gln	Tyr	Leu	Leu	Ser	Ala	Asn	Thr	Ala	Glu	Val	Leu	Thr	Ile	Phe	Leu		
	705				710					715					720		
Ser	Thr	Leu	Phe	Gly	Trp	Asp	Val	Leu	Gln	Pro	Val	His	Leu	Leu	Trp		
			725				730						735				
Ile	Asn	Leu	Val	Thr	Asp	Thr	Phe	Pro	Ala	Ile	Ala	Leu	Gly	Val	Glu		
		740					745						750				
Pro	Ala	Glu	Pro	Gly	Val	Met	Asn	His	Lys	Pro	Arg	Gly	Arg	Lys	Ala		
	755						760					765					
Ser	Phe	Ser	Gly	Gly	Val	Leu	Ser	Ser	Ile	Ile	Tyr	Gln	Gly	Val			
	770				775					780							
Leu	Gln	Ala	Ala	Leu	Val	Met	Ser	Val	Tyr	Gly	Leu	Ala	Ile	Ala	Tyr		
	785				790					795					800		
Pro	Val	His	Val	Gly	Asp	Asn	His	Ala	Ile	His	Ala	Asp	Ala	Leu	Thr		
			805					810						815			
Met	Ala	Phe	Ala	Thr	Leu	Gly	Leu	Ile	Gln	Leu	Phe	His	Ala	Tyr	Asn		
		820						825					830				
Val	Lys	Ser	Val	Tyr	Gln	Ser	Ile	Leu	Thr	Val	Gly	Pro	Phe	Lys	Ser		
	835					840						845					
Lys	Thr	Phe	Asn	Trp	Ser	Ile	Leu	Val	Ser	Phe	Ile	Leu	Leu	Met	Ala		
	850				855					860							
Thr	Ile	Val	Val	Glu	Pro	Leu	Glu	Gly	Ile	Phe	His	Val	Thr	Lys	Leu		
	865				870				875						880		
Asp	Leu	Ser	Gln	Trp	Gly	Ile	Val	Met	Ala	Gly	Ser	Phe	Ser	Met	Ile		
			885						890					895			
Ile	Ile	Val	Glu	Ile	Val	Lys	Phe	Ile	Gln	Arg	Lys	Leu	Gly	Phe	Asp		
		900						905					910				
Lys	Asn	Ala	Ile														
		915															

(2) INFORMATION FOR SEQ ID NO:2988:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...234

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2988:

Lys	Cys	Met	Thr	Lys	Arg	Val	Leu	Ile	Thr	Gly	Val	Ser	Ser	Gly	Ile
1				5					10					15	
Gly	Leu	Ala	Gln	Ala	Arg	Leu	Phe	Leu	Glu	Lys	Gly	Tyr	Gln	Val	Tyr
			20					25					30		
Gly	Val	Asp	Gln	Gly	Glu	Lys	Pro	Leu	Leu	Glu	Gly	Asp	Phe	His	Phe
		35					40					45			
Leu	Gln	Arg	Asp	Leu	Thr	Leu	Asp	Leu	Glu	Pro	Ile	Phe	Asp	Trp	Cys
	50					55				60					
Pro	Gln	Val	Asp	Val	Leu	Cys	Asn	Thr	Ala	Gly	Val	Leu	Asp	Asp	Tyr
65				70					75					80	
Lys	Pro	Leu	Leu	Glu	Gln	Thr	Ala	Gln	Asp	Ile	Gln	Glu	Ile	Phe	Glu
			85					90						95	
Ile	Asn	Tyr	Ile	Ile	Pro	Val	Glu	Leu	Thr	Arg	Tyr	Tyr	Leu	Thr	Gln
	100						105						110		
Met	Leu	Glu	Asn	Lys	Lys	Gly	Ile	Ile	Asn	Met	Cys	Ser	Ile	Ala	
	115					120				125					
Ser	Ser	Leu	Ala	Gly	Gly	Gly	Gly	His	Ala	Tyr	Thr	Ser	Ser	Lys	His
	130				135						140				
Ala	Leu	Ala	Gly	Phe	Thr	Lys	Gln	Leu	Ala	Leu	Asp	Tyr	Ala	Glu	Ala
145				150					155					160	
Gly	Ile	Gln	Val	Phe	Gly	Ile	Ala	Pro	Gly	Ala	Val	Lys	Thr	Ala	Met
			165					170						175	
Thr	Ala	Ala	Asp	Phe	Glu	Pro	Gly	Gly	Leu	Ala	Asp	Trp	Val	Ala	Ser
		180					185					190			
Glu	Thr	Pro	Ile	Lys	Arg	Trp	Ile	Glu	Pro	Glu	Glu	Ile	Ala	Glu	Leu
	195					200					205				
Ser	Leu	Phe	Leu	Ala	Ser	Gly	Lys	Ala	Ser	Ala	Met	Gln	Gly	Gln	Ile
	210				215					220					
Leu	Thr	Ile	Asp	Gly	Gly	Trp	Ser	Leu	Lys						
225					230										

(2) INFORMATION FOR SEQ ID NO:2989:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 177 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...177

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2989:

```
Glu Ile Met Thr Glu Thr Leu Ile Lys Ile Glu Asn Leu His Lys Ser
1           5           10           15
Phe Gly Lys Asn Glu Val Leu Lys Gly Ile Asn Leu Glu Ile Lys Arg
           20           25           30
Gly Glu Val Val Val Ile Ile Gly Pro Ser Gly Ser Gly Lys Ser Thr
           35           40           45
Leu Leu Arg Ser Met Asn Leu Leu Glu Glu Ala Thr Lys Gly Lys Leu
           50           55           60
Ile Phe Glu Gly Val Asp Ile Thr Asp Lys Lys Asn Asp Leu Phe Ala
65           70           75           80
Met Arg Glu Lys Met Gly Met Val Phe Gln Gln Phe Asn Leu Phe Pro
           85           90           95
Asn Met Thr Val Met Glu Asn Ile Thr Leu Ser Pro Ile Lys Thr Lys
           100          105          110
Gly Glu Ser Arg Glu Val Ala Glu Lys Arg Ala Gln Glu Leu Leu Glu
           115          120          125
Lys Val Gly Leu Pro Asp Lys Ala Asp Ala Tyr Pro Gln Ser Leu Ser
           130          135          140
Gly Gly Gln Gln Gln Arg Ile Ala Ser Arg Val Gly Trp Leu Trp Tyr
145          150          155          160
Gln Met Phe Cys Ser Leu Thr Asn Gln Leu Gln Pro Trp Ile Leu Lys
           165          170          175
Trp
```

(2) INFORMATION FOR SEQ ID NO:2990:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2990:

```
Arg Val Met Thr Leu Val Tyr Gln Ser Thr Arg Asp Ala Asn Asn Thr
1           5           10           15
Val Thr Ala Ser Gln Ala Ile Leu Gln Gly Leu Ala Thr Asp Gly Gly
           20           25           30
Leu Phe Thr Pro Asp Thr Tyr Pro Lys Val Asp Leu Asn Phe Asp Lys
           35           40           45
Leu Lys Asp Ala Ser Tyr Gln Glu Val Ala Lys Leu Val Leu Ser Ala
           50           55           60
Phe Leu Asp Asp Phe Thr Val Glu Glu Leu Asp Tyr Cys Ile Asn Asn
```

65					70					75				80
Ala	Tyr	Asp	Ser	Lys	Phe	Asp	Thr	Pro	Ala	Ile	Ala	Pro	Leu	Val Lys
				85					90					95
Leu	Asp	Gly	Gln	Tyr	Asn	Leu	Glu	Leu	Phe	His	Gly	Ser	Thr	Ile Ala
			100					105					110	
Phe	Lys	Asp	Met	Ala	Leu	Ser	Ile	Leu	Pro	Tyr	Phe	Met	Thr	Thr Ala
		115					120					125		
Ala	Lys	Lys	His	Gly	Leu	Glu	Asn	Lys	Ile	Val	Ile	Leu	Thr	Ala Thr
	130					135					140			
Ser	Gly	Asp	Thr	Gly	Lys	Ala	Ala	Met	Ala	Gly	Phe	Ala	Asn	Val Pro
145					150					155				160
Gly	Thr	Glu	Ile	Ile	Val	Phe	Tyr	Pro	Lys	Asp	Gly	Val	Ser	Lys Ile
			165					170						175
Gln	Glu	Leu	Gln	Met	Thr	Thr	Gln	Thr	Gly	Asp	Asn	Thr	His	Val Ile
		180					185					190		
Ala	Ile	Asp	Gly	Asn	Phe	Asp	Asp	Ala	Gln	Thr	Asn	Val	Lys	His Met
	195					200					205			
Phe	Asn	Asp	Val	Ala	Leu	Arg	Glu	Lys	Leu	Thr	Thr	Asn	Lys	Leu Gln
	210				215					220				
Phe	Ser	Ser	Ala	Asn	Ser	Met	Asn	Ile	Gly	Arg	Leu	Val	Pro	Gln Ile
225				230					235					240
Val	Tyr	Tyr	Val	Tyr	Ala	Tyr	Ala	Gln	Leu	Val	Lys	Thr	Gly	Glu Ile
			245					250					255	
Val	Ala	Gly	Glu	Lys	Val	Asn	Phe	Thr	Val	Pro	Thr	Gly	Asn	Phe Gly
		260					265					270		
Asn	Ile	Leu	Ala	Ala	Phe	Tyr	Ala	Lys	Gln	Ile	Gly	Leu	Pro	Val Gly
	275					280					285			
Lys	Leu	Ile	Cys	Ala	Ser	Asn	Asp	Asn	Asn	Val	Leu	Thr	Asp	Phe Phe
	290				295					300				
Lys	Thr	Arg	Val	Tyr	Asp	Lys	Lys	Arg	Glu	Phe	Lys	Val	Thr	Thr Ser
305				310					315					320
Pro	Ser	Met	Asp	Ile	Leu	Val	Ser	Ser	Asn	Leu	Glu	Arg	Leu	Ile Phe
			325					330					335	
His	Leu	Leu	Gly	Asn	Asn	Ala	Glu	Lys	Thr	Thr	Glu	Leu	Met	Asn Ala
		340					345					350		
Leu	Asn	Thr	Gln	Gly	Gln	Tyr	Lys	Leu	Thr	Asp	Phe	Asp	Ala	Glu Ile
	355					360					365			
Leu	Asp	Leu	Phe	Ala	Ala	Glu	Tyr	Ala	Thr	Glu	Glu	Glu	Thr	Ala Ala
	370				375					380				
Glu	Ile	Lys	Arg	Val	Cys	Glu	Leu	Asp	Ser	Tyr	Ile	Glu	Asp	Pro His
385				390					395					400
Thr	Ala	Val	Ala	Ser	Ala	Val	Tyr	Lys	Lys	Tyr	Gln	Ser	Ala	Thr Gly
		405					410						415	
Asp	Val	Thr	Lys	Thr	Val	Ile	Ala	Ser	Thr	Ala	Ser	Pro	Tyr	Lys Phe
		420					425					430		
Pro	Val	Val	Ala	Val	Glu	Ala	Val	Thr	Gly	Lys	Ala	Gly	Leu	Thr Asp
	435					440					445			
Phe	Glu	Ala	Leu	Ala	Gln	Leu	His	Glu	Ile	Ser	Gly	Val	Ala	Val Pro
	450				455				460					
Pro	Ala	Val	Asp	Gly	Leu	Glu	Ile	Ala	Pro	Ile	Arg	His	Lys	Thr Thr
465				470					475					480
Val	Ala	Ala	Ala	Asp	Met	Gln	Ala	Ala	Val	Glu	Ala	Tyr	Leu	Gly Leu
			485				490						495	

(2) INFORMATION FOR SEQ ID NO:2991:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...100

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2991:

```

Leu Glu Met Thr Thr Ile Arg Ser Leu Leu Leu Asn Phe Ile Ser Ile
1          5          10          15
Ser Tyr Ser Ile Phe Ile Gln Lys Ile Lys Lys Gln Thr Arg Lys Leu
20          25          30
Val Ala Gly Gly Ser Lys His Cys Phe Glu Ile Val Asp Arg Thr Asp
35          40          45
Lys Pro Cys Asn Ile Pro Ala Tyr Ile His Thr Thr Arg Arg Tyr Tyr
50          55          60
Pro Ser Leu Lys Arg Phe Ser Lys Ser Ile His Phe Cys Leu Leu Leu
65          70          75          80
Ile Ile Pro Tyr Ser His Lys Lys Thr Asn Ile Leu Ile Leu Lys Asn
85          90          95
Ala His Phe Ser
100

```

(2) INFORMATION FOR SEQ ID NO:2992:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 273 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2992:

```

Lys Phe Val Thr Ser Phe Tyr Pro Ile Tyr Ala Met Val Lys Glu Val
1          5          10          15
Ser Gly Asp Leu Asn Asp Val Arg Met Ile Gln Ser Ser Ser Gly Ile
20          25          30
His Ser Phe Glu Pro Ser Ala Asn Asp Ile Ala Ala Ile Tyr Asp Ala

```


[illegible]

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2994:

Leu	Gln	Ser	Thr	Gln	Val	Asp	Ala	His	Gly	Tyr	Met	Gly	Arg	Gly	Trp
1				5					10					15	
Asp	Trp	Ala	Asp	Met	Leu	Gly	Phe	Thr	Val	Ala	Gly	Tyr	Gly	Val	Val
		20						25					30		
Ser	Met	Asp	Val	Arg	Gly	Gln	Ser	Gly	Tyr	Ser	Gln	Asp	Gly	Leu	Arg
		35					40					45			
Ser	Pro	Leu	Gly	Asn	Thr	Val	Lys	Gly	His	Ile	Ile	Arg	Gly	Ala	Met
	50					55					60				
Glu	Gly	Arg	Asp	His	Leu	Phe	Tyr	Lys	Asp	Val	Tyr	Leu	Asp	Ile	Tyr
65					70					75					80
Gln	Leu	Val	Glu	Ile	Val	Ala	Ser	Leu	Ser	Gln	Val	Asp	Glu	Lys	Arg
				85					90					95	
Leu	Ser	Ser	Tyr	Gly	Ala	Ser	Gln	Gly	Gly	Ala	Leu	Ala	Leu	Val	Ala
			100					105					110		
Ala	Ala	Leu	Asn	Pro	Arg	Ile	Gln	Lys	Thr	Val	Ala	Ile	Tyr	Pro	Phe
		115					120					125			
Leu	Ser	Asp	Phe	Arg	Arg	Val	Ile	Glu	Ile	Gly	Asn	Thr	Ser	Glu	Ala
	130					135					140				
Tyr	Asp	Glu	Leu	Phe	Arg	Tyr	Phe	Lys	Phe	His	Asp	Pro	Phe	His	Glu
145					150					155					160
Thr	Glu	Glu	Glu	Ile	Met	Ala	Thr	Leu	Ala	Tyr	Ile	Asp	Val	Lys	Asn
				165						170				175	
Leu	Ala	His	Arg	Ile	Gln	Gly	Glu	Val	Lys	Met	Ile	Thr	Gly	Leu	Asp
			180					185					190		
Asp	Asp	Val	Cys	Tyr	Pro	Ile	Thr	Gln	Phe	Ala	Ile	Tyr	Asn	Arg	Leu
		195					200					205			
Thr	Cys	Asp	Lys	Thr	Tyr	Arg	Ile	Met	Pro	Glu	Tyr	Ala	His	Glu	Ala
	210					215					220				
Met	Asn	Val	Phe	Val	Asn	Asp	Gln	Val	Tyr	Asn	Trp	Leu	Cys	Gly	Ser
225					230					235					240
Glu	Ile	Pro	Phe	Lys	Tyr	Leu	Lys								
				245											

(2) INFORMATION FOR SEQ ID NO:2995:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 69 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...69
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2995:

Lys	Asn	Thr	Thr	Ser	Pro	Phe	Leu	Val	Asn	Thr	Val	Ser	Cys	Leu	Val
1				5					10					15	
Val	Phe	Cys	Tyr	Phe	Thr	Val	Leu	Ser	Val	Tyr	Leu	Tyr	Lys	Lys	Asn

	20		25		30										
Leu	Glu	Gly	Val	Thr	Leu	Gln	Gly	Phe	Ile	Leu	Leu	Glu	Asn	Leu	Phe
	35		40		45										
Lys	Pro	Arg	Gln	Leu	Tyr	Leu	Gln	Pro	Gln	Asn	Ser	Val	Leu	Ser	Ser
	50		55		60										
Leu	Arg	Leu	Ala	Ser											
65															

(2) INFORMATION FOR SEQ ID NO:2996:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 521 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...521
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2996:

Ile	Ala	Thr	Thr	Trp	Tyr	Ile	Tyr	Leu	Pro	Pro	Leu	Asn	Leu	Thr	Ser
1				5				10						15	
Trp	Glu	Phe	Leu	Phe	Phe	Leu	Cys	Gly	His	Leu	Leu	Val	Val	Ala	Ile
			20					25					30		
Leu	Phe	Gly	Phe	Gly	Lys	Gly	Ile	Asn	Leu	Val	Lys	Thr	Val	His	Val
		35				40						45			
Arg	His	Gly	Lys	Ala	Glu	Ala	Ala	Leu	Asn	Leu	Glu	Gly	Phe	Lys	Ile
	50				55						60				
Asn	Arg	Leu	Gly	Lys	Ile	Leu	Leu	Ala	Ser	Ile	Gly	Gly	Ile	Leu	Leu
65					70				75					80	
Leu	Ala	Ala	Leu	Val	Ser	Leu	Val	Thr	Ser	Ser	Met	Phe	Gln	Ala	Lys
			85					90						95	
Asn	Tyr	Ala	Asn	Val	Val	Thr	Val	Thr	Glu	Lys	Asp	Phe	Thr	Glu	Phe
			100					105					110		
Pro	Arg	Ser	Asp	Thr	Ser	Lys	Val	Pro	Ile	Leu	Asp	Arg	Ser	Thr	Ala
		115				120						125			
Glu	Lys	Ile	Gly	Asp	Arg	Tyr	Leu	Gly	Ser	Leu	Thr	Asp	Lys	Val	Ser
	130					135					140				
Gln	Tyr	Val	Ala	Ala	Asp	Thr	Tyr	Thr	Gln	Leu	Thr	Ile	Asp	Gly	Lys
145					150					155				160	
Pro	Tyr	Arg	Val	Thr	Pro	Leu	Glu	Tyr	Ala	Asp	Pro	Ile	Lys	Trp	Phe
			165					170					175		
Asn	Asn	Gln	Ala	Lys	Gly	Ile	Gly	Glu	Tyr	Ile	Lys	Val	Asp	Met	Val
		180				185						190			
Thr	Gly	Asn	Ala	Asp	Leu	Val	Asp	Leu	Lys	Thr	Pro	Ile	Lys	Tyr	Ser
	195				200						205				
Asp	Ser	Glu	Tyr	Phe	Asn	Arg	Asp	Val	Lys	Arg	His	Leu	Arg	Leu	Lys
	210					215					220				

```

Tyr Pro Thr Lys Ile Phe Lys Thr Pro Ser Phe Glu Val Asp Asp Glu
225                230                235                240
Gly Asn Pro Phe Tyr Val Ala Thr Val Tyr Gln Lys Gln Phe Gly Leu
                245                250                255
Ala Val Pro Arg Pro Ala Ser Val Ile Ile Leu Asp Ala Thr Asn Gly
                260                265                270
Glu Thr Lys Glu Tyr Ser Leu Ser Asp Val Pro Glu Trp Val Asp Arg
                275                280                285
Ile Tyr Pro Ala Glu Glu Thr Ile Glu Gln Ile Asn Tyr Asn Gly Lys
                290                295                300
Tyr Lys Asp Gly Phe Leu Asn Ala Met Ile Ser Lys Lys Asn Val Thr
305                310                315                320
Gln Thr Thr Lys Gly Tyr Asn Tyr Leu Ser Ile Gly Asn Asp Ile Tyr
                325                330                335
Leu Tyr Thr Gly Val Thr Ser Ala Asn Ala Asp Glu Ser Asn Leu Gly
                340                345                350
Phe Ile Leu Glu Asn Met Arg Thr Gly Glu Ile Thr Lys Tyr Ser Leu
                355                360                365
Ala Ser Ala Thr Glu Glu Ser Ala Arg Glu Ser Ala Glu Gly Ala Val
                370                375                380
Gln Glu Lys Ser Tyr Lys Ala Thr Phe Pro Ile Leu Ile Asn Leu Asn
385                390                395                400
Asp Lys Pro Leu Tyr Ile Met Gly Leu Lys Asp Asn Ala Gly Leu Val
                405                410                415
Lys Glu Tyr Ala Leu Val Asp Ala Val Glu Tyr Gln Asn Val Ile Val
                420                425                430
Ala Thr Thr Val Glu Glu Met Leu Ser Lys Tyr Ala Asn Lys Asn Asp
                435                440                445
Leu Glu Ile Asp Asn Ala Thr Thr Glu Ser Ile Asn Gly Val Val Ala
                450                455                460
Asp Leu Lys Ser Ala Val Ile Lys Gly Asp Thr Val Tyr Phe Phe Lys
465                470                475                480
Val Asp Gly Lys Ile Tyr Lys Val Lys Ala Ser Val Ser Asp Asp Tyr
                485                490                495
Pro Tyr Leu Glu Asn Gly Lys Thr Phe Glu Gly Gln Val Gly Lys Asp
                500                505                510
Asn Tyr Leu Lys Thr Phe Lys Leu Arg
                515                520

```

(2) INFORMATION FOR SEQ ID NO:2997:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2997:

Asp	Met	Thr	Thr	Asn	Arg	Lys	Asp	Glu	His	Ile	Leu	Tyr	Ala	Leu	Glu
1				5				10						15	
Gln	Lys	Ser	Ser	Tyr	Asn	Ser	Phe	Asp	Glu	Val	Glu	Leu	Ile	His	Ser
			20					25					30		
Ser	Leu	Pro	Leu	Tyr	Asn	Leu	Asp	Glu	Ile	Asp	Leu	Ser	Thr	Glu	Phe
		35					40					45			
Ala	Gly	Arg	Lys	Trp	Asp	Phe	Pro	Phe	Tyr	Ile	Asn	Ala	Met	Thr	Gly
	50					55					60				
Gly	Ser	Asn	Lys	Gly	Arg	Glu	Ile	Asn	Gln	Lys	Leu	Ala	Gln	Val	Ala
65					70				75					80	
Glu	Ser	Cys	Gly	Ile	Leu	Phe	Val	Thr	Gly	Ser	Tyr	Ser	Ala	Ala	Leu
			85						90					95	
Lys	Asn	Pro	Thr	Asp	Asp	Ser	Phe	Ser	Val	Lys	Ser	Ser	His	Pro	Asn
			100						105				110		
Leu	Leu	Leu	Gly	Thr	Asn	Ile	Gly	Leu	Asp	Lys	Pro	Val	Glu	Leu	Gly
		115					120					125			
Leu	Gln	Thr	Val	Glu	Glu	Met	Asn	Pro	Val	Leu	Leu	Gln	Val	His	Val
	130					135					140				
Asn	Val	Met	Gln	Glu	Leu	Leu	Met	Pro	Glu	Gly	Glu	Arg	Lys	Phe	Arg
145					150					155					160
Ser	Trp	Gln	Ser	His	Leu	Ala	Asp	Tyr	Ile	Lys	Gln	Ile	Pro	Val	Pro
			165						170					175	
Ile	Val	Leu	Lys	Glu	Val	Gly	Phe	Gly	Met	Asp	Ala	Lys	Thr	Ile	Glu
			180					185					190		
Arg	Ala	Tyr	Glu	Phe	Gly	Val	Arg	Thr	Val	Asp	Leu	Ser	Gly	Arg	Gly
		195					200					205			
Gly	Thr	Ser	Phe	Ala	Tyr	Ile	Glu	Asn	Arg	Arg	Ser	Gly	Gln	Arg	Asp
	210					215					220				
Tyr	Leu	Asn	Gln	Trp	Gly	Gln	Ser	Thr	Met	Gln	Ala	Leu	Leu	Asn	Ala
225					230					235					240
Gln	Glu	Trp	Lys	Asp	Lys	Val	Glu	Leu	Leu	Val	Ser	Gly	Gly	Val	Arg
			245						250					255	
Asn	Pro	Leu	Asp	Met	Ile	Lys	Cys	Leu	Val	Phe	Gly	Ala	Lys	Ala	Val
		260						265					270		
Gly	Leu	Ser	Arg	Thr	Val	Leu	Glu	Leu	Val	Glu	Thr	Tyr	Thr	Val	Glu
	275						280					285			
Glu	Val	Ile	Gly	Ile	Val	Gln	Gly	Trp	Lys	Ala	Asp	Leu	Arg	Leu	Ile
	290					295					300				
Met	Cys	Ser	Leu	Asn	Cys	Ala	Thr	Ile	Ala	Asp	Leu	Gln	Lys	Val	Asp
305				310						315					320
Tyr	Leu	Leu	Tyr	Gly	Lys	Leu	Lys	Glu	Ala	Lys	Asp	Gln	Met	Lys	Lys
			325						330					335	
Ala															

(2) INFORMATION FOR SEQ ID NO:2998:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2998:

Ala	Phe	Ala	Thr	Lys	Pro	Lys	Gln	Phe	Ile	Phe	Met	Ala	Lys	Lys	Glu
1				5					10					15	
Leu	Phe	Thr	Asn	Arg	Ile	Phe	Gly	Trp	Trp	Ile	Arg	Met	Cys	Gly	Ala
			20					25					30		
Phe	Pro	Ile	Asp	Arg	Glu	Asn	Pro	Ser	Ala	Ser	Ala	Ile	Lys	Tyr	Pro
			35				40					45			
Ile	Asn	Val	Leu	Lys	Lys	Ser	Asp	Arg	Ser	Leu	Ile	Met	Phe	Pro	Ser
	50					55					60				
Gly	Ser	Arg	His	Ser	Asn	Asp	Val	Lys	Gly	Gly	Ala	Ala	Leu	Ile	Ala
65					70					75					80
Lys	Met	Ala	Lys	Val	Arg	Ile	Met	Pro	Val	Thr	Tyr	Thr	Gly	Pro	Met
				85					90					95	
Thr	Leu	Lys	Gly	Leu	Ile	Ser	Arg	Glu	Arg	Val	Asp	Met	Asn	Phe	Gly
			100					105					110		
Asn	Pro	Ile	Asp	Ile	Ser	Asp	Ile	Lys	Lys	Met	Asn	Asp	Glu	Gly	Ile
			115				120					125			
Glu	Thr	Val	Ala	Asn	Arg	Ile	Gln	Thr	Glu	Phe	Gln	Arg	Leu	Asp	Glu
	130					135					140				
Glu	Thr	Lys	Gln	Trp	His	Asn	Asp	Lys	Lys	Pro	Asn	Pro	Leu	Trp	Trp
145					150					155					160
Phe	Ile	Arg	Ile	Pro	Ala	Leu	Ile	Leu	Ala	Ile	Ile	Leu	Ala	Ile	Leu
				165					170					175	
Thr	Ile	Ile	Phe	Ser	Phe	Ile	Ala	Ser	Phe	Ile	Trp	Asn	Pro	Asp	Lys
			180					185					190		
Lys	Arg	Glu	Lys	Leu	His	Arg	Arg	Glu							
		195					200								

(2) INFORMATION FOR SEQ ID NO:2999:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 265 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...265

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2999:

Lys	Thr	Gln	Thr	Val	Thr	Gly	Val	Pro	Lys	Met	Ser	Gln	Glu	Phe	Leu
1				5					10					15	
Ala	Arg	Ile	Leu	Glu	Gln	Lys	Ala	Arg	Glu	Val	Glu	Gln	Met	Lys	Leu
			20					25					30		
Glu	Gln	Ile	Gln	Pro	Leu	Arg	Gln	Thr	Tyr	Arg	Leu	Ala	Glu	Phe	Leu
		35					40					45			
Lys	Asn	His	Gln	Asp	Cys	Leu	Gln	Val	Ile	Ala	Glu	Val	Lys	Lys	Ala
	50					55					60				
Ser	Pro	Ser	Leu	Gly	Asp	Ile	Asn	Leu	Asp	Val	Asp	Ile	Val	Gln	Gln
65					70					75					80
Ala	Gln	Thr	Tyr	Glu	Glu	Asn	Gly	Ala	Val	Met	Ile	Ser	Val	Leu	Thr
				85				90						95	
Asp	Glu	Val	Phe	Phe	Lys	Gly	His	Leu	Asp	Tyr	Leu	Arg	Glu	Ile	Ser
			100					105					110		
Ser	Gln	Val	Glu	Ile	Pro	Thr	Leu	Asn	Lys	Asp	Phe	Ile	Ile	Asp	Glu
		115					120					125			
Lys	Gln	Ile	Ile	Arg	Ala	Arg	Asn	Ala	Gly	Ala	Thr	Val	Ile	Leu	Leu
	130					135					140				
Ile	Val	Ala	Ala	Leu	Ser	Glu	Glu	Arg	Leu	Lys	Glu	Leu	Tyr	Asp	Tyr
145					150					155					160
Ala	Thr	Glu	Leu	Gly	Leu	Glu	Val	Leu	Val	Glu	Thr	His	Asn	Leu	Ala
			165					170						175	
Glu	Leu	Glu	Val	Ala	His	Arg	Leu	Gly	Ala	Glu	Ile	Ile	Gly	Val	Asn
			180					185					190		
Asn	Arg	Asn	Leu	Thr	Thr	Phe	Glu	Val	Asp	Leu	Gln	Thr	Ser	Val	Asp
	195						200					205			
Leu	Ala	Pro	Tyr	Phe	Glu	Glu	Gly	Arg	Tyr	Tyr	Ile	Ser	Glu	Ser	Ala
	210					215					220				
Ile	Phe	Thr	Gly	Gln	Asp	Ala	Glu	Arg	Leu	Ala	Pro	Tyr	Phe	Asn	Gly
225					230					235					240
Ile	Leu	Val	Gly	Thr	Ala	Leu	Met	Gln	Ala	Glu	Asn	Val	Ala	Gln	Arg
			245					250						255	
Ile	Lys	Glu	Leu	Gln	Ile	Asp	Lys	Gly							
			260					265							

(2) INFORMATION FOR SEQ ID NO:3000:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 763 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...763
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3000:

Arg	Asn	Lys	Thr	Ile	Ile	Arg	Arg	Gln	Leu	Asn	Met	Leu	Ser	Leu	Gln
1			5					10					15		
Glu	Phe	Val	Gln	Asn	Arg	Tyr	Asn	Lys	Thr	Ile	Ala	Glu	Cys	Ser	Asn
		20					25					30			
Glu	Glu	Leu	Tyr	Leu	Ala	Leu	Leu	Asn	Tyr	Ser	Lys	Leu	Ala	Ser	Ser
	35					40					45				
Gln	Lys	Pro	Val	Asn	Thr	Gly	Lys	Lys	Lys	Val	Tyr	Tyr	Ile	Ser	Ala
	50				55					60					
Glu	Phe	Leu	Ile	Gly	Lys	Leu	Leu	Ser	Asn	Asn	Leu	Ile	Asn	Leu	Gly
65				70					75						80
Leu	Tyr	Asp	Asp	Val	Lys	Lys	Glu	Leu	Ala	Ala	Ala	Gly	Lys	Asp	Leu
			85				90							95	
Ile	Glu	Val	Glu	Glu	Val	Glu	Leu	Glu	Pro	Ser	Leu	Gly	Asn	Gly	Gly
	100					105						110			
Leu	Gly	Arg	Leu	Ala	Ala	Cys	Phe	Ile	Asp	Ser	Ile	Ala	Thr	Leu	Gly
	115					120						125			
Leu	Asn	Gly	Asp	Gly	Val	Gly	Leu	Asn	Tyr	His	Phe	Gly	Leu	Phe	Gln
	130					135					140				
Gln	Val	Leu	Lys	Asn	Asn	Gln	Gln	Glu	Thr	Ile	Pro	Asn	Ala	Trp	Leu
145				150						155					160
Thr	Glu	Gln	Asn	Trp	Leu	Val	Arg	Ser	Ser	Arg	Ser	Tyr	Gln	Val	Pro
			165					170						175	
Phe	Ala	Asp	Phe	Thr	Leu	Thr	Ser	Thr	Leu	Tyr	Asp	Ile	Asp	Val	Thr
		180						185					190		
Gly	Tyr	Glu	Thr	Ala	Thr	Lys	Asn	Arg	Leu	Arg	Leu	Phe	Asp	Leu	Asp
	195					200					205				
Ser	Val	Asp	Ser	Ser	Ile	Ile	Lys	Asp	Gly	Ile	Asn	Phe	Asp	Lys	Thr
	210				215						220				
Asp	Ile	Ala	Arg	Asn	Leu	Thr	Leu	Phe	Leu	Tyr	Pro	Asp	Asp	Ser	Asp
225				230					235						240
Arg	Gln	Gly	Glu	Leu	Leu	Arg	Ile	Phe	Gln	Gln	Tyr	Phe	Met	Val	Ser
			245					250						255	
Asn	Gly	Ala	Gln	Leu	Ile	Ile	Asp	Glu	Ala	Ile	Glu	Lys	Gly	Ser	Asn
	260						265						270		
Leu	His	Asp	Leu	Ala	Asp	Tyr	Ala	Val	Val	Gln	Ile	Asn	Asp	Thr	His
	275					280						285			
Pro	Ser	Met	Val	Ile	Pro	Glu	Leu	Ile	Arg	Leu	Leu	Thr	Ala	Arg	Gly
	290				295						300				
Ile	Asp	Leu	Asp	Glu	Ala	Ile	Ser	Ile	Val	Arg	Ser	Met	Thr	Ala	Tyr
305				310					315						320
Thr	Asn	His	Thr	Ile	Leu	Ala	Glu	Ala	Leu	Glu	Lys	Trp	Pro	Leu	Glu
			325					330						335	
Phe	Leu	Gln	Glu	Val	Val	Pro	His	Leu	Val	Pro	Ile	Ile	Glu	Glu	Leu
		340					345						350		
Asp	Arg	Arg	Val	Lys	Ala	Glu	Tyr	Lys	Asp	Pro	Ala	Val	Gln	Ile	Ile
	355						360					365			
Asp	Glu	Ser	Gly	Arg	Val	His	Met	Ala	His	Met	Asp	Ile	His	Tyr	Gly
	370				375						380				
Tyr	Ser	Val	Asn	Gly	Val	Ala	Ala	Leu	His	Thr	Glu	Ile	Leu	Lys	Asn
385				390					395						400
Ser	Glu	Leu	Lys	Ala	Phe	Tyr	Asp	Leu	Tyr	Pro	Glu	Lys	Phe	Asn	Asn
			405					410						415	
Lys	Thr	Asn	Gly	Ile	Thr	Phe	Arg	Arg	Trp	Leu	Met	His	Ala	Asn	Pro
		420					425						430		
Arg	Leu	Ser	His	Tyr	Leu	Asp	Glu	Ile	Leu	Gly	Asp	Gly	Trp	His	His
	435					440						445			

Glu	Ala	Asp	Glu	Leu	Glu	Lys	Leu	Leu	Ser	Tyr	Glu	Asp	Lys	Ala	Ala	450	455	460
Val	Lys	Glu	Lys	Leu	Glu	Ser	Ile	Lys	Ala	His	Asn	Lys	Arg	Lys	Leu	465	470	475
Ala	Arg	His	Leu	Lys	Glu	His	Gln	Gly	Val	Glu	Ile	Asn	Pro	Asn	Ser	485	490	495
Ile	Phe	Asp	Ile	Gln	Ile	Lys	Arg	Leu	His	Glu	Tyr	Lys	Arg	Gln	Gln	500	505	510
Met	Asn	Ala	Leu	Tyr	Val	Ile	His	Lys	Tyr	Leu	Asp	Ile	Lys	Ala	Gly	515	520	525
Asn	Ile	Pro	Ala	Arg	Pro	Ile	Thr	Ile	Phe	Phe	Gly	Gly	Lys	Ala	Ala	530	535	540
Pro	Ala	Tyr	Thr	Ile	Ala	Gln	Asp	Ile	Ile	His	Leu	Ile	Leu	Cys	Met	545	550	555
Ser	Glu	Val	Ile	Ala	Asn	Asp	Pro	Ala	Val	Ala	Pro	His	Leu	Gln	Val	565	570	575
Val	Met	Val	Glu	Asn	Tyr	Asn	Val	Thr	Ala	Ala	Ser	Phe	Leu	Ile	Pro	580	585	590
Ala	Cys	Asp	Ile	Ser	Glu	Gln	Ile	Ser	Leu	Ala	Ser	Lys	Glu	Ala	Ser	595	600	605
Gly	Thr	Gly	Asn	Met	Lys	Phe	Met	Leu	Asn	Gly	Ala	Leu	Thr	Leu	Gly	610	615	620
Thr	Met	Asp	Gly	Ala	Asn	Val	Glu	Ile	Ala	Glu	Leu	Val	Gly	Asp	Glu	625	630	635
Asn	Ile	Tyr	Ile	Phe	Gly	Glu	Asp	Ser	Glu	Thr	Val	Ile	Asp	Leu	Tyr	645	650	655
Ala	Lys	Ala	Ala	Tyr	Lys	Ser	Ser	Glu	Phe	Tyr	Ala	Arg	Glu	Ala	Ile	660	665	670
Lys	Pro	Leu	Val	Asp	Phe	Ile	Val	Ser	Asp	Ala	Val	Leu	Ala	Ala	Gly	675	680	685
Asn	Lys	Glu	Arg	Leu	Glu	Arg	Leu	Tyr	Asn	Glu	Leu	Ile	Asn	Lys	Asp	690	695	700
Trp	Phe	Met	Thr	Leu	Leu	Asp	Leu	Glu	Asp	Tyr	Ile	Lys	Val	Lys	Glu	705	710	715
Gln	Met	Leu	Ala	Asp	Tyr	Glu	Asp	Arg	Asp	Ala	Trp	Leu	Asp	Lys	Val	725	730	735
Ile	Val	Asn	Ile	Ser	Lys	Ala	Gly	Phe	Phe	Ser	Ser	Asp	Arg	Thr	Ile	740	745	750
Ala	Gln	Tyr	Asn	Glu	Asp	Ile	Trp	His	Leu	Asn						755	760	

(2) INFORMATION FOR SEQ ID NO:3001:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

(B) LOCATION 1...393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3001:

Lys	Asp	Lys	Thr	Lys	Met	Gly	Lys	Tyr	Asp	Phe	Thr	Ser	Leu	Pro	Asn
1				5					10					15	
Arg	Leu	Gly	His	His	Thr	Tyr	Lys	Trp	Lys	Glu	Thr	Glu	Thr	Asp	Ser
			20					25					30		
Glu	Val	Leu	Pro	Ala	Trp	Ile	Ala	Asp	Met	Asp	Phe	Val	Val	Leu	Pro
		35				40						45			
Glu	Ile	Arg	Gln	Ala	Val	Gln	Thr	Tyr	Ala	Asp	Gln	Leu	Val	Tyr	Gly
	50					55					60				
Tyr	Thr	Tyr	Ala	Ser	Glu	Asp	Leu	Ile	Lys	Glu	Val	Gln	Lys	Trp	Glu
65					70					75				80	
Ala	Thr	Gln	Tyr	Gly	Tyr	Asn	Phe	Asp	Lys	Glu	Ala	Leu	Val	Phe	Ile
				85					90					95	
Glu	Gly	Val	Val	Pro	Ala	Ile	Ser	Thr	Ala	Ile	Gln	Thr	Phe	Thr	Lys
			100					105					110		
Glu	Gly	Glu	Ala	Val	Leu	Ile	Asn	Thr	Pro	Val	Tyr	Pro	Pro	Phe	Ala
		115					120					125			
Arg	Ser	Val	Lys	Leu	Asn	Asn	Arg	Arg	Leu	Ile	Thr	Asn	Ser	Leu	Val
	130					135					140				
Glu	Lys	Asp	Gly	Leu	Phe	Glu	Ile	Asp	Phe	Asp	Gln	Leu	Glu	Lys	Asp
145					150					155				160	
Leu	Val	Glu	Glu	Glu	Val	Lys	Leu	Tyr	Ile	Leu	Cys	Asn	Pro	His	Asn
				165					170					175	
Pro	Gly	Gly	Arg	Val	Trp	Glu	Lys	Glu	Val	Leu	Glu	Lys	Ile	Gly	Gln
			180					185					190		
Leu	Cys	Gln	Lys	His	Gly	Val	Leu	Leu	Val	Ser	Asp	Glu	Ile	His	Gln
		195					200					205			
Asp	Leu	Thr	Leu	Phe	Gly	His	Lys	His	Gln	Ser	Phe	Asn	Thr	Ile	Asn
	210					215					220				
Pro	Ala	Phe	Lys	Asn	Phe	Ala	Ile	Val	Leu	Ser	Ser	Ala	Thr	Lys	Thr
225					230					235				240	
Phe	Asn	Ile	Ala	Gly	Thr	Lys	Asn	Ser	Tyr	Ala	Val	Ile	Glu	Asn	Pro
				245					250					255	
Lys	Leu	Arg	Leu	Ala	Phe	Gln	Lys	Arg	Leu	Leu	Ala	Asn	Asn	Gln	His
			260					265					270		
Glu	Ile	Ser	Gly	Leu	Gly	Tyr	Leu	Ala	Thr	Glu	Ala	Ala	Tyr	Arg	Tyr
		275					280					285			
Gly	Lys	Asp	Trp	Leu	Glu	Glu	Leu	Lys	Gln	Val	Phe	Glu	Asp	His	Ile
	290					295					300				
Asn	Tyr	Val	Val	Asp	Leu	Phe	Gly	Lys	Glu	Thr	Lys	Ile	Lys	Val	Met
305					310					315				320	
Lys	Pro	Gln	Gly	Thr	Tyr	Leu	Ile	Trp	Leu	Asp	Phe	Ser	Ala	Tyr	Asp
				325					330					335	
Leu	Thr	Asp	Glu	Thr	Leu	Gln	Glu	Leu	Leu	Arg	Asn	Glu	Ala	Lys	Val
			340					345					350		
Ile	Leu	Asn	Arg	Gly	Leu	Asp	Phe	Gly	Glu	Glu	Gly	Ser	Leu	His	Ala
		355					360					365			
Arg	Ile	Asn	Ile	Ala	Met	Pro	Lys	Ser	Leu	Leu	Gln	Glu	Val	Cys	Gln
	370					375					380				
Arg	Ile	Val	Ala	Thr	Phe	Ala	Lys	Arg							
385						390									

(2) INFORMATION FOR SEQ ID NO:3002:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 95 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...95
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3002:

Asn	Leu	Lys	Thr	Asp	Leu	Tyr	Leu	Val	Trp	Val	His	Leu	Phe	Arg	Glu
1			5					10						15	
Ala	Arg	Lys	Glu	Ala	Arg	Val	Ile	Gln	Leu	Ala	Leu	Asp	Tyr	His	Leu
		20					25					30			
Glu	Lys	Ile	Phe	Val	Gln	Ala	Met	Gln	Glu	Phe	Leu	Gly	Lys	Tyr	His
	35				40						45				
Gly	Lys	Ser	Lys	Gly	Val	Ser	Ser	Tyr	Leu	His	Ser	Phe	Trp	Ser	Ser
	50				55					60					
Ala	Ile	Val	Ser	Val	Leu	Leu	Lys	Trp	Ile	Lys	Asp	Gly	Met	Lys	Val
65				70				75						80	
Pro	Ala	Glu	Lys	Ile	Ala	Asp	Leu	Gly	Leu	Pro	Phe	Phe	Lys	Lys	
			85					90						95	

(2) INFORMATION FOR SEQ ID NO:3003:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 346 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...346
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3003:

Leu	Arg	Lys	Thr	Ser	Lys	Met	Ile	Asn	Gln	Ile	Tyr	Gln	Leu	Thr	Lys
1			5					10						15	
Pro	Lys	Phe	Ile	Asn	Val	Lys	Tyr	Gln	Glu	Glu	Ala	Ile	Asp	Gln	Glu
		20					25					30			
Asn	His	Ile	Leu	Ile	Arg	Pro	Asn	Tyr	Met	Ala	Val	Cys	His	Ala	Asp
	35					40						45			

(2) INFORMATION FOR SEQ ID NO:3004:

(A) LENGTH: 371 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: YES

(A) ORGANISM: *Streptococcus pneumoniae*

(A) NAME/KEY: misc_feature
(B) LOCATION 1...371

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3004:

Lys	Val	Lys	Thr	Met	Lys	Lys	Val	Ala	Ile	Ile	Gly	Ala	Gly	Ile	Val
1				5					10					15	
Gly	Ala	Thr	Ala	Tyr	Tyr	Leu	Ser	Arg	Glu	Ser	Asp	Leu	Glu	Val	
			20				25					30			
Thr	Val	Phe	Asp	His	Glu	Gln	Gly	Gln	Ala	Thr	Lys	Ala	Ala	Ala	Gly
		35					40					45			
Ile	Ile	Ser	Pro	Trp	Phe	Ser	Lys	Arg	Arg	Asn	Lys	Ala	Trp	Tyr	Lys
	50					55					60				
Met	Ala	Arg	Leu	Gly	Ala	Asp	Phe	Tyr	Val	Asp	Leu	Leu	Ala	Asp	Leu
65					70					75					80
Glu	Lys	Ser	Gly	Gln	Lys	Ile	Asp	Phe	Tyr	Gln	Arg	Ser	Gly	Val	Phe
				85					90					95	
Leu	Leu	Lys	Lys	Asp	Glu	Ser	Lys	Leu	Glu	Glu	Leu	Tyr	Gln	Leu	Ala
			100					105					110		
Leu	Gln	Arg	Arg	Glu	Glu	Ser	Pro	Leu	Ile	Gly	Gln	Leu	Ala	Ile	Leu
		115					120					125			
Asp	Gln	Ala	Ser	Ala	Asn	Glu	Leu	Phe	Pro	Gly	Leu	Gln	Gly	Phe	Asp
	130					135					140				
Arg	Leu	Leu	Tyr	Ala	Ser	Gly	Gly	Ala	Arg	Val	Asp	Gly	Gln	Leu	Leu
145					150					155					160
Val	Thr	Arg	Leu	Leu	Glu	Ala	Ser	His	Val	Lys	Leu	Val	Lys	Glu	Lys
				165					170					175	
Val	Thr	Leu	Thr	Leu	Leu	Ser	Ser	Gly	Tyr	Gln	Ile	Gly	Glu	Glu	Val
			180					185					190		
Phe	Asp	Gln	Val	Ile	Leu	Ala	Thr	Gly	Ala	Trp	Leu	Gly	Asp	Met	Leu
	195						200					205			
Glu	Pro	Leu	Gly	Tyr	Glu	Val	Asp	Val	Arg	Pro	Gln	Lys	Gly	Gln	Leu
	210					215					220				
Arg	Asp	Tyr	Gln	Leu	Ala	Gln	Asp	Met	Glu	Ala	Tyr	Pro	Val	Val	Met
225					230					235					240
Pro	Glu	Gly	Glu	Trp	Asp	Leu	Ile	Pro	Phe	Ala	Gly	Gly	Lys	Leu	Ser
				245					250					255	
Leu	Gly	Ala	Thr	His	Glu	Asn	Asp	Met	Gly	Phe	Asp	Leu	Thr	Val	Asp
			260					265					270		
Glu	Pro	Leu	Leu	Gln	Gln	Met	Glu	Glu	Ala	Ala	Leu	Pro	His	Tyr	Pro
	275						280					285			
Val	Leu	Ala	Arg	Ala	Thr	Ser	Arg	Ala	Glu	Arg	Val	Gly	Ile	Arg	Ala
	290					295					300				
Tyr	Thr	Ser	Asp	Phe	Ser	Pro	Phe	Phe	Gly	Gln	Val	Pro	Glu	Leu	Ala
305					310					315					320
Gly	Val	Tyr	Ala	Gly	Ser	Gly	Leu	Gly	Ser	Ser	Gly	Leu	Thr	Thr	Gly
				325					330					335	
Pro	Ile	Ile	Gly	Tyr	His	Leu	Ala	Gln	Leu	Ile	Gln	Asp	Lys	Glu	Leu
			340					345					350		
Thr	Leu	Asp	Pro	Leu	Asn	Tyr	Pro	Ile	Glu	Asn	Tyr	Val	Lys	Arg	Val
		355					360					365			
Lys	Ser	Glu													
	370														

(2) INFORMATION FOR SEQ ID NO:3005:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 211 amino acids

(B) TYPE: amino acid

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...211
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3005:

```

Arg Thr Lys Thr Ser Trp Phe Arg Leu Ile Ile Gln Lys Leu Lys Glu
1      5      10      15
Ser Lys Ile Ser Asp Gln Ser Phe Ser Thr Ser Pro Leu Thr Gln Val
      20      25      30
Ile Asn Ser Pro Ser Leu Thr Ser Gly Ala Thr His Phe Val Glu Lys
      35      40      45
Leu Ser Asp Thr Glu Gln Leu Asn Lys Lys Val Lys Ile Ile Pro Leu
      50      55      60
Glu Val Val Leu Arg Asn Tyr Thr Ala Gly Ser Phe Ser Lys Arg Phe
65      70      75      80
Gly Val Asp Glu Gly Ile Ala Leu Glu Thr Pro Ile Val Glu Phe Tyr
      85      90      95
Tyr Lys Asn Asp Asp Leu Asp Asp Pro Phe Ile Asn Asp Glu His Val
      100     105     110
Lys Phe Leu Gln Ile Ala Gly Asp Gln Gln Ile Ala Tyr Leu Lys Glu
      115     120     125
Glu Thr Arg Arg Ile Asn Glu Leu Leu Lys Val Trp Phe Thr Glu Ile
      130     135     140
Gly Leu Lys Leu Ile Asp Phe Lys Leu Glu Phe Gly Phe Asp Lys Asp
145     150     155     160
Gly Lys Ile Ile Leu Ala Asp Glu Phe Ser Pro Asp Asn Cys Arg Leu
      165     170     175
Trp Asp Ala Asp Gly Asn His Met Asp Lys Asp Val Phe Arg Arg Gly
      180     185     190
Leu Gly Glu Leu Thr Asp Val Tyr Glu Ile Val Trp Glu Lys Leu Gln
      195     200     205
Glu Leu Lys
210

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(2) INFORMATION FOR SEQ ID NO:3006:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 556 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...556

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3006:

Gly	Arg	Lys	Thr	Ala	Ser	Ser	Leu	Leu	Ser	Glu	Lys	Glu	Lys	Gln	Met
1				5					10					15	
Thr	Leu	Asp	Lys	Gly	Lys	Val	Val	Tyr	Gln	Ile	Tyr	Pro	Lys	Ser	Tyr
			20					25					30		
Lys	Asp	Thr	Thr	Glu	Asn	Gly	Ile	Gly	Asp	Phe	Arg	Gly	Ile	Ile	Glu
		35				40						45			
Lys	Ile	Pro	Tyr	Leu	Ala	Lys	Leu	Gly	Val	Asp	Met	Val	Trp	Leu	Asn
	50					55					60				
Pro	Phe	Tyr	Pro	Ser	Pro	Gln	Arg	Asp	Asn	Gly	Tyr	Asp	Ile	Ser	Asp
65					70					75					80
Tyr	Met	Ala	Val	Asp	Pro	Leu	Phe	Gly	Asp	Met	Ala	Asp	Phe	Glu	Glu
				85					90					95	
Met	Val	Cys	Val	Gly	Lys	Glu	His	Lys	Ile	Asp	Phe	Met	Leu	Asp	Met
			100					105					110		
Val	Leu	Asn	His	Cys	Ser	Thr	Glu	His	Glu	Trp	Phe	Gln	Lys	Ala	Leu
		115					120					125			
Ala	Gly	Asp	Lys	Tyr	Tyr	Gln	Asp	Phe	Phe	Phe	Ile	Gln	Asp	Gln	Pro
	130					135					140				
Thr	Asp	Trp	Gln	Ser	Lys	Phe	Gly	Gly	Ser	Ala	Trp	Ala	Pro	Phe	Gly
145					150					155					160
Asp	Thr	Gly	Lys	Tyr	Tyr	Leu	His	Leu	Phe	Asp	Glu	Thr	Gln	Ala	Asp
				165					170					175	
Leu	Asn	Trp	Arg	Asn	Pro	Asn	Val	Arg	Lys	Glu	Leu	Phe	Lys	Val	Val
			180					185					190		
Asn	Phe	Trp	Arg	Asp	Lys	Gly	Val	Lys	Gly	Phe	Arg	Phe	Asp	Val	Ile
	195					200						205			
Asn	Leu	Ile	Gly	Lys	Asp	Glu	Val	Ser	Val	Asp	Cys	Pro	Glu	Asn	Glu
	210					215					220				
Gly	Lys	Pro	Ala	Tyr	Thr	Asp	Lys	Pro	Ile	Val	His	Asn	Tyr	Leu	Arg
225					230					235					240
Met	Met	Asn	Gln	Ala	Thr	Phe	Gly	Ser	Asp	Asp	Ser	Phe	Met	Thr	Val
				245					250					255	
Gly	Glu	Met	Ser	Ser	Thr	Thr	Met	Glu	Asn	Cys	Val	Leu	Tyr	Ser	Ser
		260						265					270		
Pro	Asp	Arg	Gln	Glu	Leu	Ser	Met	Thr	Phe	Asn	Phe	His	His	Leu	Lys
		275					280					285			
Val	Asp	Tyr	Lys	Asp	Gly	Gln	Lys	Trp	Thr	Leu	Ala	Pro	Phe	Asp	Phe
	290					295					300				
Glu	Glu	Leu	Lys	Ser	Leu	Tyr	His	Ser	Trp	Gly	Lys	Glu	Met	Ser	Asp
305					310					315					320
Lys	Asp	Gly	Trp	Ser	Ala	Leu	Phe	Trp	Asn	Asn	His	Asp	Gln	Pro	Arg
				325					330					335	
Ala	Leu	Asn	Arg	Phe	Val	Asp	Ile	Gln	Asn	Phe	Arg	Lys	Glu	Gly	Ala
			340					345					350		
Thr	Met	Leu	Ala	Ala	Ser	Ile	His	Leu	Ser	Arg	Gly	Thr	Pro	Tyr	Ile
		355				360						365			
Tyr	Met	Gly	Glu	Glu	Ile	Gly	Met	Ile	Asp	Pro	Asp	Tyr	Asp	Ser	Met
	370					375					380				
Ala	Asp	Tyr	Val	Asp	Val	Glu	Ser	Leu	Asn	Ala	Tyr	Gln	Met	Leu	Leu
385					390					395					400

Glu	Glu	Gly	Lys	Ser	Gln	Gln	Glu	Ala	Phe	Gln	Ile	Ile	Gln	Ala	Lys
				405					410					415	
Ser	Arg	Asp	Asn	Ser	Arg	Ile	Pro	Met	Gln	Trp	Asp	Ala	Ser	Glu	Asn
			420					425					430		
Ala	Gly	Phe	Ser	Thr	Gly	Thr	Pro	Trp	Leu	Lys	Ala	Gly	Lys	Ser	Tyr
		435					440					445			
Lys	Tyr	Ile	Asn	Val	Glu	Asn	Glu	Ile	Gln	Gly	Pro	Ile	Phe	Thr	Phe
	450					455					460				
Tyr	Gln	Asp	Leu	Ile	Arg	Leu	Arg	Lys	Glu	Met	Pro	Ile	Ile	Ser	Glu
465					470					475					480
Gly	Ser	Tyr	Lys	Pro	Ala	Phe	Glu	Asp	Ser	Lys	Gln	Val	Tyr	Ala	Phe
				485				490						495	
Glu	Arg	Gln	Phe	Glu	Asp	Gln	Lys	Leu	Leu	Val	Leu	Asn	Asn	Phe	Tyr
			500					505					510		
Ala	Lys	Glu	Val	Glu	Ile	Asp	Leu	Pro	Ala	Val	Tyr	Gln	Asn	Gly	Gln
		515					520					525			
Ile	Leu	Ile	Ser	Asn	Tyr	Glu	Asp	Ala	Glu	Val	Ser	Glu	Lys	Ile	Leu
	530					535					540				
Leu	Lys	Pro	Tyr	Gln	Thr	Leu	Ala	Ile	Tyr	Val	Asn				
545					550					555					

(2) INFORMATION FOR SEQ ID NO:3007:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...96

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3007:

Arg	Asn	Glu	Thr	Leu	Lys	Met	Ala	Val	Lys	Ile	Arg	Leu	Thr	Arg	Met
1				5					10					15	
Gly	Ser	Lys	Lys	Lys	Pro	Phe	Tyr	Arg	Ile	Asn	Val	Ala	Asp	Ser	Arg
			20					25					30		
Ser	Pro	Arg	Asp	Gly	Arg	Phe	Ile	Glu	Thr	Val	Gly	Thr	Tyr	Asn	Pro
		35				40					45				
Leu	Val	Ala	Glu	Asn	Gln	Val	Thr	Leu	Lys	Glu	Asp	Arg	Val	Leu	Ala
	50				55					60					
Trp	Leu	Ala	Asn	Gly	Ala	Gln	Pro	Ser	Asp	Thr	Val	Arg	Asn	Ile	Leu
65					70				75					80	
Ser	Lys	Glu	Gly	Val	Leu	Lys	Lys	Phe	His	Asp	Ser	Lys	Phe	Ser	Lys
				85					90					95	

(2) INFORMATION FOR SEQ ID NO:3008:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 72 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...72

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3008:

Gln	Lys	Glu	Thr	Cys	Met	Asn	Thr	Tyr	Cys	Asn	Ile	Asn	Glu	Thr	Met
1				5					10					15	
Leu	Ser	Glu	Val	Tyr	Gly	Gly	Asn	Ser	Gly	Gly	Ala	Ala	Val	Val	Ala
			20					25					30		
Ala	Leu	Gly	Cys	Ala	Ala	Gly	Gly	Val	Lys	Tyr	Gly	Arg	Leu	Leu	Gly
		35				40					45				
Pro	Trp	Gly	Ala	Ala	Ile	Gly	Gly	Ile	Gly	Gly	Ala	Val	Val	Cys	Gly
	50					55					60				
Tyr	Leu	Ala	Tyr	Thr	Ala	Thr	Ser								
65					70										

(2) INFORMATION FOR SEQ ID NO:3009:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 284 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...284

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3009:

Arg	Lys	Glu	Thr	Ala	Met	Gln	Ser	Thr	Glu	Lys	Lys	Pro	Leu	Thr	Ala
1				5					10					15	
Phe	Thr	Val	Ile	Ser	Thr	Ile	Ile	Leu	Leu	Leu	Leu	Thr	Val	Leu	Phe
			20					25					30		
Ile	Phe	Pro	Phe	Tyr	Trp	Ile	Leu	Thr	Gly	Ala	Phe	Lys	Ser	Gln	Pro
		35				40					45				
Asp	Thr	Ile	Val	Ile	Pro	Pro	Gln	Trp	Phe	Pro	Lys	Met	Pro	Thr	Met
	50					55					60				

Glu	Asn	Phe	Gln	Gln	Leu	Met	Val	Gln	Asn	Pro	Ala	Leu	Gln	Trp	Met
65					70					75					80
Trp	Asn	Ser	Val	Phe	Ile	Ser	Leu	Val	Thr	Met	Phe	Leu	Val	Cys	Ala
				85					90					95	
Thr	Ser	Ser	Leu	Ala	Gly	Tyr	Val	Leu	Ala	Lys	Lys	Arg	Phe	Tyr	Gly
			100					105					110		
Gln	Arg	Ile	Leu	Phe	Ala	Ile	Phe	Ile	Ala	Ala	Met	Ala	Leu	Pro	Lys
		115					120					125			
Gln	Val	Val	Leu	Val	Pro	Leu	Val	Arg	Ile	Val	Asn	Phe	Met	Gly	Ile
	130					135					140				
His	Asp	Thr	Leu	Trp	Ala	Val	Ile	Leu	Pro	Leu	Ile	Gly	Trp	Pro	Phe
145					150					155					160
Gly	Val	Phe	Leu	Met	Lys	Gln	Phe	Ser	Glu	Asn	Ile	Pro	Thr	Glu	Leu
			165						170					175	
Leu	Glu	Ser	Ala	Lys	Ile	Asp	Gly	Cys	Gly	Glu	Ile	Arg	Thr	Phe	Trp
			180					185					190		
Ser	Val	Ala	Phe	Pro	Ile	Val	Lys	Pro	Gly	Phe	Ala	Ala	Leu	Ala	Ile
		195					200					205			
Phe	Thr	Phe	Ile	Asn	Thr	Trp	Asn	Asp	Tyr	Phe	Met	Gln	Leu	Val	Met
	210					215					220				
Leu	Thr	Ser	Arg	Asn	Asn	Leu	Thr	Ile	Ser	Leu	Gly	Val	Ala	Thr	Met
225					230					235					240
Gln	Ala	Glu	Met	Ala	Thr	Asn	Tyr	Gly	Leu	Ile	Met	Ala	Gly	Ala	Ala
			245					250					255		
Leu	Ala	Ala	Val	Pro	Ile	Val	Thr	Val	Phe	Leu	Val	Phe	Gln	Lys	Ser
			260				265						270		
Phe	Thr	Gln	Gly	Ile	Thr	Met	Gly	Ala	Val	Lys	Gly				
		275					280								

(2) INFORMATION FOR SEQ ID NO:3010:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...76

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3010:

Ser	Pro	Trp	Thr	Thr	Arg	Leu	Ser	Lys	Pro	Leu	Pro	Ser	Arg	Pro	Thr
1				5					10					15	
Val	Ser	Ile	Pro	Met	Trp	Met	Ser	Asn	Ser	Thr	Pro	Ser	Ser	Glu	Thr
			20					25					30		
Met	Pro	Met	Ala	Cys	Leu	Val	Gly	Lys	Arg	Thr	Val	Thr	Val	Pro	Leu
		35					40					45			
Thr	Gly	Glu	Val	Asn	Ser	Pro	Trp	Leu	Gly	Ser	Met	Thr	Arg	Pro	Cys

50	55	60
Pro Met Thr Pro Asp Ala Lys Thr Gly Ser Val Ala		
65	70	75

(2) INFORMATION FOR SEQ ID NO:3011:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...133

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3011:

Gln	Lys	Trp	Thr	Lys	Glu	Leu	Met	Val	Thr	Trp	Ile	Leu	Trp	Ala	Leu
1				5					10					15	
Ile	Leu	Ala	Met	Leu	Ala	Trp	Met	Gly	Phe	Asn	Tyr	Leu	Arg	Ile	Arg
			20					25					30		
Arg	Ala	Ala	Lys	Ile	Val	Asp	Asn	Glu	Glu	Phe	Glu	Ala	Leu	Ile	Arg
			35				40					45			
Thr	Gly	Gln	Leu	Ile	Asp	Leu	Arg	Asp	Pro	Ala	Glu	Phe	His	Arg	Lys
			50				55				60				
His	Ile	Leu	Gly	Ala	Arg	Asn	Ile	Pro	Ser	Ser	Gln	Leu	Lys	Thr	Ser
65					70				75					80	
Leu	Ala	Ala	Leu	Arg	Lys	Asp	Lys	Pro	Val	Leu	Leu	Tyr	Glu	Asn	Gln
				85					90					95	
Arg	Ala	Gln	Arg	Val	Thr	Asn	Ala	Ala	Leu	Tyr	Leu	Lys	Lys	Gln	Gly
			100				105						110		
Phe	Ser	Glu	Ile	Tyr	Ile	Leu	Ser	Tyr	Gly	Leu	Asp	Ser	Trp	Lys	Gly
		115					120					125			
Lys	Val	Lys	Thr	Ser											
															130

(2) INFORMATION FOR SEQ ID NO:3012:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...133

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3012:

```

Met Glu Trp Thr Thr Glu Arg Arg Tyr Arg Leu Tyr Gln Glu Trp Thr
1      5      10      15
Gln Glu Glu Ile Gln His Ile Asn Glu Asn Met Ala Gln Ser Pro Trp
      20      25      30
His Thr His Xaa His Val Glu Ala Lys Thr Gly Leu Leu Asn Asp Pro
      35      40      45
Asn Gly Phe Ser Tyr Phe Asp Gly Asn Trp Ile Leu Phe Asn Gln Ile
      50      55      60
Phe Pro Phe Gly Ala Xaa His Gly Leu Xaa Ser Trp Ala His Leu Lys
65      70      75      80
Ile Asn Asp Trp Val His Leu Xaa Lys Pro Glu Ile Lys Phe Trp Gln
      85      90      95
Asn Pro His Xaa Xaa Phe Arg Val Pro Thr Ser Val Arg Pro Ser Asn
      100     105     110
Leu Gly Lys Asn Tyr Ser Phe Phe Arg Arg Phe Phe Pro Ile Lys
      115     120     125
Asn Gly Ser Ser Pro
130

```

(2) INFORMATION FOR SEQ ID NO:3013:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 469 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...469

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3013:

```

Ser Ser Arg Thr Ser Ala Leu Phe Lys Gly Val Glu Met Lys Leu Thr
1      5      10      15
Ile His Glu Ile Ala Gln Val Val Gly Ala Lys Asn Asp Ile Ser Ile
      20      25      30
Phe Glu Asp Thr Gln Leu Glu Lys Ala Glu Phe Asp Ser Arg Leu Ile
      35      40      45
Gly Thr Gly Asp Leu Phe Val Pro Leu Lys Gly Ala Arg Asp Gly His
      50      55      60
Asp Phe Ile Lys Thr Ala Phe Glu Asn Gly Ala Ala Val Thr Leu Ser
65      70      75      80
Glu Lys Glu Val Ser Asn His Pro Tyr Ile Leu Val Asp Asp Val Leu
      85      90      95

```


Thr	Ala	Phe	Gln	Ser	Leu	Ala	Ser	Tyr	Tyr	Leu	Glu	Lys	Thr	Thr	Val
			100					105						110	
Asp	Val	Phe	Ala	Val	Thr	Gly	Ser	Asn	Gly	Lys	Thr	Thr	Thr	Lys	Asp
		115					120						125		
Met	Leu	Ala	His	Leu	Leu	Ser	Thr	Arg	Tyr	Lys	Thr	Tyr	Lys	Thr	Gln
	130					135					140				
Gly	Asn	Tyr	Asn	Asn	Glu	Ile	Gly	Leu	Pro	Tyr	Thr	Val	Leu	His	Met
145					150					155					160
Pro	Glu	Gly	Thr	Glu	Lys	Leu	Val	Leu	Glu	Met	Gly	Gln	Asp	His	Leu
				165					170					175	
Gly	Asp	Ile	His	Leu	Leu	Ser	Glu	Leu	Ala	Arg	Pro	Lys	Thr	Ala	Ile
			180					185					190		
Val	Thr	Leu	Val	Gly	Glu	Ala	His	Leu	Ala	Phe	Phe	Lys	Asp	Arg	Ser
		195					200					205			
Glu	Ile	Ala	Lys	Gly	Lys	Met	Gln	Ile	Ala	Asp	Gly	Met	Ala	Ser	Gly
	210					215					220				
Ser	Leu	Leu	Leu	Ala	Pro	Ala	Asp	Pro	Ile	Val	Glu	Asp	Tyr	Leu	Pro
225					230					235					240
Thr	Asp	Lys	Lys	Val	Val	Arg	Phe	Gly	Gln	Gly	Ala	Glu	Leu	Glu	Ile
			245					250						255	
Thr	Asp	Leu	Val	Glu	Arg	Lys	Asp	Ser	Leu	Thr	Phe	Lys	Ala	Asn	Phe
		260						265					270		
Leu	Glu	Gln	Ala	Leu	Asp	Leu	Pro	Val	Thr	Gly	Lys	Tyr	Asn	Ala	Thr
	275						280					285			
Asn	Ala	Met	Ile	Ala	Ser	Tyr	Val	Ala	Leu	Gln	Glu	Gly	Val	Ser	Glu
	290					295					300				
Glu	Gln	Ile	His	Gln	Ala	Phe	Gln	Gly	Leu	Glu	Leu	Thr	Arg	Asn	Arg
305					310					315					320
Thr	Glu	Trp	Lys	Lys	Ala	Ala	Asn	Gly	Ala	Asp	Ile	Leu	Ser	Asp	Val
			325					330						335	
Tyr	Asn	Ala	Asn	Pro	Thr	Ala	Met	Lys	Leu	Ile	Leu	Glu	Thr	Phe	Ser
		340						345					350		
Ala	Ile	Pro	Ala	Asn	Glu	Gly	Gly	Lys	Lys	Ile	Ala	Val	Leu	Ala	Asp
		355					360					365			
Met	Lys	Glu	Leu	Gly	Asp	Gln	Ser	Ile	Gln	Leu	His	Asn	Gln	Met	Ile
	370					375					380				
Leu	Ser	Leu	Ser	Pro	Asp	Val	Leu	Asp	Thr	Val	Ile	Phe	Tyr	Gly	Glu
385					390					395					400
Asp	Ile	Ala	Glu	Leu	Ala	Gln	Leu	Ala	Ser	Gln	Met	Phe	Pro	Ile	Gly
			405						410					415	
His	Val	Tyr	Tyr	Phe	Lys	Lys	Thr	Glu	Asp	Gln	Asp	Gln	Phe	Glu	Asp
		420						425					430		
Leu	Val	Lys	Gln	Val	Lys	Glu	Ser	Leu	Ser	Ala	Asn	Asp	Gln	Ile	Leu
		435					440					445			
Leu	Lys	Gly	Ser	Asn	Ser	Met	Asn	Leu	Ala	Met	Leu	Val	Glu	Ser	Leu
	450					455					460				
Glu	Asn	Glu	Thr	Lys											
465															

(2) INFORMATION FOR SEQ ID NO:3014:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3014:

```
Ile Arg Arg Thr Leu Ser Arg Thr Cys Leu Ala Leu Thr Gly Ala Ser
1      5      10      15
Ala Ser Thr Ser Pro Lys Arg Ser Arg Asn Leu Leu Phe Ser Lys Arg
      20      25      30
Arg Ala Val Phe Ser Ser Thr Lys Leu Leu Arg Phe Phe Leu Met Ala
      35      40      45
Ser Thr Ser Ala Lys Val Thr Asn Asn Cys Trp Glu Lys Ser Ser Ser
      50      55      60
Ala Ser Asn Asn Ser Phe Val Ser Ile Lys Gln Ala Pro Phe Leu Ser
      65      70      75      80
Leu Ser Phe Ile Phe Glu Phe Ile Phe Leu Ser Arg Pro Asp Ile Pro
      85      90      95
Trp His Phe Glu Ser
      100
```

(2) INFORMATION FOR SEQ ID NO:3015:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 367 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...367

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3015:

```
His Thr Gly Thr His Phe Lys Asn Ser Trp Phe Leu Asn Val Pro Asn
1      5      10      15
Met Ala Lys Ile Gly Leu Gly Asn Ile Pro Arg Glu Thr Pro Leu Lys
      20      25      30
Thr Val Ala Ala Glu Ser Asn Pro Thr Gly Tyr Ala Thr Lys Leu Glu
      35      40      45
Glu Val Ser Leu Gly Lys Asp Thr Met Thr Gly His Trp Glu Ile Met
      50      55      60
Gly Leu Asn Ile Thr Glu Pro Phe Asp Thr Phe Trp Asn Gly Phe Pro
      65      70      75      80
```

Glu	Glu	Ile	Leu	Thr	Lys	Ile	Glu	Glu	Phe	Ser	Gly	Arg	Lys	Val	Ile
				85					90					95	
Arg	Glu	Ala	Asn	Lys	Pro	Tyr	Ser	Gly	Thr	Ala	Val	Ile	Asp	Asp	Phe
			100					105					110		
Gly	Pro	Arg	Gln	Met	Glu	Thr	Gly	Glu	Leu	Ile	Ile	Tyr	Thr	Ser	Ala
		115					120					125			
Asp	Pro	Val	Leu	Gln	Ile	Ala	Ala	His	Glu	Asp	Ile	Ile	Pro	Leu	Asp
		130				135					140				
Glu	Leu	Tyr	Arg	Ile	Cys	Glu	Tyr	Ala	Arg	Ser	Ile	Thr	Leu	Glu	Arg
145					150					155					160
Pro	Ala	Leu	Leu	Gly	Arg	Ile	Ile	Ala	Arg	Pro	Tyr	Val	Gly	Glu	Pro
				165					170					175	
Gly	Asn	Phe	Thr	Arg	Thr	Ala	Asn	Arg	Arg	Asp	Leu	Ala	Val	Ser	Pro
			180					185					190		
Phe	Ser	Pro	Thr	Val	Leu	Asp	Lys	Leu	Asn	Glu	Ala	Gly	Ile	Asp	Thr
		195					200					205			
Tyr	Ala	Val	Gly	Lys	Ile	Asn	Asp	Ile	Phe	Asn	Gly	Ala	Gly	Ile	Asn
		210				215					220				
His	Asp	Met	Gly	His	Asn	Lys	Ser	Asn	Ser	His	Gly	Ile	Asp	Thr	Leu
225					230				235						240
Leu	Lys	Thr	Met	Gly	Leu	Ala	Glu	Phe	Glu	Lys	Gly	Phe	Ser	Phe	Thr
			245						250					255	
Asn	Leu	Val	Asp	Phe	Asp	Ala	Leu	Tyr	Gly	His	Arg	Arg	Asn	Ala	His
			260					265					270		
Gly	Tyr	Arg	Asp	Cys	Leu	His	Glu	Phe	Asp	Glu	Arg	Leu	Pro	Glu	Ile
		275					280					285			
Ile	Ala	Ala	Met	Arg	Glu	Asn	Asp	Leu	Leu	Leu	Ile	Thr	Ala	Asp	His
		290				295					300				
Gly	Asn	Asp	Pro	Thr	Tyr	Ala	Gly	Thr	Asp	His	Thr	Arg	Glu	Tyr	Ile
305					310					315					320
Pro	Leu	Leu	Ala	Tyr	Ser	Pro	Ala	Phe	Lys	Gly	Asn	Gly	Leu	Ile	Pro
			325						330					335	
Val	Gly	His	Phe	Ala	Asp	Ile	Ser	Ala	Thr	Val	Ala	Asp	Asn	Phe	Gly
			340					345					350		
Val	Glu	Thr	Ala	Met	Ile	Gly	Glu	Ser	Phe	Leu	Asp	Lys	Leu	Val	
		355					360						365		

(2) INFORMATION FOR SEQ ID NO:3016:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...288

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3016:

Glu	Phe	Tyr	Phe	Pro	Arg	Leu	Ala	Arg	Arg	Leu	Leu	Val	Asn	Asp	Asp
1				5					10					15	
Tyr	Asp	Val	Glu	Val	Ser	Phe	Thr	Ile	Met	Asn	Pro	Pro	Leu	Glu	Phe
			20					25					30		
Ser	Lys	Arg	Arg	Glu	Val	Lys	Lys	Ile	Ser	Trp	Ile	His	Gly	Ser	Ile
		35				40						45			
Glu	Glu	Leu	Leu	Lys	Asp	Ser	Ser	Lys	Arg	Glu	Ser	His	Arg	Ser	Gln
	50					55				60					
Leu	Asp	Ala	Ala	Asn	Thr	Ile	Val	Gly	Ile	Ser	Lys	Lys	Thr	Ser	Asn
65				70					75						80
Ser	Ile	Lys	Glu	Val	Tyr	Pro	Asp	Tyr	Ala	Ser	Lys	Leu	Gln	Thr	Ile
			85					90					95		
Tyr	Asn	Gly	Tyr	Asp	Phe	Gln	Thr	Ile	Leu	Glu	Lys	Ser	Gln	Glu	Lys
		100						105					110		
Ile	Asp	Ile	Glu	Ile	Ala	Pro	Gln	Ser	Ile	Cys	Thr	Ile	Gly	Arg	Ile
	115					120						125			
Glu	Glu	Asn	Lys	Gly	Ser	Asp	Arg	Val	Val	Glu	Val	Ile	Arg	Leu	Leu
	130					135					140				
His	Gln	Glu	Gly	Lys	Asn	Tyr	His	Leu	Tyr	Phe	Ile	Gly	Ala	Gly	Asp
145				150					155						160
Met	Glu	Glu	Glu	Leu	Lys	Lys	Arg	Val	Lys	Glu	Tyr	Gly	Ile	Glu	Asp
			165					170					175		
Tyr	Val	His	Phe	Leu	Gly	Tyr	Gln	Lys	Asn	Pro	Tyr	Gln	Tyr	Leu	Ser
		180					185					190			
Gln	Thr	Lys	Val	Leu	Leu	Ser	Met	Ser	Lys	Gln	Glu	Gly	Phe	Pro	Gly
		195				200						205			
Val	Tyr	Val	Glu	Ala	Leu	Ser	Leu	Gly	Leu	Pro	Phe	Ile	Ser	Thr	Asp
	210					215				220					
Val	Gly	Gly	Ala	Glu	Glu	Leu	Ser	Gln	Glu	Gly	Arg	Phe	Gly	Gln	Ile
225				230					235						240
Ile	Glu	Ser	Asn	Gln	Glu	Ala	Ala	Gln	Ala	Ile	Thr	Asn	Tyr	Met	Thr
			245					250					255		
Ser	Ala	Ser	Asn	Phe	Asp	Val	Asp	Glu	Ala	Ser	Gln	Phe	Ile	Gln	Gln
		260				265						270			
Phe	Thr	Ile	Thr	Lys	Gln	Ile	Glu	Gln	Val	Glu	Lys	Leu	Leu	Glu	Glu
		275				280						285			

(2) INFORMATION FOR SEQ ID NO:3017:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 102 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...102
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3017:

Leu	Lys	Asn	Phe	Phe	Ala	His	His	Pro	Lys	Gln	Lys	Val	Ile	Leu	Ala
				165					170					175	
Gly	His	Ser	Lys	Gly	Gly	Asn	Leu	Ala	Ile	Tyr	Ala	Ala	Ser	Gln	Ile
			180					185						190	
Glu	Gln	Ser	Leu	Gln	Asn	Gln	Ile	Thr	Ala	Val	Tyr	Thr	Phe	Asp	Ala
		195					200					205			
Pro	Gly	Leu	His	Gln	Glu	Leu	Thr	Gln	Thr	Ala	Gly	Tyr	Gln	Arg	Ile
	210					215					220				
Met	Asp	Arg	Ser	Lys	Ile	Phe	Ile	Pro	Gln	Gly	Ser	Ile	Ile	Gly	Met
225					230					235					240
Met	Leu	Glu	Ile	Pro	Ala	His	Gln	Ile	Ile	Val	Gln	Ser	Thr	Ala	Leu
				245					250					255	
Gly	Gly	Ile	Ala	Gln	His	Asp	Thr	Phe	Ser	Trp	Gln	Ile	Glu	Asp	Lys
			260					265					270		
His	Phe	Val	Gln	Leu	Asp	Lys	Thr	Asn	Ser	Asp	Ser	Gln	Gln	Val	Asp
		275					280					285			
Thr	Thr	Phe	Lys	Glu	Trp	Val	Ala	Thr	Val	Pro	Asp	Glu	Glu	Leu	Gln
	290					295					300				
Leu	Tyr	Phe	Asp	Leu	Phe	Phe	Gly	Thr	Ile	Leu	Glu	Ala	Gly	Ile	Ser
305					310					315					320
Ser	Ile	Asn	Asp	Leu	Ala	Ser	Leu	Lys	Ala	Leu	Glu	Tyr	Ile	His	His
				325					330					335	
Leu	Phe	Val	Gln	Ala	Gln	Ser	Leu	Thr	Pro	Glu	Glu	Arg	Glu	Thr	Leu
			340					345					350		
Gly	Arg	Leu	Thr	Gln	Leu	Leu	Ile	Asp	Thr	Arg	Tyr	Gln	Ala	Trp	Lys
		355					360					365			
Asn	Arg														
	370														

(2) INFORMATION FOR SEQ ID NO:3019:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3019:

Met	Asn	Ile	Ala	Lys	Ile	Val	Arg	Glu	Ala	Arg	Glu	Gln	Ser	Arg	Leu
1				5					10					15	
Thr	Thr	Leu	Asp	Phe	Ala	Thr	Gly	Ile	Phe	Asp	Glu	Phe	Ile	Gln	Leu
			20					25					30		
His	Gly	Asp	Arg	Ser	Phe	Arg	Asp	Asp	Gly	Ala	Val	Val	Gly	Gly	Ile
		35					40					45			
Gly	Trp	Leu	Gly	Asp	Gln	Ala	Val	Thr	Val	Val	Gly	Ile	Gln	Lys	Gly
	50					55					60				

Lys	Ser	Leu	Gln	Asp	Asn	Leu	Lys	Arg	Asn	Phe	Gly	Gln	Pro	His	Pro
65					70					75					80
Glu	Gly	Tyr	Arg	Lys	Ala	Leu	Arg	Leu	Met	Lys	Gln	Ala	Glu	Lys	Phe
				85					90					95	
Gly	Arg	Pro	Val	Thr	Phe	Ile	Asn	Thr	Ala	Gly	Ala	Tyr	Pro	Gly	
			100				105					110			
Val	Gly	Ala	Glu	Glu	Arg	Gly	Gln	Gly	Glu	Ala	Ile	Ala	Arg	Asn	Leu
		115				120						125			
Met	Glu	Met	Ser	Asp	Leu	Lys	Val	Pro	Ile	Ile	Ala	Ile	Ile	Ile	Gly
	130					135					140				
Glu	Gly	Gly	Ser	Gly	Gly	Ala	Leu	Ala	Leu	Ala	Val	Ala	Asp	Arg	Val
145					150					155					160
Trp	Met	Leu	Glu	Asn	Ser	Ile	Tyr	Ala	Ile	Leu	Ser	Pro	Glu	Gly	Phe
				165					170					175	
Ala	Ser	Ile	Leu	Trp	Lys	Asp	Gly	Thr	Arg	Ala	Met	Glu	Ala	Ala	Glu
			180					185					190		
Leu	Met	Lys	Ile	Thr	Ser	His	Glu	Leu	Leu	Glu	Met	Asp	Val	Val	Asp
		195					200					205			
Lys	Val	Ile	Ser	Glu	Val	Gly	Leu	Ser	Ser	Lys	Glu	Leu	Ile	Lys	Ser
	210					215					220				
Val	Lys	Lys	Glu	Leu	Gln	Thr	Glu	Leu	Ala	Arg	Leu	Ser	Gln	Lys	Pro
225					230					235					240
Leu	Glu	Glu	Leu	Leu	Glu	Glu	Arg	Tyr	Gln	Arg	Phe	Arg	Lys	Tyr	
				245					250					255	

(2) INFORMATION FOR SEQ ID NO:3020:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...203

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3020:

Tyr	Asp	Ile	Ala	Glu	Ser	His	Phe	Tyr	Ala	Ser	Ala	Asn	Asn	Val	Ile
1				5				10						15	
Arg	Asp	Asp	Ala	Ser	Ser	Phe	His	Thr	Phe	Tyr	Phe	Asp	Pro	Glu	Thr
			20					25					30		
Gly	Gln	Pro	Phe	Lys	Gly	Val	Thr	Arg	Gln	Gly	Tyr	Ser	Asp	Asp	Ser
		35					40					45			
Cys	Trp	Ala	Arg	Gly	Gln	Ser	Trp	Gly	Val	Tyr	Gly	Ile	Pro	Leu	Thr
	50					55				60					
Tyr	Arg	His	Leu	Lys	Asp	Glu	Ser	Cys	Phe	Asp	Leu	Phe	Lys	Gly	Val
65					70					75					80
Thr	Asn	Phe	Phe	Leu	Asn	Arg	Leu	Pro	Lys	Asp	His	Val	Ser	Tyr	Trp
			85					90						95	

Asp	Leu	Ile	Phe	Asn	Asp	Gly	Ser	Asp	Gln	Ser	Arg	Asp	Ser	Ser	Ala
			100					105					110		
Thr	Ala	Ile	Ala	Val	Cys	Gly	Ile	His	Glu	Met	Leu	Lys	His	Leu	Pro
		115					120					125			
Glu	Val	Asp	Ala	Asp	Lys	Asp	Ile	Tyr	Lys	His	Ala	Met	His	Ala	Met
	130					135					140				
Leu	Arg	Ser	Leu	Ile	Glu	His	Tyr	Ala	Asn	Asp	Gln	Phe	Thr	Pro	Gly
145					150					155					160
Gly	Thr	Ser	Leu	Leu	His	Gly	Val	Tyr	Ser	Trp	His	Ser	Gly	Lys	Gly
				165					170					175	
Val	Asp	Glu	Gly	Asn	Ile	Trp	Gly	Asp	Tyr	Tyr	Tyr	Leu	Glu	Ala	Leu
			180					185					190		
Ile	Arg	Phe	Tyr	Lys	Asp	Trp	Asn	Leu	Tyr	Trp					
		195					200								

(2) INFORMATION FOR SEQ ID NO:3021:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 61 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...61
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3021:

Pro	Ala	Ile	Ala	Ser	Thr	Thr	Leu	Pro	Ser	Phe	Glu	Tyr	Cys	Ser	Arg
1				5					10					15	
Tyr	Leu	Ala	Lys	Phe	Pro	Ser	Thr	Pro	Ser	Ser	Lys	Phe	His	Lys	Lys
		20					25						30		
Asn	Arg	Asn	His	Ala	Ser	Asn	Asn	Arg	Met	Lys	Leu	Val	Val	Asn	Val
	35					40					45				
Ile	Val	Arg	Asn	Pro	Arg	Ile	Lys	Gly	Ala	Ile	Asp	Lys			
	50				55						60				

(2) INFORMATION FOR SEQ ID NO:3022:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 357 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...357

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3022:

Lys	Leu	Ile	Ala	Ala	Phe	Tyr	Asn	Met	Tyr	Lys	Lys	Arg	Ser	Val	Ala
1				5					10					15	
Arg	Ser	Cys	Leu	Pro	Arg	Arg	Ala	Tyr	Ser	Leu	Tyr	Lys	Thr	Tyr	Pro
			20					25					30		
Leu	Ile	Ser	Gln	Tyr	Leu	Ser	Gly	Thr	Thr	Ala	Ser	Gly	Leu	Tyr	Glu
		35					40					45			
Ala	Lys	Leu	Ala	Arg	Glu	Glu	Phe	Pro	Gly	Glu	Val	His	Val	Phe	Ala
	50					55					60				
Pro	Ala	Phe	Lys	Asp	Ala	Asp	Leu	Glu	Glu	Leu	Leu	Glu	Ile	Met	Asp
65				70						75				80	
His	Ile	Val	Phe	Asn	Ser	Glu	Arg	Gln	Leu	Arg	Lys	His	Gly	Pro	Arg
			85					90						95	
Cys	Arg	Glu	Ala	Gly	Val	Ser	Val	Gly	Leu	Arg	Leu	Asn	Pro	Gln	Cys
			100					105					110		
Ser	Thr	Gln	Gly	Asp	His	Ala	Leu	Tyr	Asp	Pro	Cys	Ala	Pro	Gly	Ser
		115					120					125			
Arg	Phe	Gly	Val	Thr	Ile	Asp	Lys	Ile	Pro	Ser	Asp	Leu	Leu	Asp	Leu
	130					135					140				
Val	Asp	Gly	Leu	His	Phe	His	Thr	Leu	Cys	Glu	Gln	Gly	Ala	Asp	Asp
145				150						155				160	
Leu	Gln	Thr	Thr	Leu	Lys	Ala	Val	Glu	Glu	Gln	Phe	Gly	Pro	Tyr	Leu
			165					170						175	
His	Glu	Val	Lys	Trp	Leu	Asn	Met	Gly	Gly	Gly	His	His	Ile	Thr	Arg
		180					185						190		
Glu	Gly	Tyr	Asp	Val	Asp	Leu	Leu	Ile	Ser	Glu	Ile	Lys	Arg	Ile	Arg
		195				200						205			
Lys	Thr	Tyr	Asn	Leu	Glu	Ile	Tyr	Ile	Glu	Pro	Gly	Glu	Ala	Ile	Ala
	210					215					220				
Leu	Asn	Ala	Gly	Tyr	Leu	Ala	Thr	Glu	Val	Leu	Asp	Ile	Val	Glu	Asn
225				230						235				240	
Gly	Met	Glu	Ile	Leu	Val	Leu	Asp	Ala	Ser	Ala	Thr	Cys	His	Met	Pro
			245					250						255	
Asp	Val	Leu	Glu	Met	Pro	Tyr	Arg	Pro	Ser	Leu	Arg	Asn	Gly	Phe	Glu
		260					265						270		
Ala	Gln	Glu	Lys	Ala	His	Thr	Tyr	Arg	Leu	Ser	Ser	Asn	Thr	Cys	Leu
	275					280						285			
Thr	Gly	Asp	Val	Ile	Gly	Asp	Tyr	Ser	Phe	Glu	Asn	Pro	Val	Gln	Ile
	290					295					300				
Gly	Asp	Arg	Leu	Tyr	Phe	Gln	Asp	Met	Ala	Ile	Tyr	Ser	Phe	Val	Lys
305				310						315				320	
Asn	Asn	Thr	Phe	Asn	Gly	Ile	Gly	Leu	Pro	Ser	Leu	Tyr	Leu	Met	Asp
			325					330						335	
Glu	Gln	Gly	Asp	Cys	Ser	Leu	Leu	Lys	Ala	Phe	Gly	Tyr	Gln	Asp	Phe
		340					345						350		
Lys	Gly	Arg	Leu	Ser											
	355														

(2) INFORMATION FOR SEQ ID NO:3023:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 290 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...290
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3023:

```

Met Arg Ile Ala Asp Tyr Ser Val Thr Lys Ala Val Leu Glu Arg His
1      5      10      15
Gly Phe Thr Phe Lys Lys Ser Phe Gly Gln Asn Phe Leu Thr Asp Thr
      20      25      30
Asn Ile Leu Gln Lys Ile Val Asp Thr Ala Glu Ile Asp Asp Gln Val
      35      40      45
Asn Val Ile Glu Ile Gly Pro Gly Ile Gly Ala Leu Thr Glu Phe Leu
      50      55      60
Ala Glu Arg Ala Ala Gln Val Met Ala Phe Glu Ile Asp His Arg Leu
65      70      75      80
Val Pro Ile Leu Ala Asp Thr Leu Arg Asp Phe Asp Asn Val Thr Val
      85      90      95
Val Asn Glu Asp Ile Leu Lys Val Asp Leu Ala Gln His Ile Gln Asn
      100     105     110
Phe Lys Asn Pro Asn Leu Pro Ile Lys Val Val Ala Asn Leu Pro Tyr
      115     120     125
Tyr Ile Thr Thr Pro Ile Leu Met His Leu Ile Glu Ser Gly Ile Pro
      130     135     140
Phe Ser Glu Phe Val Val Met Met Gln Lys Glu Val Ala Asp Arg Ile
145     150     155     160
Ser Ala Gln Pro Asn Thr Lys Ala Tyr Gly Ser Leu Ser Ile Ala Val
      165     170     175
Gln Tyr Tyr Met Thr Ala Lys Val Ala Phe Ile Val Pro Arg Thr Val
      180     185     190
Phe Val Pro Ala Pro Asn Val Asp Ser Ala Ile Leu Lys Met Val Arg
      195     200     205
Arg Pro Glu Pro Ala Val Ala Val Glu Asp Glu Asn Phe Phe Phe Lys
210     215     220
Val Ser Lys Ala Ser Phe Thr His Arg Arg Lys Thr Leu Trp Asn Asn
225     230     235     240
Leu Thr Gly Tyr Phe Gly Lys Thr Glu Glu Val Lys Asp Lys Leu Thr
      245     250     255
Lys Ala Leu Asp Gln Ala Asp Leu Ser Pro Ser Val Arg Gly Glu Ala
      260     265     270
Leu Ser Leu Ala Glu Phe Ala Gly Leu Ala Asp Ala Leu Lys Gly Gln
      275     280     285
Gly Leu
290

```

(2) INFORMATION FOR SEQ ID NO:3024:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...283

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3024:

Pro	Met	Ile	Ala	Glu	Phe	Ile	Asp	Gly	Leu	Gln	Lys	Phe	His	Phe	Leu
1				5					10					15	
Gln	Asn	Ala	Leu	Ile	Thr	Ala	Ile	Val	Val	Gly	Ile	Val	Ala	Gly	Ala
			20					25					30		
Val	Gly	Cys	Phe	Ile	Ile	Leu	Arg	Gly	Met	Ser	Leu	Met	Gly	Asp	Ala
		35					40					45			
Ile	Ser	His	Ala	Val	Leu	Pro	Gly	Val	Ala	Leu	Ser	Phe	Ile	Leu	Gly
	50					55				60					
Leu	Asp	Phe	Phe	Ile	Gly	Ala	Ile	Val	Phe	Gly	Leu	Leu	Ala	Ala	Ile
65				70					75						80
Ile	Ile	Thr	Tyr	Ile	Lys	Gly	Asn	Ser	Ile	Ile	Lys	Ser	Asp	Thr	Ala
			85					90						95	
Ile	Gly	Ile	Thr	Phe	Ser	Ser	Phe	Leu	Ala	Leu	Gly	Ile	Ile	Leu	Asn
			100					105					110		
Gly	Val	Ser	Lys	Ser	Ser	Thr	Glu	Leu	Phe	His	Ile	Leu	Phe	Gly	Tyr
	115					120						125			
Ile	Leu	Ala	Val	Gln	Asp	Thr	Asp	Met	Phe	Ile	Thr	Met	Gly	Val	Gly
	130					135						140			
Ala	Ala	Ile	Leu	Leu	Leu	Ile	Trp	Ile	Phe	Phe	Lys	Gln	Leu	Leu	Ile
145				150					155						160
Thr	Ser	Phe	Asp	Glu	Leu	Leu	Ala	Lys	Ala	Met	Gly	Met	Pro	Val	Asn
			165					170						175	
Phe	Tyr	His	Tyr	Leu	Leu	Met	Val	Leu	Leu	Thr	Leu	Val	Ser	Val	Thr
			180					185					190		
Ala	Met	Gln	Ser	Val	Gly	Thr	Ile	Leu	Ile	Val	Ala	Met	Leu	Ile	Thr
	195					200						205			
Pro	Ala	Ala	Thr	Ala	Tyr	Leu	Tyr	Ala	Asn	Ser	Leu	Lys	Ser	Met	Ile
	210					215					220				
Phe	Leu	Ser	Ser	Thr	Phe	Gly	Ala	Thr	Ala	Ser	Val	Leu	Gly	Leu	Phe
225				230					235						240
Ile	Gly	Tyr	Ser	Phe	Asn	Val	Ala	Ala	Gly	Ser	Ser	Ile	Val	Leu	Thr
			245					250						255	
Ala	Ala	Ser	Phe	Phe	Leu	Ile	Ser	Phe	Phe	Ile	Ala	Pro	Lys	Gln	Arg
			260					265					270		
Tyr	Leu	Lys	Leu	Lys	Asn	Lys	His	Leu	Leu	Lys					
	275						280								

(2) INFORMATION FOR SEQ ID NO:3025:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 154 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...154
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3025:

Pro	Met	Ile	Ala	Lys	Glu	Phe	Glu	Thr	Phe	Leu	Leu	Gly	Gln	Glu	Glu
1				5					10					15	
Thr	Phe	Leu	Thr	Pro	Ala	Lys	Asn	Leu	Ala	Val	Leu	Ile	Asp	Thr	His
			20					25					30		
Asn	Ala	Asp	His	Ala	Thr	Leu	Leu	Leu	Ser	Gln	Met	Thr	Tyr	Thr	Arg
		35					40					45			
Val	Pro	Val	Val	Thr	Asp	Glu	Lys	Gln	Phe	Val	Gly	Thr	Ile	Gly	Leu
	50					55				60					
Arg	Asp	Ile	Met	Ala	Tyr	Gln	Met	Glu	His	Asp	Leu	Ser	Gln	Glu	Ile
65				70					75					80	
Met	Ala	Asp	Thr	Asp	Ile	Val	His	Met	Thr	Lys	Thr	Asp	Val	Ala	Val
			85						90				95		
Val	Ser	Pro	Asp	Phe	Thr	Ile	Thr	Glu	Val	Leu	His	Lys	Leu	Val	Asp
		100						105					110		
Glu	Ser	Phe	Leu	Pro	Val	Val	Asp	Thr	Glu	Gly	Ile	Phe	Gln	Gly	Ile
	115						120					125			
Ile	Thr	Arg	Lys	Ser	Ile	Leu	Lys	Ala	Val	Asn	Ala	Leu	Leu	His	Asp
	130					135					140				
Phe	Ser	Lys	Glu	Tyr	Glu	Ile	Arg	Cys	Gln						
145					150										

(2) INFORMATION FOR SEQ ID NO:3026:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 130 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3026:

```

Asn Asn Val Ala Ile Gly Val Thr Phe Ser Gly Glu Ala Ser Gln Met
1      5      10      15
Leu Glu Lys Asn Glu Asn Leu Arg Tyr Val Val Pro Thr Glu Ala Ser
      20      25      30
Asn Leu Trp Cys Asp Asn Met Val Ile Pro Lys Thr Val Lys Asn Gln
      35      40      45
Asn Ser Ala Tyr Ala Phe Ile Asn Phe Met Leu Lys Pro Glu Asn Ala
      50      55      60
Leu Gln Asn Ala Glu Tyr Val Gly Tyr Ser Thr Pro Asn Leu Pro Ala
      65      70      75      80
Lys Glu Leu Leu Pro Glu Glu Thr Lys Glu Asp Lys Ala Phe Tyr Pro
      85      90      95
Asp Val Glu Thr Met Lys His Leu Glu Val Tyr Glu Lys Phe Asp His
      100     105     110
Lys Trp Thr Gly Lys Tyr Ser Asp Leu Phe Leu Gln Phe Lys Met Tyr
      115     120     125
Arg Lys
      130

```

(2) INFORMATION FOR SEQ ID NO:3027:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 73 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...73

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3027:

```

Ser Gln Val Ala Gln Asn Thr Val Leu Arg Leu Trp Ile Glu Leu Thr
1      5      10      15
Lys Ser Ala Gln Asn Thr Val Leu Arg Leu Gln Ile Glu Leu Thr Lys
      20      25      30
Ser Val Thr Ser Ile Arg Gln Gly Glu Ala Asp His Gly Leu Lys Arg
      35      40      45
Phe Ser Lys Ser Ile Ile Ser Ser His Ser Lys Ser Tyr Gln His Lys
      50      55      60
Thr His Ser Ile Lys Val Phe Ile Thr
      65      70

```

(2) INFORMATION FOR SEQ ID NO:3028:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 66 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...66

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3028:

```

Pro Gln Val Ala Gln Ser Thr Ala Leu Arg Leu Gln Ile Glu Leu Thr
1      5      10      15
Lys Ser Ala Gln Asn Thr Val Leu Arg Leu Gln Ile Glu Leu Thr Lys
      20      25      30
Ser Val Thr Tyr Ile Ala Ala Lys Ala Thr Leu Thr Arg Phe Glu Glu
      35      40      45
Ile Phe Glu Glu Tyr Glu Thr Lys Arg Arg Leu Val Ile Val Pro Ala
      50      55      60
Ser Phe
65

```

(2) INFORMATION FOR SEQ ID NO:3029:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 66 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...66

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3029:

```

Leu Gly Val Ala Pro Cys Glu Ile Gly Lys Ser Leu Ser Ser Arg Glu
1      5      10      15
Phe Ser Ser Ala Gly Arg Ala Ser Ala Leu Gln Ala Glu Gly Gln Arg
      20      25      30
Phe Asp Pro Val Asn Ser Gln Arg Ser Arg Ser Val Ala Val Ile Thr
      35      40      45
Ser Pro Cys His Gly Glu Asp Arg Gly Phe Asp Ser Arg Arg Asp Arg
      50      55      60

```

Leu Arg
65

(2) INFORMATION FOR SEQ ID NO:3030:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 66 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...66
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3030:

Leu	Gly	Val	Ala	Pro	Cys	Glu	Ile	Gly	Lys	Ser	Leu	Ser	Ser	Arg	Glu
1				5				10						15	
Phe	Ser	Ser	Ala	Gly	Arg	Ala	Ser	Ala	Leu	Gln	Ala	Glu	Gly	Gln	Arg
			20				25					30			
Phe	Asp	Pro	Val	Asn	Ser	Gln	Arg	Ser	Arg	Ser	Val	Ala	Val	Ile	Thr
		35				40					45				
Ser	Pro	Cys	His	Gly	Glu	Asp	Arg	Gly	Phe	Asp	Ser	Arg	Arg	Asp	Arg
	50					55					60				
Leu	Arg														
65															

(2) INFORMATION FOR SEQ ID NO:3031:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 82 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...82
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3031:

Leu	Gly	Val	Ala	Pro	Cys	Glu	Ile	Gly	Lys	Ser	Leu	Ser	Ser	Arg	Glu
1				5				10						15	
Phe	Ser	Ser	Ala	Gly	Arg	Ala	Ser	Ala	Leu	Gln	Ala	Glu	Gly	Gln	Arg

		20					25				30			
Phe	Asp	Pro	Val	Asn	Ser	His	Phe	Ser	Gly	Cys	Ser	Leu	Val	Lys
		35					40					45		
Leu	Gln	Pro	Ser	Lys	Leu	Leu	Ser	Arg	Val	Arg	Phe	Ser	Ser	Pro
		50					55				60			Ala
Leu	Asn	Phe	Val	Leu	Cys	Thr	Lys	Phe	Leu	Thr	Trp	Ala	Arg	Ser
65					70					75				80
Gly	Gly													

(2) INFORMATION FOR SEQ ID NO:3032:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 975 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...975

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3032:

Met	Ser	Tyr	Phe	Arg	Asn	Arg	Asp	Ile	Asp	Ile	Glu	Arg	Ile	Ser	Met
1				5				10					15		
Asn	Arg	Ser	Val	Gln	Glu	Arg	Lys	Cys	Arg	Tyr	Ser	Ile	Arg	Lys	Leu
			20					25				30			
Ser	Val	Gly	Ala	Val	Ser	Met	Ile	Val	Gly	Ala	Val	Val	Phe	Gly	Thr
		35					40					45			
Ser	Pro	Val	Leu	Ala	Gln	Glu	Gly	Ala	Ser	Glu	Gln	Pro	Leu	Ala	Asn
		50					55				60				
Glu	Thr	Gln	Leu	Ser	Gly	Glu	Ser	Ser	Thr	Leu	Thr	Asp	Thr	Glu	Lys
65					70					75					80
Ser	Gln	Pro	Ser	Ser	Glu	Thr	Glu	Leu	Ser	Gly	Asn	Lys	Gln	Glu	Gln
				85				90					95		
Glu	Arg	Lys	Asp	Lys	Gln	Glu	Glu	Lys	Ile	Ser	Arg	Asp	Tyr	Tyr	Ala
			100					105					110		
Arg	Asp	Leu	Glu	Asn	Val	Glu	Thr	Val	Ile	Glu	Lys	Glu	Asp	Val	Glu
			115				120						125		
Thr	Asn	Ala	Ser	Asn	Gly	Gln	Arg	Val	Asp	Leu	Ser	Ser	Glu	Leu	Asp
						135					140				
Lys	Leu	Lys	Lys	Leu	Glu	Asn	Ala	Thr	Val	His	Met	Glu	Phe	Lys	Pro
145					150					155					160
Asp	Ala	Lys	Ala	Pro	Ala	Phe	Tyr	Asn	Leu	Phe	Ser	Val	Ser	Ser	Ala
				165					170					175	
Thr	Lys	Lys	Asp	Glu	Tyr	Phe	Thr	Met	Ala	Val	Tyr	Asn	Asn	Thr	Ala
			180					185					190		
Thr	Leu	Glu	Gly	Arg	Gly	Ser	Asp	Gly	Lys	Gln	Phe	Tyr	Gly	Asn	Tyr
		195					200					205			
Asn	Asp	Ala	Pro	Leu	Lys	Val	Lys	Pro	Gly	Gln	Trp	Asn	Ser	Val	Thr

210		215		220
Phe Thr Val Glu Lys Pro Thr Pro Glu Leu Pro Lys Gly Arg Val Arg				
225		230		240
Leu Tyr Val Asn Gly Val Leu Ser Arg Thr Ser Leu Lys Ser Gly Asn				
	245		250	255
Phe Ile Lys Asp Met Pro Asp Val Thr His Val Gln Ile Gly Ala Thr				
	260		265	270
Lys Arg Ala Asn Asn Thr Val Trp Gly Ser Asn Leu Gln Ile Arg Asn				
	275		280	285
Leu Thr Val Tyr Asn Arg Ala Leu Thr Pro Glu Glu Val Gln Lys Arg				
	290		295	300
Ser Gln Leu Phe Lys Arg Ser Asp Leu Glu Lys Lys Leu Pro Glu Gly				
305		310		320
Ala Val Leu Thr Glu Lys Thr Asp Ile Phe Glu Ser Gly Arg Asn Gly				
	325		330	335
Lys Pro Asn Lys Asp Gly Ile Lys Ser Tyr Arg Ile Pro Ala Leu Leu				
	340		345	350
Lys Thr Asp Lys Gly Thr Leu Ile Ala Gly Ala Asp Glu Arg Arg Leu				
	355		360	365
His Ser Ser Asp Trp Gly Asp Ile Gly Met Val Ile Arg Arg Ser Glu				
	370		375	380
Asp Asn Gly Lys Thr Trp Gly Asp Arg Val Thr Ile Thr Asn Leu Arg				
385		390		400
Asp Asn Pro Lys Ala Ser Asp Pro Ser Ile Gly Ser Pro Val Asn Ile				
	405		410	415
Asp Met Val Leu Val Gln Asp Pro Glu Thr Lys Arg Ile Phe Ser Ile				
	420		425	430
Tyr Asp Met Phe Pro Glu Gly Lys Gly Ile Phe Gly Met Ser Ser Gln				
	435		440	445
Lys Glu Glu Ala Tyr Lys Lys Ile Asp Gly Lys Thr Tyr Gln Ile Leu				
	450		455	460
Tyr Arg Glu Gly Glu Lys Gly Ala Tyr Thr Ile Arg Glu Asn Gly Thr				
465		470		480
Val Tyr Thr Pro Asp Gly Lys Ala Thr Asp Tyr Arg Val Val Val Asp				
	485		490	495
Pro Val Lys Pro Ala Tyr Ser Asp Lys Gly Asp Leu Tyr Lys Gly Asp				
	500		505	510
Gln Leu Leu Gly Asn Ile Tyr Phe Thr Thr Asn Lys Thr Ser Pro Phe				
	515		520	525
Arg Ile Ala Lys Asp Ser Tyr Leu Trp Met Ser Tyr Ser Asp Asp Asp				
	530		535	540
Gly Lys Thr Trp Ser Ala Pro Gln Asp Ile Thr Pro Met Val Lys Ala				
545		550		560
Asp Trp Met Lys Phe Leu Gly Val Gly Pro Gly Thr Gly Ile Val Leu				
	565		570	575
Arg Asn Gly Pro His Lys Gly Arg Ile Leu Ile Pro Val Tyr Thr Thr				
	580		585	590
Asn Asn Val Ser His Leu Asp Gly Ser Gln Ser Ser Arg Val Ile Tyr				
	595		600	605
Ser Asp Asp His Gly Lys Thr Trp His Ala Gly Glu Ala Val Asn Asp				
	610		615	620
Asn Arg Gln Val Asp Gly Gln Lys Ile His Ser Ser Thr Met Asn Asn				
625		630		640
Lys Arg Ala Gln Asn Thr Glu Ser Thr Val Val Gln Leu Asn Asn Gly				
	645		650	655
Asp Val Lys Leu Phe Met Arg Gly Leu Thr Gly Asp Leu Gln Val Ala				
	660		665	670

Thr	Ser	Lys	Asp	Gly	Gly	Val	Thr	Trp	Glu	Lys	Asp	Ile	Lys	Arg	Tyr	675	680	685
Pro	Gln	Val	Lys	Asp	Val	Tyr	Val	Gln	Met	Ser	Ala	Ile	His	Thr	Met	690	695	700
His	Glu	Gly	Lys	Glu	Tyr	Ile	Ile	Leu	Ser	Asn	Ala	Gly	Gly	Pro	Lys	705	710	715
Arg	Glu	Asn	Gly	Met	Val	His	Leu	Ala	Arg	Val	Glu	Glu	Asn	Gly	Glu	725	730	735
Leu	Thr	Trp	Leu	Lys	His	Asn	Pro	Ile	Gln	Lys	Gly	Glu	Phe	Ala	Tyr	740	745	750
Asn	Ser	Leu	Gln	Glu	Leu	Gly	Asn	Gly	Glu	Tyr	Gly	Ile	Leu	Tyr	Glu	755	760	765
His	Thr	Glu	Lys	Gly	Gln	Asn	Ala	Tyr	Thr	Leu	Ser	Phe	Arg	Lys	Phe	770	775	780
Asn	Trp	Glu	Phe	Leu	Ser	Lys	Asn	Leu	Ile	Ser	Pro	Thr	Glu	Ala	Lys	785	790	795
Val	Lys	Arg	Thr	Arg	Glu	Met	Gly	Lys	Gly	Val	Ile	Gly	Leu	Glu	Phe	805	810	815
Asp	Ser	Glu	Val	Leu	Val	Asn	Lys	Ala	Pro	Thr	Leu	Gln	Leu	Ala	Asn	820	825	830
Gly	Lys	Thr	Ala	Thr	Phe	Leu	Thr	Gln	Tyr	Asp	Ser	Lys	Thr	Leu	Leu	835	840	845
Phe	Ala	Val	Asp	Lys	Glu	Asp	Ile	Gly	Gln	Glu	Ile	Ile	Gly	Ile	Ala	850	855	860
Lys	Gly	Ser	Ile	Glu	Ser	Met	His	Asn	Leu	Pro	Val	Asn	Leu	Ala	Gly	865	870	875
Ala	Arg	Val	Pro	Gly	Gly	Val	Asn	Gly	Ser	Lys	Ala	Ala	Val	His	Glu	885	890	895
Val	Pro	Glu	Phe	Thr	Gly	Gly	Val	Asn	Gly	Thr	Glu	Pro	Ala	Val	His	900	905	910
Glu	Ile	Ala	Glu	Tyr	Lys	Gly	Ser	Asp	Ser	Leu	Val	Thr	Leu	Thr	Thr	915	920	925
Lys	Glu	Asp	Tyr	Thr	Tyr	Lys	Ala	Pro	Leu	Ala	Gln	Gln	Ala	Leu	Pro	930	935	940
Glu	Thr	Gly	Asn	Lys	Glu	Ser	Asp	Leu	Leu	Ala	Ser	Leu	Gly	Leu	Thr	945	950	955
Ala	Phe	Phe	Leu	Gly	Leu	Phe	Thr	Leu	Gly	Lys	Lys	Arg	Glu	Gln		965	970	975

(2) INFORMATION FOR SEQ ID NO:3033:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 655 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...655

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3033:

Arg	Leu	Ser	Ala	Thr	Ala	Gly	Leu	Val	Leu	Leu	Ala	Ala	Gly	Val	Leu
1				5					10					15	
Ala	Ala	Cys	Ser	Ser	Ser	Lys	Ser	Ser	Asp	Ser	Ser	Ala	Pro	Lys	Ala
			20					25					30		
Tyr	Gly	Tyr	Val	Tyr	Thr	Ala	Asp	Pro	Glu	Thr	Leu	Asp	Tyr	Leu	Ile
		35					40					45			
Ser	Ser	Lys	Asn	Ser	Thr	Thr	Val	Val	Thr	Ser	Asn	Gly	Ile	Asp	Gly
		50				55					60				
Leu	Phe	Thr	Asn	Asp	Asn	Tyr	Gly	Asn	Leu	Ala	Pro	Ala	Val	Ala	Glu
65					70					75					80
Asp	Trp	Glu	Val	Ser	Lys	Asp	Gly	Leu	Thr	Tyr	Thr	Tyr	Lys	Ile	Arg
				85					90					95	
Lys	Gly	Val	Lys	Trp	Phe	Thr	Ser	Asp	Gly	Glu	Glu	Tyr	Ala	Glu	Val
			100					105					110		
Thr	Ala	Lys	Asp	Phe	Val	Asn	Gly	Leu	Lys	His	Ala	Ala	Asp	Lys	Lys
		115					120					125			
Ser	Glu	Ala	Met	Tyr	Leu	Ala	Glu	Asn	Ser	Val	Lys	Gly	Leu	Ala	Asp
	130					135					140				
Tyr	Leu	Ser	Gly	Thr	Ser	Thr	Asp	Phe	Ser	Thr	Val	Gly	Val	Lys	Ala
145					150					155					160
Val	Asp	Asp	Tyr	Thr	Leu	Gln	Tyr	Thr	Leu	Asn	Gln	Pro	Glu	Pro	Phe
				165					170					175	
Trp	Asn	Ser	Lys	Leu	Thr	Tyr	Ser	Ile	Phe	Trp	Pro	Leu	Asn	Glu	Glu
			180					185					190		
Phe	Glu	Thr	Ser	Lys	Gly	Ser	Asp	Phe	Ala	Lys	Pro	Thr	Asp	Pro	Thr
		195					200					205			
Ser	Leu	Leu	Tyr	Asn	Gly	Pro	Phe	Leu	Leu	Lys	Gly	Leu	Thr	Ala	Lys
	210					215					220				
Ser	Ser	Val	Glu	Phe	Val	Lys	Asn	Glu	Gln	Tyr	Trp	Asp	Lys	Glu	Asn
225					230					235					240
Val	His	Leu	Asp	Thr	Ile	Asn	Leu	Ala	Tyr	Tyr	Asp	Gly	Ser	Asp	Gln
				245					250					255	
Glu	Ser	Leu	Glu	Arg	Asn	Phe	Thr	Ser	Gly	Ala	Tyr	Ser	Tyr	Ala	Arg
		260						265					270		
Leu	Tyr	Pro	Thr	Ser	Ser	Asn	Tyr	Ser	Lys	Val	Ala	Glu	Glu	Tyr	Lys
		275					280					285			
Asp	Asn	Ile	Tyr	Tyr	Thr	Gln	Ser	Gly	Ser	Gly	Ile	Ala	Gly	Leu	Gly
	290					295					300				
Val	Asn	Ile	Asp	Arg	Gln	Ser	Tyr	Asn	Tyr	Thr	Ser	Lys	Thr	Thr	Asp
305					310					315					320
Ser	Glu	Lys	Val	Ala	Thr	Lys	Lys	Ala	Leu	Leu	Asn	Lys	Asp	Phe	Arg
				325					330					335	
Gln	Ala	Leu	Asn	Phe	Ala	Leu	Asp	Arg	Ser	Ala	Tyr	Ser	Ala	Gln	Ile
			340					345					350		
Asn	Gly	Lys	Asp	Gly	Ala	Ala	Leu	Ala	Val	Arg	Asn	Leu	Phe	Val	Lys
		355					360					365			
Pro	Asp	Phe	Val	Ser	Ala	Gly	Glu	Lys	Thr	Phe	Gly	Asp	Leu	Val	Ala
	370					375					380				
Ala	Gln	Leu	Pro	Ala	Tyr	Gly	Asp	Glu	Trp	Lys	Gly	Val	Asn	Leu	Ala
385					390					395					400
Asp	Gly	Gln	Asp	Gly	Leu	Phe	Asn	Ala	Asp	Lys	Ala	Lys	Ala	Glu	Phe
				405					410					415	
Ala	Lys	Ala	Lys	Lys	Ala	Leu	Glu	Ala	Asp	Gly	Val	Gln	Phe	Pro	Ile
			420					425					430		
His	Leu	Asp	Val	Pro	Val	Asp	Gln	Ala	Ser	Lys	Asn	Tyr	Ile	Ser	Arg

		435						440						445			
Ile	Gln	Ser	Phe	Lys	Gln	Ser	Val	Glu	Thr	Val	Leu	Gly	Val	Glu	Asn		
	450					455					460						
Val	Val	Val	Asp	Ile	Gln	Gln	Met	Thr	Ser	Asp	Glu	Phe	Leu	Asn	Ile		
465					470					475					480		
Thr	Tyr	Tyr	Ala	Ala	Asn	Ala	Ser	Ser	Glu	Asp	Trp	Asp	Val	Ser	Gly		
				485					490					495			
Gly	Val	Ser	Trp	Gly	Pro	Asp	Tyr	Gln	Asp	Pro	Ser	Thr	Tyr	Leu	Asp		
			500					505					510				
Ile	Leu	Lys	Thr	Thr	Ser	Ser	Glu	Thr	Thr	Lys	Thr	Tyr	Leu	Gly	Phe		
		515					520					525					
Asp	Asn	Pro	Asn	Ser	Pro	Ser	Val	Val	Gln	Val	Gly	Leu	Lys	Glu	Tyr		
	530					535					540						
Asp	Lys	Leu	Val	Asp	Glu	Ala	Ala	Arg	Glu	Thr	Ser	Asp	Leu	Asn	Val		
545					550					555					560		
Arg	Tyr	Glu	Lys	Tyr	Ala	Ala	Ala	Gln	Ala	Trp	Leu	Thr	Asp	Ser	Ser		
				565					570					575			
Leu	Phe	Ile	Pro	Ala	Met	Ala	Ser	Ser	Gly	Ala	Ala	Pro	Val	Leu	Ser		
			580						585				590				
Arg	Ile	Val	Pro	Phe	Thr	Gly	Ala	Ser	Ala	Gln	Thr	Gly	Ser	Lys	Gly		
		595					600					605					
Ser	Asp	Val	Tyr	Phe	Lys	Tyr	Leu	Lys	Leu	Gln	Asp	Lys	Val	Val	Thr		
	610					615					620						
Lys	Glu	Glu	Tyr	Glu	Lys	Ala	Arg	Glu	Lys	Trp	Leu	Lys	Glu	Lys	Ala		
625					630					635					640		
Glu	Ser	Asn	Glu	Lys	Ala	Gln	Lys	Glu	Leu	Ala	Ser	His	Val	Lys			
				645					650					655			

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3034:

Leu	Glu	Ser	Val	Phe	Ser	Asp	Ile	Pro	Pro	Gln	Ala	Val	Lys	Thr	Gly
65					70					75					80
Met	Leu	Ala	Thr	Thr	Glu	Ile	Met	Glu	Ile	Ile	Gln	Pro	Tyr	Leu	Lys
				85					90					95	
Lys	Leu	Asp	Cys	Pro	Tyr	Val	Leu	Asp	Pro	Val	Met	Val	Ala	Thr	Ser
			100					105					110		
Gly	Asp	Ala	Leu	Ile	Asp	Ser	Asn	Ala	Arg	Asp	Tyr	Leu	Lys	Thr	Asn
		115					120						125		
Leu	Leu	Pro	Leu	Ala	Thr	Ile	Ile	Thr	Pro	Asn	Leu	Pro	Glu	Ala	Glu
		130					135					140			
Glu	Ile	Val	Gly	Phe	Ser	Ile	His	Asp	Pro	Glu	Asp	Met	Gln	Arg	Ala
145					150					155					160
Gly	Arg	Leu	Ile	Leu	Lys	Glu	Phe	Gly	Pro	Gln	Ser	Val	Val	Ile	Lys
				165					170					175	
Gly	Gly	His	Leu	Lys	Gly	Gly	His	Leu	Lys	Gly	Gly	Ala	Lys	Asp	Phe
			180					185					190		
Leu	Phe	Thr	Lys	Asn	Glu	Gln	Phe	Val	Trp	Glu	Ser	Pro	Arg	Ile	Gln
		195					200					205			
Thr	Cys	His	Thr	His	Gly	Thr	Gly	Cys	Thr	Phe	Ala	Ala	Val	Ile	Thr
	210				215						220				
Ala	Glu	Leu	Ala	Lys	Gly	Lys	Ser	Leu	Tyr	Gln	Ala	Val	Asp	Lys	Ala
225					230					235					240
Lys	Ala	Phe	Ile	Thr	Lys	Ala	Ile	Gln	Asp	Ala	Pro	Gln	Leu	Gly	His
				245					250					255	
Gly	Ser	Gly	Pro	Val	Asn	His	Thr	Thr	Phe	Lys	Asp				
			260					265							

(2) INFORMATION FOR SEQ ID NO:3035:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...308

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3035:

Arg	Arg	Pro	Ala	Thr	Gly	His	Gly	His	Ala	Gly	Pro	Ala	Pro	Pro	Arg
1				5					10					15	
Arg	Arg	Ala	Gly	Ala	Val	Ala	Pro	Ala	Gly	Ala	Pro	His	Gly	Phe	Arg
			20					25					30		
Leu	Arg	Trp	Arg	Pro	Gly	Cys	Ala	Pro	Ala	Arg	His	Leu	Ala	Gly	Ala
		35				40						45			
Arg	Asp	Arg	Pro	Ala	Ala	Val	Ala	Gly	Ser	Arg	Ser	Met	Pro	Ala	Gly
	50				55					60					
Val	Pro	Ala	Gly	Gly	Arg	Arg	Gly	Phe	Ala	Trp	Gln	Ala	Met	Ala	Gln
65					70					75					80

Ser Lys Thr Thr Ile Asp Thr Thr Val Ser Ser Lys Leu Phe Asn Asn
50 55 60
Arg Val Val Ile
65

(2) INFORMATION FOR SEQ ID NO:3037:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 302 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...302

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3037:

Glu	Leu	Thr	Ala	Asp	Ser	Pro	Leu	Phe	Met	Val	Lys	Thr	Met	Thr	Ile	1	5	10	15
Ala	Thr	Ile	Asp	Ile	Gly	Gly	Thr	Gly	Ile	Lys	Phe	Ala	Ser	Leu	Thr	20	25	30	
Pro	Asp	Gly	Lys	Ile	Leu	Tyr	Lys	Thr	Ser	Ile	Ser	Thr	Pro	Glu	Asn	35	40	45	
Leu	Glu	Asp	Leu	Leu	Ala	Trp	Leu	Asp	Gln	Arg	Leu	Ser	Glu	Gln	Asp	50	55	60	
Tyr	Ser	Gly	Ile	Ala	Met	Ser	Val	Pro	Gly	Ala	Val	Asn	Gln	Glu	Thr	65	70	75	80
Gly	Val	Ile	Asp	Gly	Phe	Ser	Ala	Val	Pro	Tyr	Ile	His	Gly	Phe	Ser	85	90	95	
Trp	Tyr	Glu	Ala	Leu	Ser	Ser	Tyr	Gln	Leu	Pro	Val	His	Leu	Glu	Asn	100	105	110	
Asp	Ala	Asn	Cys	Val	Gly	Leu	Ser	Glu	Leu	Leu	Ala	His	Pro	Asp	Leu	115	120	125	
Glu	Asn	Ala	Ala	Cys	Val	Val	Ile	Gly	Thr	Gly	Ile	Gly	Gly	Ala	Met	130	135	140	
Ile	Ile	Asn	Gly	Arg	Leu	His	Arg	Gly	Arg	His	Gly	Leu	Gly	Gly	Glu	145	150	155	160
Phe	Gly	Tyr	Met	Thr	Thr	Leu	Ala	Pro	Ala	Glu	Lys	Leu	Asn	Asn	Trp	165	170	175	
Ser	Gln	Leu	Ala	Ser	Thr	Gly	Asn	Met	Val	Arg	Tyr	Val	Ile	Glu	Lys	180	185	190	
Ser	Gly	His	Thr	Asp	Trp	Asp	Gly	Arg	Lys	Ile	Tyr	Gln	Glu	Ala	Ala	195	200	205	
Ala	Gly	Asn	Ala	Leu	Cys	Gln	Glu	Ala	Ile	Glu	Arg	Met	Asn	Arg	Asn	210	215	220	
Leu	Ala	Gln	Gly	Leu	Leu	Asn	Ile	Gln	Tyr	Leu	Ile	Asp	Pro	Asp	Val	225	230	235	240
Ile	Ser	Leu	Gly	Gly	Ser	Ile	Ser	Gln	Asn	Pro	Asp	Phe	Ile	Gln	Asp	245	250	255	

Val	Lys	Lys	Ala	Val	Asp	Asn	Phe	Val	Asp	Thr	Tyr	Glu	Glu	Tyr	Thr
			260					265					270		
Val	Ala	Pro	Val	Ile	Gln	Thr	Cys	Thr	Tyr	His	Ala	Asp	Ala	Asn	Leu
		275					280					285			
Tyr	Gly	Ala	Leu	Val	Asn	Trp	Leu	Gln	Glu	Glu	Lys	Gln	Trp		
	290					295					300				

(2) INFORMATION FOR SEQ ID NO:3038:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 67 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...67
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3038:

Arg	Thr	Thr	Ala	Arg	Met	Ala	Ala	Phe	Ile	Pro	Gly	Ala	Ser	Pro	Pro
1			5					10					15		
Leu	Val	Lys	Thr	Ala	Ile	Arg	Phe	Ile	Leu	Val	Tyr	Ala	Pro	Phe	Ser
			20				25					30			
Phe	Asn	Ile	Leu	Leu	Asp	Tyr	Ile	Thr	Phe	Asp	Phe	Lys	Ile	Leu	Leu
		35				40					45				
Phe	Ser	Val	Phe	Leu	Ala	Ile	Asn	Arg	Phe	His	Asn	Asp	Phe	Ile	Gln
	50					55					60				
Phe	Leu	Leu													
65															

(2) INFORMATION FOR SEQ ID NO:3039:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 794 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...794
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3039:

Gly	Lys	Thr	Ala	Arg	His	His	Thr	Met	Phe	Glu	Met	Leu	Gly	Asn	Phe
1				5					10					15	
Ser	Ile	Gly	Asp	Tyr	Phe	Arg	Asp	Glu	Ala	Ile	Thr	Trp	Ala	Tyr	Glu
			20					25					30		
Leu	Leu	Thr	Ser	Pro	Glu	Trp	Phe	Asp	Phe	Pro	Ala	Glu	Lys	Leu	Tyr
		35					40					45			
Met	Thr	Tyr	Tyr	Pro	Asp	Asp	Lys	Asp	Ser	Tyr	Asn	Arg	Trp	Ile	Glu
	50					55					60				
Val	Gly	Val	Asp	Pro	Ser	His	Leu	Ile	Pro	Ile	Glu	Asp	Asn	Phe	Trp
65					70					75					80
Glu	Ile	Gly	Ala	Gly	Pro	Ser	Gly	Pro	Asp	Thr	Glu	Ile	Phe	Phe	Asp
				85					90					95	
Arg	Gly	Glu	Ala	Phe	Asp	Pro	Glu	Asn	Ile	Gly	Leu	Arg	Leu	Leu	Ala
			100					105					110		
Glu	Asp	Ile	Glu	Asn	Asp	Arg	Tyr	Ile	Glu	Ile	Trp	Asn	Ile	Val	Leu
	115						120					125			
Ser	Gln	Phe	Asn	Ala	Asp	Pro	Ala	Val	Pro	Arg	Ser	Glu	Tyr	Lys	Glu
	130					135					140				
Leu	Pro	His	Lys	Asn	Ile	Asp	Thr	Gly	Ala	Gly	Leu	Glu	Arg	Leu	Val
145					150					155					160
Ala	Val	Ile	Gln	Gly	Ala	Lys	Thr	Asn	Phe	Glu	Thr	Asp	Leu	Phe	Met
				165					170					175	
Pro	Ile	Ile	Arg	Glu	Val	Glu	Lys	Leu	Ser	Gly	Lys	Val	Tyr	Asp	Gln
			180					185					190		
Asp	Gly	Asp	Asn	Met	Ser	Phe	Lys	Val	Ile	Ala	Asp	His	Ile	Arg	Ser
	195						200					205			
Leu	Ser	Phe	Ala	Ile	Gly	Asp	Gly	Ala	Leu	Pro	Gly	Asn	Glu	Gly	Arg
	210					215					220				
Gly	Tyr	Val	Leu	Arg	Arg	Leu	Leu	Arg	Arg	Ala	Ser	Met	His	Gly	Gln
225					230					235					240
Lys	Leu	Gly	Ile	Asn	Glu	Pro	Phe	Leu	Tyr	Lys	Leu	Val	Pro	Thr	Val
				245					250					255	
Gly	Lys	Ile	Met	Glu	Ser	Tyr	Tyr	Pro	Glu	Val	Leu	Glu	Lys	Arg	Asp
			260					265					270		
Phe	Ile	Glu	Lys	Ile	Val	Lys	Ser	Glu	Glu	Glu	Ser	Phe	Ala	Arg	Thr
	275						280					285			
Leu	His	Ser	Gly	Gln	His	Phe	Ala	Gln	Gly	Ile	Val	Ala	Asp	Leu	Lys
	290					295					300				
Glu	Lys	Gly	Gln	Ser	Val	Ile	Ala	Gly	Gln	Asp	Val	Phe	Lys	Leu	Tyr
305					310					315					320
Asp	Thr	Tyr	Gly	Phe	Pro	Val	Glu	Leu	Thr	Glu	Glu	Ile	Ala	Glu	Glu
				325					330					335	
Ala	Gly	Met	Thr	Val	Asp	Arg	Glu	Gly	Phe	Glu	Ala	Ala	Met	Lys	Glu
			340					345					350		
Gln	Gln	Glu	Arg	Ala	Arg	Ala	Ser	Ala	Val	Lys	Gly	Gly	Ser	Met	Gly
			355				360					365			
Met	Gln	Asn	Glu	Thr	Leu	Gln	Asn	Ile	Thr	Val	Glu	Ser	Val	Phe	Asn
	370					375					380				
Tyr	Asn	Ala	Ser	Gln	Leu	Ser	Ser	Lys	Leu	Val	Ala	Ile	Val	Ala	Asp
385					390					395					400
Asn	Ala	Glu	Val	Gly	Ala	Val	Ser	Glu	Gly	Thr	Ala	Ser	Leu	Ile	Phe
				405					410					415	
Ala	Glu	Thr	Ser	Phe	Tyr	Ala	Glu	Met	Gly	Gly	Gln	Val	Ala	Asp	Tyr
			420					425					430		
Gly	Gln	Ile	Leu	Asp	Glu	Ser	Gly	Lys	Val	Val	Ala	Thr	Val	Thr	Asn
		435					440					445			

Val	Gln	Lys	Ala	Pro	Asn	Gly	Gln	Ala	Leu	His	Thr	Val	Glu	Val	Leu
450						455					460				
Ala	Pro	Leu	Ala	Leu	Asn	Gln	Glu	Tyr	Thr	Leu	Ala	Ile	Asp	Ser	Asn
465					470					475					480
Arg	Arg	His	Arg	Val	Met	Lys	Asn	His	Thr	Ala	Thr	His	Leu	Leu	His
				485					490					495	
Ala	Ala	Leu	His	Asn	Ile	Leu	Gly	Asn	His	Ala	Thr	Gln	Ala	Gly	Ser
			500					505					510		
Leu	Asn	Glu	Val	Glu	Phe	Leu	Arg	Phe	Asp	Phe	Thr	His	Phe	Gln	Ala
		515					520					525			
Val	Thr	Ala	Glu	Glu	Leu	Arg	Ala	Ile	Glu	Gln	Gln	Val	Asn	Glu	Lys
	530					535					540				
Ile	Trp	Glu	Ala	Leu	Glu	Val	Lys	Thr	Val	Glu	Thr	Asp	Ile	Asp	Thr
545					550					555					560
Ala	Lys	Glu	Met	Gly	Ala	Met	Ala	Leu	Phe	Gly	Glu	Lys	Tyr	Gly	Lys
				565					570					575	
Glu	Val	Arg	Val	Val	Thr	Ile	Gly	Asp	Tyr	Ser	Ile	Glu	Leu	Cys	Gly
			580					585					590		
Gly	Thr	His	Val	Gly	Asn	Thr	Ser	Glu	Ile	Gly	Leu	Phe	Lys	Ile	Val
	595						600					605			
Lys	Glu	Glu	Gly	Ile	Gly	Ser	Gly	Thr	Arg	Arg	Ile	Leu	Ala	Val	Thr
	610					615					620				
Gly	Lys	Glu	Ala	Phe	Glu	Ala	Tyr	Arg	Glu	Gln	Glu	Asp	Ala	Leu	Lys
625					630					635					640
Ala	Val	Ala	Ala	Thr	Leu	Lys	Ala	Pro	Gln	Val	Lys	Glu	Val	Pro	His
				645					650					655	
Lys	Val	Glu	Gly	Leu	Gln	Glu	Gln	Leu	Arg	Gln	Leu	Gln	Lys	Glu	Asn
			660					665					670		
Ala	Glu	Leu	Lys	Glu	Lys	Ala	Ala	Ala	Ala	Ala	Ala	Gly	Asp	Ile	Phe
		675					680					685			
Lys	Asp	Val	Lys	Glu	Val	Asn	Gly	His	Arg	Tyr	Ile	Ala	Ser	Gln	Val
	690					695					700				
Ser	Val	Ser	Asp	Ala	Gly	Ala	Leu	Arg	Thr	Phe	Ala	Asp	Asn	Trp	Lys
705					710					715					720
Gln	Lys	Asp	Tyr	Ser	Asp	Leu	Leu	Val	Leu	Val	Ala	Ala	Ile	Gly	Asp
				725					730					735	
Lys	Val	Asn	Val	Leu	Val	Ala	Ser	Lys	Thr	Lys	Asp	Leu	His	Ala	Gly
		740						745				750			
Asn	Leu	Val	Lys	Glu	Leu	Ala	Pro	Ile	Ile	Asp	Gly	Arg	Gly	Gly	Gly
	755					760					765				
Lys	Pro	Asp	Met	Ala	Met	Ala	Gly	Gly	Ser	Asn	Gln	Ala	Lys	Ile	Gln
	770					775					780				
Glu	Leu	Leu	Asp	Ala	Val	Ala	Gly	Lys	Leu						
785					790										

(2) INFORMATION FOR SEQ ID NO:3040:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...309

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3040:

Tyr	Asn	Tyr	Phe	Met	Ile	Ile	Thr	Ile	Pro	Ile	Lys	Asn	Gln	Lys	Asp
1				5					10					15	
Ile	Gly	Thr	Pro	Ser	Asp	Ser	Val	Val	Val	Leu	Gly	Tyr	Phe	Asp	Gly
			20					25					30		
Ile	His	Lys	Gly	His	Gln	Glu	Leu	Phe	Arg	Val	Ala	Asn	Lys	Ala	Ala
		35					40					45			
Arg	Lys	Asp	Leu	Leu	Pro	Ile	Val	Val	Met	Thr	Phe	Asn	Glu	Ser	Pro
	50					55					60				
Lys	Ile	Ala	Leu	Glu	Pro	Tyr	His	Pro	Asp	Leu	Phe	Leu	His	Ile	Leu
65					70				75					80	
Asn	Pro	Ala	Glu	Arg	Glu	Arg	Lys	Leu	Lys	Arg	Glu	Gly	Val	Glu	Glu
			85						90					95	
Leu	Tyr	Leu	Leu	Asp	Phe	Ser	Ser	Gln	Phe	Ala	Ser	Leu	Thr	Ala	Gln
		100						105					110		
Glu	Phe	Phe	Ala	Thr	Tyr	Ile	Lys	Ala	Met	Asn	Ala	Lys	Ile	Ile	Val
		115					120					125			
Ala	Gly	Phe	Asp	Tyr	Thr	Phe	Gly	Ser	Asp	Lys	Lys	Thr	Ala	Glu	Asp
	130					135					140				
Leu	Lys	Asp	Tyr	Phe	Asp	Gly	Glu	Val	Ile	Ile	Val	Pro	Pro	Val	Glu
145					150				155						160
Asp	Glu	Lys	Gly	Lys	Ile	Ser	Ser	Thr	Arg	Ile	Arg	Gln	Ala	Ile	Leu
			165					170						175	
Asp	Gly	Asn	Val	Lys	Glu	Ala	Gly	Lys	Leu	Leu	Gly	Ala	Pro	Leu	Pro
		180						185				190			
Ser	Arg	Gly	Met	Val	Val	His	Gly	Asn	Ala	Arg	Gly	Arg	Thr	Ile	Gly
		195					200					205			
Tyr	Pro	Thr	Ala	Asn	Leu	Val	Leu	Leu	Asp	Arg	Thr	Tyr	Met	Pro	Ala
	210					215					220				
Asp	Gly	Val	Tyr	Val	Val	Asp	Val	Glu	Ile	Gln	Arg	Gln	Lys	Tyr	Arg
225					230					235					240
Ala	Met	Ala	Ser	Val	Gly	Lys	Asn	Val	Thr	Phe	Asp	Gly	Glu	Glu	Ala
			245						250					255	
Arg	Phe	Glu	Val	Asn	Ile	Phe	Asp	Phe	Asn	Gln	Asp	Ile	Tyr	Gly	Glu
		260					265						270		
Thr	Val	Met	Val	Tyr	Trp	Leu	Asp	Arg	Ile	Arg	Asp	Met	Thr	Lys	Phe
		275					280					285			
Asp	Ser	Val	Asp	Gln	Leu	Val	Asp	Gln	Leu	Lys	Ala	Asp	Glu	Glu	Val
	290					295					300				
Thr	Arg	Asn	Trp	Ser											
305															

(2) INFORMATION FOR SEQ ID NO:3041:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 200 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...200
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3041:

```

Val Asn Tyr Leu Asn Lys Met Glu Arg Asn Ile Asn Met Lys Lys Trp
1      5      10      15
Gln Thr Cys Val Leu Gly Ala Gly Ser Leu Leu Cys Leu Thr Ala Cys

      20      25      30
Ser Gly Lys Ser Val Thr Ser Glu His Gln Thr Lys Asp Glu Met Lys
      35      40      45
Thr Glu Gln Thr Ala Ser Lys Thr Ser Ala Ala Lys Gly Lys Glu Val
      50      55      60
Ala Asp Phe Glu Leu Met Gly Val Asp Gly Lys Thr Tyr Arg Leu Ser
65      70      75      80
Asp Tyr Lys Gly Lys Lys Val Tyr Leu Lys Phe Trp Ala Ser Trp Cys
      85      90      95
Ser Ile Cys Leu Ala Ser Leu Pro Asp Thr Asp Glu Ile Ala Lys Glu
      100     105     110
Ala Gly Asp Asp Tyr Val Val Leu Thr Val Val Ser Pro Gly His Lys
      115     120     125
Gly Glu Gln Ser Glu Ala Asp Phe Lys Asn Trp Tyr Lys Gly Leu Asp
      130     135     140
Tyr Lys Asn Leu Pro Val Leu Val Asp Pro Ser Gly Lys Leu Leu Glu
145     150     155     160
Thr Tyr Gly Val Arg Ser Tyr Pro Thr Gln Ala Phe Ile Asp Lys Glu
      165     170     175
Gly Lys Leu Val Lys Thr His Pro Gly Phe Met Glu Lys Asp Ala Ile
      180     185     190
Leu Gln Thr Leu Lys Glu Leu Ala
      195     200

```

(2) INFORMATION FOR SEQ ID NO:3042:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 63 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature

(B) LOCATION 1...63

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3042:

```
Asn Phe Tyr Ala Lys Ser Leu Gly Ile Asn Phe Tyr Leu Phe Leu Pro
1          5          10          15
Thr His Leu Ser Thr Ile Leu Leu Arg Lys His Gly Pro Ile Ser Lys
          20          25          30
Ser Thr Ser Lys Arg Tyr Tyr Gln Val Val Ala Ile Pro Phe Thr Arg
          35          40          45
Leu Phe Cys Pro Ala Leu Val Ser Ile Asp Tyr Ser Arg Leu Lys
          50          55          60
```

(2) INFORMATION FOR SEQ ID NO:3043:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...77

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3043:

```
Asn Phe Tyr Ala Arg Ser Leu Gly Ile Asn Phe Tyr Leu Phe Leu Pro
1          5          10          15
Thr His Leu Ser Thr Ile Leu Leu Arg Lys His Gly Leu Ile Ser Lys
          20          25          30
Ser Thr Ser Lys Arg Tyr Tyr Gln Val Ala Ile Pro Phe Met Arg Leu
          35          40          45
Phe Cys Pro Ala Leu Val Ser Ile Asp Tyr Ser Ser Arg Ile Gln Leu
          50          55          60
Gly Lys Lys Leu Leu Asn Ile Trp Arg Val Leu Leu Gly
          65          70          75
```

(2) INFORMATION FOR SEQ ID NO:3044:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 235 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...235

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3044:

```
Met Ile Tyr Ala Gly Ile Leu Ala Gly Gly Thr Gly Thr Arg Met Gly
1           5           10           15
Ile Ser Asn Leu Pro Lys Gln Phe Leu Glu Leu Gly Asp Arg Pro Ile
          20           25           30
Leu Ile His Thr Ile Glu Lys Phe Val Leu Glu Pro Ser Ile Glu Lys
          35           40           45
Ile Val Val Gly Val His Gly Asp Trp Val Leu His Ala Glu Asp Leu
          50           55           60
Val Asp Lys Tyr Leu Pro Leu His Lys Glu Arg Ile Ile Ile Thr Lys
65           70           75           80
Gly Gly Ala Asp Arg Asn Thr Ser Ile Glu Asn Ile Ile Glu Ala Ile
          85           90           95
Asp Ala Tyr Arg Pro Leu Thr Pro Glu Asp Ile Val Val Thr His Asp
          100          105          110
Ser Val Arg Pro Phe Ile Thr Leu Arg Met Ile Gln Asp Ser Ile Lys
          115          120          125
Leu Ala Gln Asn His Asp Ala Val Asp Thr Val Val Glu Ala Val Asp
          130          135          140
Thr Ile Val Glu Ser Thr Asn Gly Gln Phe Ile Thr Gly Ile Pro Asn
145          150          155          160
Arg Ala His Leu Tyr Gln Gly Gln Thr Pro Gln Thr Phe Arg Cys Lys
          165          170          175
Asp Phe Met Asp Leu Tyr Gly Ser Leu Ser Asp Glu Glu Lys Glu Ile
          180          185          190
Leu Thr Asp Ala Cys Lys Ile Phe Val Ile Lys Gly Lys Asp Val Ala
          195          200          205
Leu Ala Lys Gly Glu Tyr Ser Asn Leu Lys Ile Thr Thr Val Thr Asp
          210          215          220
Leu Lys Ile Ala Lys Ser Met Ile Glu Lys Asp
225          230          235
```

(2) INFORMATION FOR SEQ ID NO:3045:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 340 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3045:

Glu	Met	His	Ala	Lys	Met	Arg	Asn	Lys	Thr	Gln	Ile	His	Leu	Gly	Ile	1	5	10	15
Ile	Phe	Val	Ile	Cys	Leu	Gly	Leu	Leu	Ile	Thr	Ile	Phe	Leu	Ser	Leu	20	25	30	
Lys	Leu	Gly	Thr	Lys	Glu	Ile	Asn	Ile	Arg	Asp	Phe	Leu	Ala	Ala	Phe	35	40	45	
Gly	Met	Gly	Asn	Thr	Asn	Asp	Asp	Phe	Ile	Lys	Ser	Ile	Ile	Tyr	Lys	50	55	60	
Arg	Ile	Pro	Arg	Thr	Ile	Phe	Ala	Ile	Leu	Ala	Gly	Ser	Ser	Leu	Ala	65	70	75	
Ile	Ser	Gly	Val	Leu	Met	Gln	Ser	Val	Thr	Arg	Asn	Pro	Ile	Ala	Asp	85	90	95	
Pro	Gly	Ile	Leu	Gly	Ile	Asn	Thr	Gly	Ala	Ser	Leu	Ser	Val	Val	Ile	100	105	110	
Gly	Leu	Ser	Phe	Leu	Gly	Ile	Ser	Ser	Ser	Ile	Ser	His	Ile	Ser	Phe	115	120	125	
Ala	Ile	Ile	Gly	Gly	Leu	Val	Ser	Val	Ile	Phe	Val	Tyr	Ala	Ile	Ala	130	135	140	
Val	Ser	Gly	Lys	Ala	Gly	Leu	Thr	Pro	Ile	Lys	Leu	Ala	Leu	Ser	Gly	145	150	155	
Thr	Cys	Val	Ser	Met	Ala	Leu	Ser	Ser	Phe	Val	Ser	Phe	Leu	Ile	Leu	165	170	175	
Pro	Asn	Asn	Asn	Val	Leu	Asp	Lys	Phe	Arg	Phe	Trp	Gln	Ile	Gly	Ser	180	185	190	
Leu	Gly	Ala	Ala	Thr	Leu	Ser	Ser	Ile	Ser	Thr	Leu	Leu	Pro	Phe	Ile	195	200	205	
Ile	Leu	Gly	His	Leu	Ile	Ala	Ile	Phe	Ile	Ser	Ser	Asp	Leu	Asn	Ala	210	215	220	
Leu	Ala	Met	Gly	Asp	Glu	Met	Ala	Val	Gly	Leu	Gly	Val	Asn	Val	Asn	225	230	235	
Arg	Ile	Arg	Ser	Leu	Ala	Ile	Ile	Ala	Ser	Val	Leu	Leu	Cys	Ser	Ser	245	250	255	
Ile	Thr	Ala	Ile	Gly	Gly	Pro	Ile	Gly	Phe	Val	Gly	Leu	Ile	Val	Pro	260	265	270	
His	Phe	Cys	Gly	Leu	Phe	Ile	Ser	Lys	Asp	Ile	Arg	Thr	Met	Thr	Ile	275	280	285	
Ser	Ser	Ser	Phe	Ile	Gly	Ala	Glu	Leu	Leu	Leu	Ile	Cys	Asp	Ile	Ile	290	295	300	
Gly	Arg	Met	Leu	Gly	Lys	Pro	Gly	Glu	Ile	Glu	Val	Gly	Ile	Ile	Thr	305	310	315	
Ala	Ile	Ile	Gly	Gly	Pro	Val	Leu	Ile	Tyr	Val	Thr	Met	Lys	Asn	Arg	325	330	335	
Gly	Val	Asn	Asn													340			

(2) INFORMATION FOR SEQ ID NO:3046:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...180

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3046:

```

Ser His Asp Ala Gln Asn Thr Val Leu Arg Trp Gln Ile Glu Leu Thr
1          5          10          15
Lys Ser Ala Gln Asn Thr Val Leu Arg Trp Gln Ile Glu Leu Thr Lys
          20          25          30
Ser Ala Gln Asn Thr Val Leu Arg Trp Gln Ile Glu Leu Thr Lys Ser
          35          40          45
Ala Gln Asn Thr Val Leu Arg Trp Gln Ile Glu Leu Thr Lys Ser Ala
          50          55          60
Gln Asn Thr Val Leu Arg Trp Gln Ile Glu Leu Thr Lys Ser Ala Gln
65          70          75          80
Asn Thr Val Leu Arg Trp Gln Ile Glu Leu Thr Lys Ser Ala Gln Asn
          85          90          95
Thr Val Leu Arg Trp Gln Ile Glu Leu Thr Lys Ser Ala Gln Asn Thr
          100         105         110
Val Leu Arg Trp Gln Ile Glu Leu Thr Lys Ser Ala Gln Asn Thr Val
          115         120         125
Leu Arg Trp Gln Ile Glu Leu Thr Lys Ser Ala Gln Asn Thr Val Leu
          130         135         140
Arg Trp Gln Ile Glu Leu Thr Lys Ser Ala Gln Asn Thr Val Leu Arg
145          150         155         160
Trp Gln Ile Glu Leu Thr Lys Ser Val Thr Tyr Ile Arg Gln Gly Glu
          165         170         175
Ala Asp Val Val
          180
  
```

(2) INFORMATION FOR SEQ ID NO:3047:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 100 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...100

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3047:

```

Pro Leu Asp Ala Gly Gln Arg Phe Arg Tyr Gly Val Ser Ile Ile Pro
1          5          10          15
Asp Asp Tyr Asp Pro Ile Ala Tyr Val Val Ser Lys Ser Met Glu Pro
  
```


(2) INFORMATION FOR SEQ ID NO:3048:

(A) LENGTH: 251 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...251

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3048:

2058

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...282
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3050:

```

Met Ile Phe Ala Thr Ser Gln Val Asn Pro Leu Thr Asn Ser Ser Val
1      5      10      15
Arg Asn Leu Arg Pro Lys Gln Arg Arg Leu Phe Met Phe Trp Asn Leu
20      25      30
Val His Tyr Glu Phe Lys Asn Val Asn Lys Trp Tyr Leu Ala Leu Tyr
35      40      45
Ala Ala Val Leu Val Leu Ser Ala Leu Ile Gly Ile Gln Thr Gln Gly
50      55      60
Phe Lys Asn Leu Pro Tyr Gln Glu Ser Gln Ala Thr Met Leu Leu Phe
65      70      75      80
Leu Ala Thr Val Phe Gly Gly Leu Met Leu Thr Leu Ala Ile Ser Thr
85      90      95
Ile Phe Leu Ile Ile Lys Arg Phe Lys Gly Ser Val Tyr Asp Arg Gln
100     105     110
Gly Tyr Leu Thr Leu Thr Leu Pro Val Ser Glu His His Ile Ile Thr
115     120     125
Ala Lys Leu Ile Gly Ala Phe Ile Trp Ser Leu Ile Ser Thr Ala Val
130     135     140
Leu Ala Leu Ser Ala Val Ile Ile Leu Ala Leu Thr Ala Pro Glu Trp
145     150     155     160
Ile Pro Leu Ser Tyr Val Ile Thr Phe Val Glu Thr His Leu Pro Gln
165     170     175
Ile Phe Leu Thr Gly Ile Ser Phe Leu Leu Asn Thr Ile Ser Gly Ile
180     185     190
Leu Cys Ile Tyr Leu Ala Ile Ser Ile Gly Gln Leu Phe Asn Glu Tyr
195     200     205
Arg Thr Ala Leu Ala Val Ala Ala Tyr Ile Gly Ile Gln Ile Val Ile
210     215     220
Gly Phe Ile Glu Leu Phe Phe Asn Leu Ser Ser Asn Phe Tyr Val Asn
225     230     235     240
Ser Leu Val Gly Leu Asn Asp His Phe Tyr Met Gly Ala Gly Ile Ala
245     250     255
Ile Val Lys Glu Leu Ile Phe Ile Ala Ile Phe Tyr Leu Gly Thr Tyr
260     265     270
Tyr Ile Leu Arg Asn Lys Val Asn Leu Leu
275     280

```

(2) INFORMATION FOR SEQ ID NO:3051:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 90 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...90
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3051:

```

Asp Cys Leu Ala Thr Thr Leu Leu Asp Asn Leu Cys Tyr Phe Arg Ile
1          5          10          15
Asn Phe Leu Lys Val Ile Ala Asp Ile Leu Gln Gly Glu Asn Gln Leu
20          25          30
Leu Lys Gln Val Leu His Gly Lys Leu Met Ile Gly Ile Leu Lys Glu
35          40          45
Asn Ala Asn Leu Leu Asp Thr Cys Asp Asp Arg Lys Leu Thr Asp Leu
50          55          60
Ala Pro Ile Tyr Gln Asp Leu Thr Thr Ile Gly Lys Arg Thr Asp Leu
65          70          75          80
Gly Asn Asp Leu Lys Lys Ala Gly Phe Ser
85          90

```

(2) INFORMATION FOR SEQ ID NO:3052:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 125 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...125
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3052:

```

Lys Ser Ile Ala Leu Lys Lys Gln Leu Ala Asn His Ser Gly Lys Lys
1          5          10          15
Lys Phe His Ala Met Lys Ala Gln Ala Ile Val Thr Ser Gln Gly Arg
20          25          30
Ile Val Ser Leu Asp Ile Thr Val Asn Tyr Cys His Asp Met Lys Leu
35          40          45
Phe Lys Met Ser Cys Arg Asn Ile Gly Gln Ala Gly Lys Ile Leu Ala
50          55          60
Asp Ser Gly Tyr Gln Gly Leu Met Lys Ile Tyr Pro Gln Ala Gln Thr
65          70          75          80
Pro Arg Lys Ser Ser Lys Leu Lys Pro Leu Thr Ala Glu Asp Lys Ala

```

			85					90					95			
Tyr	Asn	His	Ala	Leu	Ser	Lys	Glu	Arg	Ser	Lys	Val	Glu	Asn	Ile	Phe	
			100					105					110			
Ala	Lys	Val	Lys	Thr	Phe	Lys	Met	Phe	Ser	Thr	Thr	Tyr				
			115				120					125				

(2) INFORMATION FOR SEQ ID NO:3053:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 149 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...149
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3053:

Lys	Ser	Ile	Ala	Leu	Lys	Lys	Gln	Leu	Ala	Asn	Asp	Phe	Gly	Lys	Lys
1				5					10					15	
Lys	Phe	His	Ala	Met	Lys	Ala	Gln	Ala	Ile	Val	Thr	Ser	Gln	Gly	Arg
			20				25						30		
Ile	Val	Ser	Leu	Asp	Ile	Ala	Val	Asn	Tyr	Cys	His	Asp	Met	Lys	Leu
			35				40					45			
Phe	Lys	Met	Ser	Arg	Arg	Asn	Ile	Gly	Gln	Ala	Gly	Lys	Ile	Leu	Ala
			50			55				60					
Asp	Ser	Gly	Tyr	Gln	Gly	Pro	Met	Lys	Ile	Tyr	Pro	Gln	Ala	Gln	Thr
65				70					75					80	
Pro	Arg	Lys	Ser	Ser	Lys	Leu	Lys	Pro	Leu	Thr	Val	Glu	Asp	Lys	Ala
			85				90						95		
Cys	Asn	His	Ala	Leu	Ser	Lys	Glu	Arg	Ser	Lys	Val	Glu	Asn	Ile	Phe
			100				105						110		
Ala	Lys	Val	Lys	Thr	Phe	Lys	Met	Phe	Ser	Thr	Thr	Tyr	Arg	Asn	His
			115				120					125			
Arg	Lys	Arg	Phe	Gly	Leu	Arg	Met	Asn	Leu	Ile	Ala	Gly	Ile	Ile	Asn
			130			135					140				
His	Glu	Leu	Gly	Phe											
145															

(2) INFORMATION FOR SEQ ID NO:3054:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 149 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...149

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3054:

```

Lys Ser Ile Ala Leu Lys Lys Glu Leu Ala Asn Tyr Ser Gly Lys Lys
1      5      10      15
Lys Cys Tyr Ala Met Lys Ala Gln Ala Ile Val Thr Ser Gln Gly Arg
20      25      30
Ile Val Ser Leu Asp Ile Thr Val Asn Tyr Cys His Asp Met Lys Leu
35      40      45
Phe Lys Met Ser Arg Arg Asn Ile Gly Gln Ala Gly Lys Ile Leu Ala
50      55      60
Asp Ser Gly Tyr Gln Gly Leu Met Lys Ile Tyr Pro Gln Ala Gln Thr
65      70      75      80
Pro Arg Lys Ser Ser Lys Phe Lys Pro Leu Thr Val Glu Asp Lys Thr
85      90      95
Tyr Asn His Ala Leu Ser Lys Glu Arg Ser Lys Val Glu Asn Ile Phe
100     105     110
Ala Lys Val Glu Thr Phe Lys Met Phe Ser Thr Thr Tyr Arg Asn His
115     120     125
Arg Lys Arg Phe Gly Leu Arg Met Asn Leu Ile Ala Gly Ile Ile Asn
130     135     140
His Glu Leu Gly Phe
145
  
```

(2) INFORMATION FOR SEQ ID NO:3055:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 322 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...322

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3055:

```

Ile Met Val Ala Lys Leu Thr Asp Val Ala Lys Leu Ala Gly Val Ser
1      5      10      15
Pro Thr Thr Val Ser Arg Val Ile Asn Lys Lys Gly Tyr Leu Ser Glu
20      25      30
Lys Thr Ile Gln Lys Val Asn Glu Ala Met Arg Glu Leu Gly Tyr Lys
35      40      45
  
```

Pro	Asn	Asn	Leu	Ala	Arg	Ser	Leu	Gln	Gly	Lys	Ser	Ala	Lys	Leu	Ile
50						55					60				
Gly	Leu	Ile	Phe	Pro	Asn	Ile	Ser	Asn	Val	Phe	Tyr	Ala	Glu	Leu	Ile
65					70					75					80
Asp	Lys	Leu	Glu	His	Gln	Leu	Phe	Lys	Asn	Gly	Tyr	Lys	Thr	Ile	Ile
				85					90					95	
Cys	Asn	Ser	Glu	His	Asp	Ser	Glu	Lys	Glu	Arg	Glu	Tyr	Ile	Glu	Met
			100					105					110		
Leu	Glu	Ala	Asn	Gln	Val	Asp	Gly	Ile	Ile	Ser	Gly	Ser	His	Asn	Leu
		115					120					125			
Gly	Ile	Glu	Asp	Tyr	Asn	Arg	Val	Thr	Ala	Pro	Ile	Ile	Ser	Phe	Asp
	130					135					140				
Arg	Asn	Leu	Ser	Pro	Asp	Ile	Pro	Val	Val	Ser	Ser	Asp	Asn	Tyr	Ala
145					150					155					160
Gly	Gly	Val	Leu	Ala	Ala	Gln	Thr	Leu	Val	Lys	Thr	Gly	Ala	Gln	Ser
				165					170					175	
Ile	Ile	Met	Ile	Thr	Gly	Asn	Asp	Asn	Ser	Asn	Ser	Pro	Thr	Gly	Leu
		180					185						190		
Arg	His	Ala	Gly	Phe	Ala	Ser	Val	Leu	Pro	Lys	Ala	Pro	Ile	Ile	Asn
	195					200						205			
Val	Ser	Ser	Asp	Phe	Ser	Pro	Val	Arg	Lys	Glu	Met	Glu	Ile	Lys	Asn
	210					215					220				
Ile	Leu	Thr	Arg	Glu	Lys	Pro	Asp	Ala	Ile	Phe	Ala	Ser	Asp	Asp	Leu
225					230					235					240
Thr	Ala	Ile	Leu	Val	Ile	Lys	Ile	Ala	Gln	Glu	Leu	Gly	Ile	Ser	Val
				245					250					255	
Pro	Lys	Glu	Leu	Lys	Val	Ile	Gly	Tyr	Asp	Gly	Thr	Tyr	Phe	Ile	Glu
			260					265					270		
Asn	Tyr	Tyr	Pro	Gln	Leu	Ala	Thr	Ile	Lys	Gln	Pro	Leu	Glu	Glu	Ile
	275						280					285			
Ala	Cys	Leu	Thr	Ile	Asp	Leu	Leu	Leu	Gln	Lys	Ile	Glu	Gly	Lys	Glu
	290					295					300				
Val	Ala	Thr	Thr	Gly	Tyr	Phe	Leu	Pro	Val	Thr	Leu	Leu	Pro	Gly	Lys
305					310					315					320
Ser	Ile														

(2) INFORMATION FOR SEQ ID NO:3056:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...330

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3056:

Val	Ala	Val	Ala	Ile	Pro	Leu	Glu	Leu	Leu	Val	Phe	Thr	Ile	Ser	Thr
1				5					10					15	
Gly	Val	Lys	Ser	Gln	Ile	His	Gln	Asp	Phe	His	Pro	Trp	Thr	Met	Lys
			20					25					30		
Tyr	Gln	Gly	Leu	Lys	Thr	Ser	Ile	Arg	Leu	Ser	Gln	Arg	Leu	Leu	Leu
		35					40					45			
Leu	Ala	Glu	Ile	Val	Ser	Ser	Val	Leu	Val	Pro	Ile	Pro	Met	Ser	Arg
	50					55					60				
Leu	Val	Pro	Ser	Asn	Gln	Leu	Leu	Lys	Arg	Val	Leu	Leu	Gln	Pro	Ser
65				70					75					80	
Val	Leu	Thr	Ile	Thr	Cys	Asn	Ser	Leu	Val	Lys	Leu	Lys	Ile	Val	Glu
			85						90				95		
Lys	Pro	Ile	Lys	Lys	Ser	Ala	Lys	Lys	Phe	Gln	Asn	Lys	Glu	Lys	Pro
			100					105					110		
Met	Ser	Gln	Tyr	Lys	Ile	Ala	Pro	Ser	Ile	Leu	Ala	Ala	Asp	Tyr	Ala
		115					120					125			
Asn	Phe	Glu	Arg	Glu	Ile	Lys	Arg	Leu	Glu	Ala	Thr	Gly	Ala	Glu	Tyr
	130					135					140				
Ala	His	Ile	Asp	Ile	Met	Asp	Ser	His	Phe	Val	Pro	Gln	Ile	Ser	Phe
145				150					155					160	
Gly	Ala	Gly	Val	Val	Glu	Ser	Leu	Arg	Pro	His	Ser	Lys	Met	Val	Phe
			165						170				175		
Asp	Cys	His	Leu	Met	Val	Ser	Asn	Pro	Glu	His	His	Leu	Glu	Asp	Phe
		180						185					190		
Ala	Arg	Ala	Gly	Ala	Asp	Ile	Ile	Ser	Ile	His	Val	Glu	Ala	Thr	Pro
		195					200					205			
His	Ile	His	Gly	Ala	Leu	Gln	Lys	Ile	Arg	Ser	Leu	Gly	Val	Lys	Pro
	210					215					220				
Ser	Val	Val	Ile	Asn	Pro	Gly	Thr	Pro	Val	Glu	Ala	Ile	Lys	His	Val
225				230						235				240	
Leu	His	Leu	Val	Asp	Gln	Val	Leu	Val	Met	Thr	Val	Asn	Pro	Gly	Phe
			245						250				255		
Gly	Gly	Gln	Ala	Phe	Leu	Pro	Glu	Thr	Met	Asp	Lys	Val	Arg	Glu	Leu
		260					265						270		
Val	Ala	Leu	Arg	Glu	Glu	Lys	Gly	Leu	Asn	Phe	Glu	Ile	Glu	Val	Asp
	275						280				285				
Gly	Gly	Ile	Asp	Asp	Gln	Thr	Ile	Ala	Gln	Ala	Lys	Glu	Ala	Gly	Ala
	290					295					300				
Thr	Val	Phe	Val	Ala	Gly	Ser	Tyr	Val	Phe	Lys	Gly	Glu	Val	Asn	Glu
305				310						315				320	
Arg	Val	Gln	Thr	Leu	Arg	Lys	Gln	Leu	Asp						
			325					330							

(2) INFORMATION FOR SEQ ID NO:3057:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3057:

Thr	Asn	Tyr	Phe	Gly	Arg	Lys	Lys	Met	Lys	Asn	Arg	Phe	Tyr	Tyr	Tyr
1				5					10					15	
Gln	Leu	Leu	Asp	Glu	Arg	Glu	Glu	Gln	Leu	Phe	Asn	Lys	Ala	Gly	Ser
			20					25					30		
Glu	Ser	Phe	Tyr	Ile	Cys	Ile	Ala	Leu	Ser	Leu	Leu	Ser	Tyr	Ile	Ile
		35					40					45			
Ser	Val	Leu	Ala	Pro	Ser	Leu	Phe	Asn	Ser	Asn	Met	Leu	Leu	Ile	Val
	50					55					60				
Ile	Ile	Ile	Gly	Thr	Phe	Tyr	Phe	Phe	Asn	Arg	Ala	Arg	Tyr	Leu	Gly
65					70				75					80	
Val	Thr	Tyr	Tyr	Ser	Arg	Phe	His	Phe	Thr	Ile	Leu	Gly	Cys	Phe	Phe
			85						90					95	
Leu	Thr	Leu	Ala	Ile	Thr	Ala	Leu	Leu	Met	Leu	Gln	Asn	Tyr	Gln	Phe
			100					105					110		
Asn	Ile	Glu	Ile	Tyr	Gln	His	Asn	Pro	Leu	Asn	Phe	Lys	Tyr	Leu	Ser
		115					120					125			
Ala	Trp	Val	Ile	Thr	Tyr	Val	Ile	Tyr	Leu	Pro	Trp	Val	Phe	Ile	Gly
	130					135					140				
Asn	Leu	Gly	Leu	Lys	Ser	Tyr	Gly	Glu	Trp	Ala	Gln	Lys	Lys	Phe	Glu
145					150					155					160
Gln	Asp	Met	Asp	Glu	Leu	Glu	Ser	Gly	Glu						
			165						170						

(2) INFORMATION FOR SEQ ID NO:3058:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3058:

Phe	Ile	Pro	Ala	Thr	Leu	Phe	His	Phe	Ile	Leu	Phe	Glu	Asn	Leu	Phe
1				5				10						15	
Lys	Pro	His	Gly	Gln	Leu	Leu	Ser	Ser	Thr	Pro	Thr	Ile	Val	Cys	Ala
			20					25					30		
Val	Glu	Thr	Thr	Cys	Gly	Ala	Arg	Leu	Pro	Leu	Cys	Leu	Thr	Leu	Val
		35				40					45				
Met	Phe	Leu	Leu	Thr	Ile	Ser	Asp	Cys	His	Cys	Lys				
	50					55					60				

(2) INFORMATION FOR SEQ ID NO:3059:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...65

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3059:

Gly	Gly	Thr	Ala	Leu	Pro	Thr	Pro	Ser	His	Gly	Ser	Ile	Phe	Cys	Val
1				5					10					15	
Trp	Ala	Phe	Phe	Tyr	Pro	Ser	Phe	Ala	Leu	Ser	Phe	Ile	Arg	Ala	Leu
			20					25					30		
Ser	Arg	Phe	Asp	Glu	Leu	Glu	Phe	Tyr	Leu	Gln	Leu	Leu	Pro	Pro	Thr
		35					40					45			
Lys	Ser	Lys	Gln	Lys	Gly	Trp	Thr	Asn	Thr	Lys	Lys	Ala	Ser	Asn	Thr
	50					55					60				
Gln															
65															

(2) INFORMATION FOR SEQ ID NO:3060:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...169

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3060:

Lys	Ser	Tyr	Ala	Lys	Ala	Gln	Leu	Asn	Glu	Lys	Ile	Phe	Leu	Leu	Gly
1				5					10					15	
Cys	Gln	Arg	Phe	Leu	Leu	Arg	Arg	Leu	Glu	Met	Leu	Arg	Asp	Leu	Gln
			20					25					30		
Glu	Thr	Asp	Val	Lys	Ala	Ile	Cys	Asp	Ile	Asn	Gln	Glu	Thr	Leu	Gly

(2) INFORMATION FOR SEQ ID NO:3062:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 110 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...110
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3062:

Met	Lys	Asn	Ala	Leu	Val	Phe	His	Gln	Asn	Thr	Phe	Pro	Leu	Phe	Leu
1				5					10					15	
Leu	Glu	Ile	Lys	Phe	Ile	Tyr	Val	Thr	Lys	Thr	Phe	Ile	Ile	Leu	Val
			20					25					30		
Tyr	Tyr	Leu	Leu	Ser	Ile	Glu	Lys	Ala	Val	Tyr	Leu	Asn	Tyr	Thr	Leu
		35					40					45			
Asn	Leu	Gln	Lys	Ser	Leu	Lys	Ile	Glu	Met	Arg	Phe	His	Thr	Leu	Phe
		50					55				60				
Tyr	Ile	Ile	Trp	Gly	Tyr	Asn	Asn	Thr	Tyr	His	Glu	Ile	Tyr	Thr	Val
65					70					75					80
Gly	Val	Thr	His	Ile	Thr	Asn	Arg	Ser	Lys	Asn	Gly	Leu	Arg	Gln	Leu
			85						90					95	
Arg	Arg	Ile	Pro	Ser	Ile	Gln	Leu	Pro	Cys	Ala	Asp	Glu	Arg		
			100					105					110		

(2) INFORMATION FOR SEQ ID NO:3063:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 334 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...334
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3063:

Ile	Pro	Cys	Ala	Thr	Val	Ser	Leu	Pro	Leu	Lys	Met	Ala	Val	Ser	Phe
1				5					10					15	

(2) INFORMATION FOR SEQ ID NO:3064:

(A) LENGTH: 122 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: YES

(A) ORGANISM: *Streptococcus pneumoniae*

2070

(A) NAME/KEY: misc_feature
(B) LOCATION 1...122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3064:

```
Ser Arg Cys Ala Ala Trp Arg Ser Val Cys Ser Cys Ala Ala Ala Arg
1          5          10          15
Thr Arg Ser Asn Trp Arg Pro Trp Ala Arg Ser Ala Arg Ser Arg Arg
          20          25          30
Arg Arg Arg Thr Arg Asn Ser Ser Ala Arg Leu Met Arg Arg Gly Ser
          35          40          45
Ala Thr Ala Arg Arg Pro Val Arg Asn Arg Trp Phe Arg Gly Tyr Pro
          50          55          60
Gly Ala Ala Thr Gly Gly Ser Pro Arg Ser Ser Arg Trp Pro Gly Arg
65          70          75          80
Leu Arg Cys Pro Gly Leu Ser Gly Ile Arg Arg Ser Ser Ala Ala Thr
          85          90          95
Arg Leu Pro Arg Thr Ser Pro Ala Ile Arg Ala Ser Val Arg Pro His
          100         105         110
Gly Ala Asp Arg Arg Arg Arg Ser Gly Ser
          115         120
```

(2) INFORMATION FOR SEQ ID NO:3065:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 158 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...158

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3065:

```
Ser Gly Leu Ala Lys Asn Pro Leu Leu Leu Gln Leu Ile Phe Ile Tyr
1          5          10          15
Tyr Val Leu Pro Ser Ile Gly Ile Arg Leu Asp Arg Leu Pro Ala Ala
          20          25          30
Ile Ile Ala Phe Val Leu Asn Tyr Ala Ala Tyr Phe Ala Glu Ile Phe
          35          40          45
Arg Gly Gly Ile Asp Thr Ile Pro Arg Gly Gln Tyr Glu Ala Ala Lys
          50          55          60
Val Leu Lys Phe Ser Pro Phe Asp Arg Val Arg Tyr Ile Ile Leu Pro
65          70          75          80
Gln Val Thr Lys Ile Val Leu Pro Ser Val Phe Asn Glu Val Met Ser
          85          90          95
Leu Val Lys Asp Thr Ser Leu Val Tyr Ala Leu Gly Ile Ser Asp Leu
          100         105         110
Ile Leu Ala Ser Arg Thr Ala Ala Asn Arg Asp Ala Ser Leu Val Pro
```

	115		120		125	
Met	Phe	Leu	Ala	Gly	Ala	Ile
	130		135		140	
Ile	Ile	Ser	Lys	Lys	Val	Glu
145			150		155	

(2) INFORMATION FOR SEQ ID NO:3066:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 522 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...522
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3066:

Val	Cys	Leu	Ala	Ile	Asp	Ile	Leu	Ser	Leu	Ile	Lys	Phe	Leu	Gly	Asp
1			5				10				15				
Phe	Val	Met	Asp	Tyr	Asn	Phe	Asn	Leu	Glu	His	Pro	Phe	Phe	Phe	Thr
			20				25				30				
Asn	Asn	Asp	Tyr	Ser	Thr	Asp	Thr	Ser	Ile	Lys	Tyr	Gln	Val	Ser	Leu
			35				40				45				
Pro	Phe	Asn	Trp	His	Glu	Val	Met	Asn	Asn	Asp	Glu	Trp	Val	Tyr	Gln
			50				55				60				
Tyr	Pro	Ile	Gly	Lys	Phe	Val	Glu	Arg	Gln	Gly	Trp	Lys	Ile	His	Ile
65							70				75				80
Ser	Ser	Glu	Tyr	Asn	Ser	Ser	His	Glu	Leu	Leu	Gln	Asp	Val	Ala	Lys
Ile	Cys	His	Glu	Met	Arg	Ile	Pro	Phe	Lys	His	Leu	Ser	Thr	Glu	Asp
			100				105				110				
Lys	Phe	Ile	Met	Arg	Asn	Gly	Lys	Leu	Val	Ser	Arg	Gly	Phe	Ser	Gly
			115				120				125				
Lys	Phe	Ile	Thr	Cys	Tyr	Pro	Asn	Gln	Asn	Glu	Leu	Glu	Ser	Val	Leu
			130				135				140				
Gln	Arg	Leu	Glu	Ser	Ala	Leu	Lys	Gln	Tyr	Asn	Gly	Pro	Tyr	Ile	Leu
145							150				155				160
Ser	Asp	Lys	Arg	Trp	Asp	Glu	Ala	Pro	Ile	Tyr	Leu	Arg	Tyr	Gly	Val
Phe	Arg	Pro	Ser	Arg	Asp	Asp	Glu	Lys	Lys	Val	Ala	Ile	Asp	Glu	Leu
Ile	Val	Gly	Asp	Glu	Val	Val	Lys	Asp	Glu	Arg	Leu	Pro	Val	Phe	Lys
Ile	Pro	Lys	Gly	Ile	Val	Pro	Pro	Asp	Phe	Leu	Asn	Lys	Trp	Leu	Asp
Lys	Lys	Asp	Lys	Lys	Gln	Gly	Asp	Phe	Pro	Phe	Ile	Ile	Asp	Asn	Ala
225							230				235				240
Ile	Arg	Phe	Ser	Asn	Ser	Gly	Gly	Ile	Tyr	Asn	Ala	Arg	Leu	Lys	Glu

(2) INFORMATION FOR SEO ID NO:3067:

(A) LENGTH: 309 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: YES

(A) ORGANISM: *Streptococcus pneumoniae*

(A) NAME/KEY: misc_feature
(B) LOCATION 1...309

Glu Arg Leu Ala Leu Ser Phe Gln Thr Lys Ser Lys Pro Phe Arg Leu

1				5					10					15	
Phe	Phe	Val	Ile	Leu	Glu	Lys	Tyr	Ile	Tyr	Arg	Ile	Phe	Ala	Leu	Phe
			20					25					30		
Leu	Gly	Lys	Ser	Asp	Val	Phe	Leu	Val	Ser	Thr	Val	Lys	Val	Leu	Lys
		35					40					45			
Lys	Lys	Gly	Thr	Ile	Met	Ser	Val	Leu	Glu	Ile	Lys	Asp	Leu	His	Val
	50					55					60				
Glu	Ile	Glu	Gly	Lys	Glu	Ile	Leu	Lys	Gly	Val	Asn	Leu	Thr	Leu	Lys
65					70					75					80
Thr	Gly	Glu	Ile	Ala	Ala	Ile	Met	Gly	Pro	Asn	Gly	Thr	Gly	Lys	Ser
				85					90					95	
Thr	Leu	Ser	Ala	Ala	Ile	Met	Gly	Asn	Pro	Asn	Tyr	Glu	Val	Thr	Lys
			100					105					110		
Gly	Glu	Val	Leu	Phe	Asp	Gly	Val	Asn	Ile	Leu	Glu	Leu	Glu	Val	Asp
		115					120					125			
Glu	Arg	Ala	Arg	Met	Gly	Leu	Phe	Leu	Ala	Met	Gln	Tyr	Pro	Ser	Glu
	130					135					140				
Ile	Pro	Gly	Ile	Thr	Asn	Ala	Glu	Phe	Leu	Arg	Ala	Ala	Met	Asn	Ala
145					150					155					160
Gly	Lys	Glu	Asp	Asp	Glu	Lys	Ile	Ser	Val	Arg	Glu	Phe	Ile	Thr	Lys
			165					170						175	
Leu	Asp	Glu	Lys	Met	Glu	Leu	Leu	Asn	Met	Lys	Glu	Glu	Met	Ala	Glu
		180						185					190		
Arg	Tyr	Leu	Asn	Glu	Gly	Phe	Ser	Gly	Gly	Glu	Lys	Lys	Arg	Asn	Glu
		195					200					205			
Ile	Leu	Gln	Leu	Leu	Met	Leu	Glu	Pro	Thr	Phe	Ala	Leu	Leu	Asp	Glu
	210					215					220				
Ile	Asp	Ser	Gly	Leu	Asp	Ile	Asp	Ala	Leu	Lys	Val	Val	Ser	Lys	Gly
225					230					235					240
Val	Asn	Ala	Met	Arg	Gly	Glu	Gly	Phe	Gly	Ala	Met	Ile	Ile	Thr	His
				245					250					255	
Tyr	Gln	Arg	Leu	Leu	Asn	Tyr	Ile	Thr	Pro	Asp	Val	Val	His	Val	Met
			260				265						270		
Met	Glu	Gly	Arg	Val	Val	Leu	Ser	Gly	Gly	Pro	Glu	Leu	Ala	Ala	Arg
		275					280					285			
Leu	Glu	Arg	Glu	Gly	Tyr	Ala	Lys	Leu	Ala	Glu	Glu	Leu	Gly	Tyr	Asp
	290					295					300				
Tyr	Lys	Glu	Glu	Leu											
305															

(2) INFORMATION FOR SEQ ID NO:3068:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3068:

```
His Phe Ile Ala Ile Ala Val Ile Asp Leu Leu Leu Phe Ala Phe Phe
1      5      10      15
Ile Ile Arg Leu Glu Thr Ser Phe Glu Trp Leu Leu Leu Ser Asp Leu
20      25      30
Ile Phe Phe Leu Thr Gln Gly Leu Leu Leu Phe Leu Leu Ile Val Arg
35      40      45
Leu Lys His Gln Phe Ala Glu Ile Tyr Pro Gln Ile Asn Lys Lys Ile
50      55      60
Arg Phe Tyr Tyr Leu Gly Val Leu Thr Ile Asp Phe Leu Phe Phe Val
65      70      75      80
Leu Leu Ala Phe Ile Ser Ser Gln Arg Phe Ser Ser Leu Met Pro Ile
85      90      95
Ile Thr Ala Cys His Ser Thr Phe Tyr Tyr Met Thr Ala Asp Tyr Leu
100     105     110
Arg Glu Asn Tyr Pro Asp Phe Tyr Asp Lys His Ile Ser Leu Trp Glu
115     120     125
Cys Leu
130
```

(2) INFORMATION FOR SEQ ID NO:3069:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3069:

```
Ala Arg Ser Ala Gly Met His Tyr Asp Ala Ser Tyr Ile Ser Phe Asp
1      5      10      15
Gly Ile Leu Arg Lys Glu Ile Leu Met Thr Leu Leu Asp Val Lys His
20      25      30
Val Gln Lys Ile Tyr Lys Thr Arg Phe Gln Gly Asn Gln Val Glu Ala
35      40      45
Leu Lys Asp Ile His Phe Thr Val Glu Lys Gly Asp Tyr Val Ala Ile
50      55      60
Met Gly Glu Ser Gly Ser Gly Lys Ser Thr Leu Leu Asn Ile Leu Ala
65      70      75      80
Met Leu Asp Lys Pro Ser Arg Gly Gln Val Tyr Leu Asn Gly Thr Asp
85      90      95
Thr Ala Thr Ile Lys Asn Ser Gln Ala Ser Ser Phe Arg Arg Glu Lys
100     105     110
```

Leu	Gly	Phe	Val	Phe	Gln	Asp	Phe	Asn	Leu	Leu	Asp	Thr	Leu	Ser	Val
		115					120					125			
Lys	Asp	Asn	Ile	Leu	Leu	Pro	Leu	Val	Leu	Ser	Arg	Arg	Pro	Ile	Thr
	130					135					140				
Glu	Met	Met	Lys	Lys	Leu	Val	Val	Thr	Ala	Glu	Asn	Leu	Gly	Ile	Asn
145					150					155					160
Gln	Leu	Gln	Glu	Lys	Tyr	Pro	Tyr	Glu	Ile	Ser	Gly	Gly	Gln	Lys	Gln
				165					170					175	
Arg	Val	Ala	Val	Ala	Arg	Ala	Ile	Ile	Thr	Glu	Pro	Glu	Ile	Leu	Leu
		180						185					190		
Ala	Asp	Glu	Pro	Thr	Gly	Ala	Leu	Asp	Ser	Lys	Ser	Ser	Ala	Ala	Leu
	195						200					205			
Leu	Asp	Val	Phe	Asp	Glu	Ile	Asn	Glu	Arg	Gly	Gln	Thr	Ile	Leu	Met
	210					215					220				
Val	Thr	His	Ser	Thr	Ala	Ala	Ala	Ser	Arg	Ala	Lys	Arg	Val	Leu	Phe
225					230					235					240
Ile	Lys	Asp	Gly	Ile	Leu	Tyr	Asn	Gln	Ile	Tyr	Arg	Gly	Glu	Lys	Thr
				245					250					255	
Glu	Arg	Gln	Met	Phe	Gln	Glu	Ile	Ser	Asp	Thr	Leu	Thr	Val	Met	Ala
			260					265					270		
Ser	Glu	Val	Asn												
			275												

(2) INFORMATION FOR SEQ ID NO:3070:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 345 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3070:

Met	Lys	Ser	Ala	Val	Tyr	Thr	Lys	Ala	Gly	Gln	Val	Gly	Leu	Ala	Ser
1				5					10					15	
Ile	Glu	Arg	Pro	Gln	Ile	Ile	Glu	Ala	Asp	Asp	Val	Ile	Ile	Arg	Val
			20					25					30		
Val	Arg	Ala	Cys	Val	Cys	Gly	Ser	Asp	Leu	Trp	Arg	Tyr	Arg	Asn	Pro
		35				40						45			
Glu	Thr	Lys	Ala	Gly	His	Lys	Asn	Ser	Gly	His	Glu	Ala	Ile	Gly	Ile
	50					55					60				
Val	Glu	Glu	Ala	Gly	Glu	Ala	Ile	Thr	Thr	Val	Lys	Pro	Gly	Asp	Phe
65					70					75					80
Val	Ile	Val	Pro	Phe	Thr	His	Gly	Cys	Gly	Glu	Cys	Asp	Ala	Cys	Leu
			85					90						95	
Ala	Gly	Phe	Asp	Gly	Ser	Cys	Asp	Asn	His	Ile	Gly	Asn	Asn	Leu	Gly
			100					105					110		

Gly	Asp	Phe	Gln	Ala	Glu	Tyr	Ile	Arg	Phe	His	Tyr	Ala	Asn	Trp	Ala	115	120	125
Leu	Val	Lys	Ile	Pro	Gly	Gln	Pro	Ser	Asp	Tyr	Thr	Glu	Gly	Met	Leu	130	135	140
Lys	Ser	Leu	Leu	Thr	Leu	Ala	Asp	Val	Met	Pro	Thr	Gly	Tyr	His	Ala	145	150	155
Ala	Arg	Val	Ala	Asn	Val	Gln	Lys	Gly	Asp	Lys	Val	Val	Val	Ile	Gly	165	170	175
Asp	Gly	Ala	Val	Gly	Gln	Cys	Ala	Val	Ile	Ala	Ala	Lys	Met	Arg	Gly	180	185	190
Ala	Ser	Gln	Ile	Ile	Leu	Met	Ser	Arg	His	Glu	Asp	Arg	Gln	Lys	Met	195	200	205
Ala	Met	Glu	Ser	Gly	Ala	Thr	Ala	Val	Val	Ala	Glu	Arg	Gly	Gln	Glu	210	215	220
Gly	Ile	Thr	Lys	Val	Arg	Glu	Ile	Leu	Gly	Gly	Gly	Ala	Asp	Ala	Ala	225	230	235
Leu	Glu	Cys	Val	Gly	Thr	Glu	Ala	Ala	Ile	Glu	Gln	Ala	Leu	Gly	Val	245	250	255
Leu	His	Asn	Gly	Gly	Arg	Met	Gly	Phe	Val	Gly	Val	Pro	His	Tyr	Asn	260	265	270
Asn	Arg	Ala	Leu	Gly	Ser	Thr	Phe	Met	Gln	Asn	Ile	Ser	Val	Ala	Gly	275	280	285
Gly	Ala	Ala	Ser	Ala	Thr	Thr	Tyr	Asp	Lys	Gln	Phe	Leu	Leu	Lys	Ala	290	295	300
Val	Leu	Asp	Gly	Asp	Ile	Asn	Pro	Gly	Arg	Val	Phe	Thr	Ser	Ser	Tyr	305	310	315
Lys	Leu	Glu	Asp	Ile	Asp	Gln	Ala	Tyr	Lys	Asp	Met	Asp	Glu	Arg	Lys	325	330	335
Thr	Ile	Lys	Ser	Met	Ile	Val	Ile	Glu								340	345	

(2) INFORMATION FOR SEQ ID NO:3071:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...147

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3071:

Ala	Ala	Thr	Ala	Arg	Pro	Arg	Leu	Pro	Gly	Glu	Asn	Arg	Ser	Arg	Gly	1	5	10	15
Arg	Val	His	Gly	Ala	Gly	Gln	Cys	Pro	Gly	Leu	Ala	Ala	Arg	Ala	Asp	20	25	30	
Ser	Gly	Arg	Arg	Arg	Pro	Arg	Arg	Gly	Ala	Ser	Ala	Thr	Arg	Arg	Asn	35	40	45	

Arg	Ser	Ile	Arg	Thr	Ala	Pro	Arg	Arg	Pro	Ser	Ala	Cys	Ala	Ile	Ala
50						55					60				
Cys	His	Ala	Asn	Pro	Arg	Arg	Pro	Pro	Ala	Gly	Thr	Pro	Ala	Gly	Ile
65				70						75					80
Glu	Arg	Glu	Pro	Ala	Thr	Ala	Ala	Gly	Arg	Ser	Arg	Ala	Pro	Ala	Arg
				85				90						95	
Cys	Arg	Ala	Gly	Ala	His	Pro	Gly	Arg	Gln	Arg	Ser	Arg	Lys	Pro	Cys
			100					105					110		
Gly	Ala	Pro	Ala	Gly	Ala	Thr	Ala	Pro	Ala	Arg	Arg	Arg	Gly	Gly	Ala
			115					120					125		
Gly	Pro	Ala	Trp	Pro	Trp	Pro	Val	Ala	Gly	Arg	Leu	His	His	Glu	Pro
			130				135				140				
Gly	Gly	Pro													
145															

(2) INFORMATION FOR SEQ ID NO:3072:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 86 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...86
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3072:

Arg	Ile	Thr	Ala	Ile	Leu	Lys	Arg	Ser	Gly	Leu	Ile	Ile	Asn	Lys	Lys
1				5					10					15	
Lys	Val	Gln	Arg	Leu	Val	Gln	Lys	Leu	Lys	Leu	Gln	Val	Lys	Ser	Tyr
			20					25					30		
Ser	Arg	Lys	Ser	Arg	Lys	Tyr	Ser	Ser	Tyr	Lys	Gly	Gln	Val	Gly	Lys
		35				40						45			
Ile	Ser	Asp	Asn	Lys	Ile	Lys	Arg	Asn	Ile	Tyr	Tyr	Arg	Lys	Lys	Gly
						55					60				
Glu	Ile	Glu	Ser	Ser	Thr	Asn	Arg	Leu	Ile	Tyr	Ser	Lys	Lys	Ile	Phe
65					70					75					80
Thr	Arg	Trp	Lys	Asn	Ser										
					85										

(2) INFORMATION FOR SEQ ID NO:3073:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 282 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...282

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3073:

Lys	Met	Thr	Ala	Gly	Gln	Thr	Lys	Leu	Ala	Thr	Met	Val	Asn	Pro	Glu
1				5					10					15	
Val	Met	Ala	Asp	Met	Val	Ala	Ala	Lys	Leu	Pro	Lys	Leu	Ile	Lys	Phe
			20					25					30		
Thr	Pro	Leu	Ala	Tyr	Val	Glu	Thr	Lys	Leu	Glu	Gly	Gln	Pro	Gly	Ser
			35					40				45			
Thr	Leu	Thr	Val	Pro	Ala	Trp	Glu	Tyr	Ala	Gly	Asp	Ala	Thr	Glu	Ile
			50			55					60				
Glu	Glu	Gly	Gln	Ala	Ile	Thr	Pro	Asp	Gln	Leu	Thr	Thr	Lys	Lys	Thr
65					70					75					80
Thr	Met	Thr	Ile	Lys	Lys	Ala	Gly	Lys	Gly	Tyr	Glu	Ile	Thr	Asp	Glu
				85					90					95	
Ser	Leu	Leu	Ser	Gly	Leu	Gly	Asp	Pro	Leu	Gly	Gln	Ala	Thr	Tyr	Gln
			100					105					110		
Leu	Gly	Leu	Ala	Ile	Ala	Asn	Lys	Ile	Asp	Asn	Asp	Leu	Val	Ala	Val
			115				120					125			
Ala	Lys	Thr	Ala	Thr	Gln	His	Ile	Thr	Glu	Thr	Pro	Thr	Thr	Leu	Glu
			130			135					140				
Ala	Ile	Asp	Lys	Ala	Leu	Asp	Ile	Phe	Glu	Asp	Glu	Glu	Asp	Ala	Gln
145					150					155					160
Tyr	Val	Ala	Ile	Ile	Asn	Pro	Lys	Asp	Ala	Thr	Lys	Leu	Lys	Thr	Ala
				165					170					175	
Val	Ala	Lys	Glu	Trp	Ile	Lys	Gly	Ser	Glu	Leu	Gly	Ala	Asn	Met	Val
			180					185					190		
Val	Ser	Gly	Thr	Phe	Gly	Glu	Val	Asp	Gly	Val	Gln	Ile	Val	Arg	Ser
			195				200					205			
Lys	Lys	Val	Asp	Glu	Gly	Lys	Gly	Phe	Leu	Val	Lys	Val	Ser	Pro	Ser
			210			215					220				
Gln	Thr	Gln	Thr	Asp	Asp	Ala	Asn	Lys	Tyr	Gly	Ala	Phe	Val	Ile	Leu
225					230					235					240
Leu	Lys	Arg	Asp	Val	Ala	Ile	Glu	Thr	Asp	Arg	Asp	Ile	Leu	Lys	Lys
				245					250					255	
Thr	Thr	Val	Ile	Thr	Gly	Asp	Glu	His	Tyr	Gly	Val	Tyr	Leu	Tyr	Asp
			260					265						270	
Pro	Thr	Arg	Val	Val	Lys	Phe	Gly	Gly	Ala						
			275				280								

(2) INFORMATION FOR SEQ ID NO:3074:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...154

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3074:

Lys	Trp	Thr	Ala	Val	Gln	Glu	Leu	Glu	Arg	Thr	Leu	Arg	Gly	Val	Glu
1				5					10					15	
Met	Ile	Thr	Ile	Lys	Lys	Gln	Glu	Ile	Val	Lys	Leu	Glu	Asp	Val	Leu
			20					25					30		
His	Leu	Tyr	Gln	Ala	Val	Gly	Trp	Thr	Asn	Tyr	Thr	His	Gln	Pro	Glu
		35					40					45			
Met	Leu	Glu	His	Ala	Leu	Ser	His	Ser	Leu	Val	Ile	Tyr	Leu	Ala	Leu
	50					55					60				
Asp	Gly	Asp	Ala	Val	Val	Gly	Leu	Ile	Arg	Leu	Val	Gly	Asp	Gly	Phe
65				70					75						80
Ser	Ser	Val	Phe	Val	Gln	Asp	Leu	Ile	Val	Leu	Pro	Ile	Tyr	Gln	Arg
			85					90						95	
Gln	Gly	Ile	Gly	Ser	Ala	Leu	Met	Lys	Glu	Ala	Leu	Lys	Asp	Tyr	Lys
		100						105					110		
Asp	Ala	Tyr	Gln	Val	Gln	Leu	Val	Thr	Glu	Glu	Thr	Glu	Lys	Asn	Val
		115					120					125			
Gly	Phe	Tyr	Arg	Ser	Met	Gly	Phe	Glu	Ile	Leu	Ser	Thr	Tyr	Asn	Cys
	130					135					140				
Ile	Gly	Met	Thr	Trp	Ala	Asn	Arg	Glu	Lys						
145						150									

(2) INFORMATION FOR SEQ ID NO:3075:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...71

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3075:

Arg	Tyr	Gln	Ala	Lys	Lys	Ser	Ile	Ala	Ala	Ile	Lys	Asn	Ser	Phe	Phe
1				5					10					15	
Pro	Arg	Leu	Glu	Gly	Ala	Ile	Leu	Leu	Ala	Ile	Asp	Tyr	Phe	Tyr	Thr
		20					25					30			
Leu	Arg	Lys	Ser	Leu	Gln	Thr	Thr	Ser	Ala	Leu	Pro	Cys	Arg	Ile	Tyr

	35		40		45
Val	Thr	Asp	Phe	Val	Met
				Ser	Tyr
				Leu	Gln
				Pro	Gln
				Asn	Ser
				Val	Leu
50				55	
				60	
Ser	Ser	Leu	Arg	Leu	Ala
				Ser	
65				70	

(2) INFORMATION FOR SEQ ID NO:3076:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...191

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3076:

Lys	Lys	Gln	Ala	Tyr	Asp	Glu	Lys	Asn	Lys	Lys	Val	Ile	Tyr	Leu	Leu
1				5				10						15	
Leu	Asp	Glu	Lys	Arg	Lys	Asn	Tyr	Val	Glu	Asp	Lys	Arg	Gln	Asn	Phe
			20					25					30		
Pro	Ser	Leu	Pro	Asn	Trp	Lys	Met	Asp	Leu	Phe	Ser	Glu	Glu	Glu	Lys
			35				40					45			
Arg	Asn	Tyr	Phe	Gln	Thr	Thr	Cys	Glu	Ile	Ser	Ser	Lys	Asp	Ser	Ala
			50			55					60				
Ile	Asn	Lys	Tyr	Lys	Met	Glu	Lys	Ile	Ile	Lys	Arg	Ser	Asn	Lys	Gly
65				70				75						80	
Asn	Val	Tyr	Arg	Ala	Ile	Arg	Lys	Ser	Asp	Gly	Gln	Lys	Val	Ile	Ile
			85					90						95	
Lys	Gln	Ser	Arg	Pro	Phe	Val	Asn	Tyr	Asp	Ala	Glu	Gly	Glu	Trp	Thr
			100					105					110		
Ala	Leu	Asp	Asp	Ile	Lys	Asn	Glu	Ala	His	Met	Leu	Lys	Lys	Leu	Ala
			115				120					125			
Asp	Lys	Ser	Tyr	Thr	Thr	Asn	Leu	Thr	Asp	Glu	Phe	Tyr	Ile	Val	Asp
			130			135					140				
Asp	Tyr	Phe	Leu	Val	Gln	Glu	Gln	Val	Asp	Gly	Leu	Asn	Phe	Glu	Glu
145				150						155				160	
Phe	Ile	Arg	Glu	Thr	Glu	His	Ser	Leu	Asn	Ile	Arg	Glu	Lys	Thr	Leu
			165					170						175	
Tyr	Asn	Ile	Val	Asn	Ile	Val	Ser	Asp	Ile	His	Lys	Leu	Gly	Ile	
			180					185					190		

(2) INFORMATION FOR SEQ ID NO:3077:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...66
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3077:

```

Lys Met Gln Ala Phe Tyr Ile Lys Lys Glu Lys Lys Leu Ser Asn Asp
1          5          10          15
Tyr His Glu Ile Asn Thr Gly Asn Gln Ser Asn Phe Tyr Glu Asn Val
          20          25          30
Lys Asp Asn Glu Ile Lys Tyr Phe Leu Thr Lys Val Ser Asn Leu Phe
          35          40          45
Phe Lys Glu Phe Leu Met Lys Gln Ser Lys Thr Ile Asn Leu Lys Leu
50          55          60
Ala His
65

```

(2) INFORMATION FOR SEQ ID NO:3078:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 476 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...476
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3078:

```

Gln Met Tyr Leu Gly Asp Leu Met Glu Lys Ala Glu Cys Gly Gln Phe
1          5          10          15
Ser Ile Leu Ser Phe Leu Leu Gln Glu Ser Gln Thr Thr Val Lys Ala
          20          25          30
Val Met Glu Glu Thr Gly Phe Ser Lys Ala Thr Leu Thr Lys Tyr Val
          35          40          45
Thr Leu Leu Asn Asp Lys Ala Leu Asp Ser Gly Leu Glu Leu Thr Ile
50          55          60
His Ser Glu Asp Glu Asn Leu Arg Leu Ser Ile Gly Ala Ala Thr Lys
65          70          75          80
Gly Arg Asp Ile Arg Ser Leu Phe Leu Asp Ser Ala Val Lys Tyr Gln
          85          90          95

```


- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...511
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3079:

```

Val Ala Lys Ala Arg Trp Asn Ser Ile Gln Met Ser Val Thr Phe Phe
1      5      10      15
Ile Gly Glu Gln Arg Leu Lys Thr Lys Ile Gly Leu Ala Ser Ile Cys
      20      25      30
Leu Leu Gly Leu Ala Thr Ser His Val Ala Ala Asn Glu Thr Glu Val
      35      40      45
Ala Lys Thr Ser Gln Asp Thr Thr Thr Ala Ser Ser Ser Ser Glu Gln
      50      55      60
Asn Gln Ser Ser Asn Lys Thr Gln Thr Ser Ala Glu Val Gln Thr Asn
      65      70      75      80
Ala Ala Ala His Trp Asp Gly Asp Tyr Tyr Val Lys Asp Asp Gly Ser
      85      90      95
Lys Ala Gln Ser Glu Trp Ile Phe Asp Asn Tyr Tyr Lys Ala Trp Phe
      100     105     110
Tyr Ile Asn Ser Asp Gly Arg Tyr Ser Gln Asn Glu Trp His Glu Asn
      115     120     125
Tyr Tyr Leu Lys Ser Gly Gly Tyr Met Ala Gln Asn Glu Trp Ile Tyr
      130     135     140
Asp Ser Asn Tyr Lys Ser Trp Phe Tyr Leu Lys Ser Asp Gly Ala Tyr
      145     150     155     160
Ala His Gln Glu Trp Gln Leu Ile Gly Asn Lys Trp Tyr Tyr Phe Lys
      165     170     175
Lys Trp Gly Tyr Met Ala Lys Ser Gln Trp Gln Gly Ser Tyr Phe Leu
      180     185     190
Asn Gly Gln Gly Ala Met Met Gln Asn Glu Trp Leu Tyr Asp Pro Ala
      195     200     205
Tyr Ser Ala Tyr Phe Tyr Leu Lys Ser Asp Gly Thr Tyr Ala Asn Gln
      210     215     220
Glu Trp Gln Lys Val Gly Gly Lys Trp Tyr Tyr Phe Lys Lys Trp Gly
      225     230     235     240
Tyr Met Ala Arg Asn Glu Trp Gln Gly Asn Tyr Tyr Leu Thr Gly Ser
      245     250     255
Gly Ala Met Ala Thr Asp Glu Val Ile Met Asp Gly Ala Arg Tyr Ile
      260     265     270
Phe Ala Ala Ser Gly Glu Leu Lys Glu Lys Lys Asp Leu Asn Val Gly
      275     280     285
Trp Val His Arg Asp Gly Lys Arg Tyr Phe Phe Asn Asn Arg Glu Glu
      290     295     300
Gln Val Gly Thr Glu His Ala Lys Lys Ile Ile Asp Ile Ser Glu His
      305     310     315     320
Asn Gly Arg Ile Asn Asp Trp Lys Lys Val Ile Asp Glu Asn Glu Val
      325     330     335
Asp Gly Val Ile Val Arg Leu Gly Tyr Ser Gly Lys Glu Asp Lys Glu

```

			340					345					350			
Leu	Ala	His	Asn	Ile	Lys	Glu	Leu	Asn	Arg	Leu	Gly	Ile	Pro	Tyr	Gly	
		355					360					365				
Val	Tyr	Leu	Tyr	Thr	Tyr	Ala	Glu	Asn	Glu	Thr	Asp	Ala	Glu	Asn	Asp	
	370					375					380					
Ala	Lys	Gln	Thr	Ile	Glu	Leu	Ile	Lys	Lys	Tyr	Asn	Met	Asn	Leu	Ser	
385					390					395					400	
Tyr	Pro	Ile	Tyr	Tyr	Asp	Val	Glu	Asn	Trp	Glu	Tyr	Val	Asn	Lys	Ser	
				405					410					415		
Lys	Arg	Ala	Pro	Ser	Asp	Thr	Asp	Thr	Trp	Val	Lys	Ile	Ile	Asn	Lys	
			420					425					430			
Tyr	Met	Asp	Thr	Met	Lys	Gln	Ala	Gly	Tyr	Gln	Asn	Val	Tyr	Val	Tyr	
		435					440					445				
Ser	Tyr	Arg	Ser	Leu	Leu	Gln	Thr	Arg	Leu	Lys	His	Pro	Asp	Ile	Leu	
	450					455					460					
Lys	His	Val	Asn	Trp	Val	Ala	Ala	Tyr	Thr	Asn	Ala	Leu	Glu	Trp	Glu	
465					470					475					480	
Asn	Pro	Tyr	Tyr	Ser	Gly	Glu	Lys	Gly	Trp	Gln	Tyr	Thr	Ser	Ser	Glu	
				485					490					495		
Tyr	Met	Lys	Gly	Ile	Gln	Gly	Arg	Val	Asp	Val	Ser	Val	Trp	Tyr		
			500					505					510			

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3080:

(2) INFORMATION FOR SEQ ID NO:3081:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...219

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3081:

Arg	Arg	Arg	Ala	Asn	Asp	Tyr	Lys	Lys	Ala	Asn	Ile	Thr	Ile	Glu	Glu
1				5					10					15	
Tyr	Ile	Glu	Met	Ser	Glu	Val	Asp	Phe	Asn	Glu	Ala	Val	Asn	Tyr	Glu
			20					25					30		
Phe	Thr	Ser	Asp	Thr	Cys	Gln	Leu	Ala	Asn	Ser	Ile	Tyr	Gln	Ser	Leu
			35				40					45			
Phe	Lys	Phe	Phe	Asp	Lys	Lys	Asn	Phe	Ser	Gly	Asp	Leu	Ile	Phe	Thr
	50				55					60					
Trp	Lys	Ser	Pro	Ser	Leu	Val	Lys	Glu	Gly	Asp	Tyr	Ile	Gly	Lys	Arg
65					70				75					80	
Asp	Ser	Gln	Val	Asp	Asn	Leu	Arg	Val	Ile	Gly	Asn	Ile	Phe	Pro	Asn
				85					90					95	
Tyr	Leu	Thr	Asn	Arg	Lys	Tyr	Ser	Leu	Asn	Met	Asn	Arg	Asn	Gly	Cys
			100					105					110		
Met	Gly	Asp	Phe	Pro	His	Asp	Phe	Phe	Asp	Ile	Tyr	Leu	Asp	His	Val
		115					120					125			
Ala	Lys	Tyr	Ala	Tyr	Glu	Gln	Lys	Val	Asn	Asn	Ile	Lys	Glu	Tyr	Tyr
	130					135					140				
Pro	Leu	Lys	Arg	Ala	Ile	Leu	His	Gln	Glu	Asn	Ala	Leu	Tyr	Phe	Arg
145					150					155				160	
Phe	Phe	Ser	Asn	Phe	Asp	Asp	Phe	Leu	Glu	Lys	Asn	Tyr	Leu	Lys	Thr
			165						170					175	
Ile	Trp	Gln	Val	Ser	Lys	Glu	Thr	Pro	Phe	Ser	Glu	Met	Asp	Phe	Asn
			180					185					190		
Met	Phe	Lys	Asn	Ile	Ser	Glu	Lys	Ile	Ile	Phe	Glu	Arg	Gly	Ser	Lys
		195					200					205			
Met	Leu	Asn	Asp	Leu	Lys	Ser	Asn	Tyr	Lys	Lys					
	210						215								

(2) INFORMATION FOR SEQ ID NO:3082:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3082:

Tyr	Asn	Arg	Ala	Met	Ser	Arg	Ile	Leu	Asp	Asn	Glu	Ile	Met	Gly	Asp
1				5					10					15	
Glu	Glu	Leu	Val	Glu	Arg	Thr	Leu	Arg	Pro	Gln	Tyr	Leu	Arg	Glu	Tyr
			20					25					30		
Ile	Gly	Gln	Asp	Lys	Val	Lys	Asp	Gln	Leu	Gln	Ile	Phe	Ile	Glu	Ala
			35				40						45		
Ala	Lys	Met	Arg	Asp	Glu	Ala	Leu	Asp	His	Val	Leu	Leu	Phe	Gly	Pro
	50					55					60				
Pro	Gly	Leu	Gly	Lys	Thr	Thr	Met	Ala	Phe	Val	Ile	Ala	Asn	Glu	Leu
65				70					75					80	
Gly	Val	Asn	Leu	Lys	Gln	Thr	Ser	Gly	Pro	Val	Ile	Glu	Lys	Ala	Gly
			85					90					95		
Asp	Leu	Val	Ala	Ile	Leu	Asn	Glu	Leu	Glu	Pro	Gly	Asp	Val	Leu	Phe
			100				105						110		
Ile	Asp	Glu	Ile	His	Arg	Leu	Pro	Met	Ser	Val	Glu	Glu	Val	Leu	Tyr
	115					120						125			
Ser	Ala	Met	Glu	Asp	Phe	Tyr	Ile	Asp	Ile	Met	Ile	Gly	Ala	Gly	Glu
	130				135						140				
Gly	Ser	Arg	Ser	Val	His	Leu	Glu	Leu	Pro	Pro	Phe	Thr	Leu	Ile	Gly
145				150					155					160	
Ala	Thr	Thr	Arg	Ala	Gly	Met	Leu	Ser	Asn	Pro	Leu	Arg	Ala	Arg	Phe
			165					170					175		
Gly	Ile	Thr	Gly	His	Met	Glu	Tyr	Tyr	Ala	His	Ala	Asp	Leu	Thr	Glu
			180				185					190			
Ile	Val	Glu	Arg	Thr	Ala	Asp	Ile	Phe	Glu	Met	Glu	Ile	Thr	His	Glu
	195				200							205			
Ala	Ala	Ser	Glu	Leu	Ala	Leu	Arg	Ser	Arg	Gly	Thr	Pro	Arg	Ile	Ala
	210				215					220					
Asn	Arg	Leu	Leu	Lys	Arg	Val	Arg	Asp	Phe	Ala	Gln	Ile	Met	Gly	Asn
225				230					235					240	
Gly	Val	Ile	Asp	Asp	Ile	Ile	Thr	Asp	Lys	Ala	Leu	Thr	Met	Leu	Asp
			245					250					255		
Val	Asp	His	Glu	Gly	Leu	Asp	Tyr	Val	Asp	Gln	Lys	Ile	Leu	Arg	Thr
		260				265						270			
Met	Ile	Glu	Met	Tyr	Ser	Gly	Gly	Pro	Val	Gly	Leu	Gly	Thr	Leu	Ser
	275					280					285				
Val	Asn	Ile	Ala	Glu	Glu	Arg	Glu	Thr	Val	Glu	Asp	Met	Tyr	Glu	Pro
	290				295					300					
Tyr	Leu	Ile	Gln	Lys	Gly	Phe	Ile	Met	Arg	Thr	Arg	Ser	Gly	Arg	Val
305				310					315					320	
Ala	Thr	Ala	Lys	Ala	Tyr	Glu	His	Leu	Gly	Tyr	Glu	Tyr	Ser	Glu	Lys
			325					330						335	

(2) INFORMATION FOR SEQ ID NO:3083:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 94 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...94

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3083:

```

Leu Asn Arg Ala Asn Arg Gly Glu Lys Ile Ser Gly Pro Pro Leu Leu
1      5      10      15
Asp Asp Asn Glu Thr Lys Ile Leu Pro Thr Ser Ser Ser Arg Phe
      20      25      30
Gly Tyr Ala Asn Pro Lys Asp His Gly Phe Ser Gln Glu Thr Leu Lys
      35      40      45
Ile Gln Val Glu Pro Ser Ile His Lys Ser Arg Arg Ile Glu Asn Thr
      50      55      60
Lys Arg Asn Val Phe Asn Ser Lys Leu Asn Lys Ile Leu Phe Ala Val
65      70      75      80
Ile Phe Leu Leu Ile Leu Leu Val Leu Ala Met Lys Leu Leu
      85      90

```

(2) INFORMATION FOR SEQ ID NO:3084:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 264 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...264

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3084:

```

Ser Met Arg Ala Pro Met Ser Pro Phe Lys Lys Met Gly Lys Pro Lys
1      5      10      15
Ser Arg Arg Ala Ile Ser Val Leu Glu His Val Cys Ile Ser Tyr Asp
      20      25      30
Gly Lys His Pro Ile Leu Asp Asp Ile Ser Phe Ser Val Asn Lys Gly
      35      40      45

```

Glu	Thr	Ile	Ala	Phe	Val	Gly	His	Thr	Gly	Ser	Gly	Lys	Ser	Ser	Ile
50						55					60				
Ile	Asn	Val	Leu	Met	Arg	Phe	Tyr	Glu	Phe	Gln	Ser	Gly	Arg	Val	Leu
65					70					75					80
Leu	Asp	Asp	Val	Asp	Ile	Arg	Asp	Phe	Ser	Gln	Glu	Glu	Leu	Arg	Lys
				85					90					95	
Asn	Ile	Gly	Leu	Val	Leu	Gln	Glu	Pro	Phe	Leu	Tyr	His	Gly	Thr	Ile
			100					105					110		
Lys	Ser	Asn	Ile	Ala	Met	Tyr	Gln	Glu	Ile	Ser	Asp	Glu	Gln	Val	Gln
		115					120					125			
Ala	Ala	Ala	Ala	Phe	Val	Asp	Ala	Asp	Ser	Phe	Ile	Gln	Glu	Leu	Pro
	130					135					140				
Gln	Gly	Tyr	Asp	Ser	Pro	Val	Ser	Glu	Arg	Gly	Ser	Ser	Phe	Ser	Thr
145					150					155					160
Gly	Gln	Arg	Gln	Leu	Phe	Ala	Phe	Ala	Arg	Thr	Val	Ala	Ser	Gln	Pro
				165					170					175	
Lys	Ile	Leu	Ile	Leu	Asp	Glu	Ala	Thr	Ala	Asn	Ile	Asp	Ser	Glu	Thr
			180					185					190		
Glu	Ser	Leu	Val	Gln	Ala	Ser	Leu	Ala	Lys	Met	Arg	Gln	Gly	Arg	Thr
	195						200					205			
Thr	Ile	Ala	Ile	Ala	His	Arg	Leu	Ser	Thr	Ile	Gln	Asp	Ala	Asn	Cys
	210					215					220				
Ile	Tyr	Val	Leu	Asp	Lys	Gly	Arg	Ile	Ile	Glu	Ser	Gly	Thr	His	Glu
225					230					235					240
Glu	Leu	Leu	Thr	Leu	Gly	Gly	Thr	Tyr	His	Lys	Met	Tyr	Ser	Leu	Gln
				245					250						255
Ala	Gly	Ala	Met	Ala	Tyr	Thr	Leu								
			260												

(2) INFORMATION FOR SEQ ID NO:3085:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...80

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3085:

Asn	Gln	Gly	Ala	Leu	Pro	Leu	Ile	His	Lys	Glu	Val	Phe	Met	Thr	His
1				5					10					15	
Tyr	Val	Ala	Asn	Pro	Glu	Val	Val	Ile	Leu	Glu	Gly	Gly	Ile	Met	Gly
		20						25					30		
Gln	Glu	Ala	Ile	Leu	Lys	Pro	Lys	Ile	Arg	Ala	Ala	Leu	Lys	Glu	Val
		35				40						45			
Leu	Val	Pro	Ser	Leu	Ala	Glu	Asn	Thr	Arg	Leu	Glu	Phe	Ala	His	His
	50					55					60				

Gln	Asn	Thr	Ala	Gly	Met	Leu	Gly	Ala	Tyr	Tyr	His	Phe	Lys	Ile	Lys
65					70				75						80

(2) INFORMATION FOR SEQ ID NO:3086:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 230 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...230

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3086:

Glu	Gly	Gly	Ala	Ser	Met	Lys	Lys	Ile	Tyr	Ser	Phe	Leu	Ala	Gly	Ile
1				5				10						15	
Ala	Ala	Ile	Ile	Leu	Val	Leu	Trp	Gly	Ile	Ala	Thr	His	Leu	Asp	Ser
			20					25					30		
Lys	Ile	Asn	Ser	Arg	Asp	Ser	Gln	Lys	Leu	Val	Ile	Tyr	Asn	Trp	Gly
		35					40					45			
Asp	Tyr	Ile	Asp	Pro	Glu	Leu	Leu	Thr	Gln	Phe	Thr	Glu	Glu	Thr	Gly
	50					55					60				
Ile	Gln	Val	Gln	Tyr	Glu	Thr	Phe	Asp	Ser	Asn	Glu	Ala	Met	Tyr	Thr
65					70					75					80
Lys	Ile	Lys	Gln	Gly	Gly	Thr	Thr	Tyr	Asp	Ile	Ala	Ile	Pro	Ser	Glu
			85					90						95	
Tyr	Met	Ile	Asn	Lys	Met	Lys	Asp	Glu	Asp	Leu	Leu	Val	Pro	Leu	Asp
			100					105					110		
Tyr	Ser	Lys	Ile	Glu	Gly	Ile	Glu	Asn	Ile	Gly	Pro	Glu	Phe	Leu	Asn
		115					120					125			
Gln	Ser	Phe	Asp	Pro	Gly	Asn	Lys	Phe	Ser	Ile	Pro	Tyr	Phe	Trp	Gly
	130					135					140				
Thr	Leu	Gly	Ile	Val	Tyr	Asn	Glu	Thr	Met	Val	Asp	Glu	Ala	Pro	Glu
145				150						155					160
His	Trp	Asp	Asp	Leu	Trp	Lys	Pro	Glu	Tyr	Lys	Asn	Ser	Ile	Met	Leu
			165					170						175	
Phe	Asp	Gly	Ala	Arg	Glu	Val	Leu	Gly	Leu	Gly	Leu	Asn	Ser	Leu	Gly
		180					185					190			
Tyr	Ser	Leu	Asn	Ser	Lys	Asp	Leu	Gln	Gln	Leu	Glu	Glu	Thr	Val	Asp
	195					200					205				
Lys	Leu	Tyr	Lys	Leu	Thr	Pro	Asn	Ile	Lys	Ala	Ile	Val	Ala	Asp	Glu
	210					215					220				
Met	Lys	Gly	Tyr	Met	Ile										
225					230										

(2) INFORMATION FOR SEQ ID NO:3087:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 73 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...73

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3087:

Val	Ala	Leu	Ala	Lys	Glu	Gln	Asp	Ile	Pro	Phe	Lys	Leu	Asp	Ile	Tyr
1				5					10					15	
Pro	Phe	Tyr	Gly	Ser	Asp	Ala	Ser	Ala	Ala	Met	Ser	Ala	Gly	Ala	Glu
			20					25					30		
Val	Lys	His	Ala	Leu	Leu	Gly	Ala	Gly	Ile	Glu	Ser	Ser	His	Ser	Tyr
		35					40					45			
Glu	Arg	Thr	His	Ile	Asp	Ser	Val	Val	Ala	Thr	Glu	Arg	Ile	Val	Asp
	50					55					60				
Ala	Tyr	Leu	Lys	Ser	Glu	Ala	Val	Ser							
65						70									

(2) INFORMATION FOR SEQ ID NO:3088:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 377 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3088:

Ile	Ser	Leu	Ala	Ser	Ser	Lys	Pro	Ser	Ser	Ile	Ser	Tyr	Phe	Ser	Val
1				5					10					15	
Ala	Phe	Asp	Ala	Leu	Cys	Ile	Ile	Asn	Arg	Ile	Gly	Glu	Val	Met	Ala
			20					25					30		
Asp	Asp	Lys	Leu	Arg	Ala	Thr	Pro	Ala	Ala	Arg	Lys	Leu	Ala	Asp	Asp
		35					40					45			
Leu	Gly	Ile	Asn	Leu	Tyr	Asp	Val	Ser	Gly	Ser	Gly	Ala	Asn	Gly	Arg
	50					55					60				

Val	His	Lys	Glu	Asp	Val	Glu	Thr	Tyr	Lys	Asp	Thr	Asn	Val	Val	Arg
65					70				75					80	
Ile	Ser	Pro	Leu	Ala	Lys	Arg	Ile	Ala	Leu	Glu	His	Asn	Ile	Ala	Trp
				85					90					95	
Gln	Glu	Ile	Gln	Gly	Thr	Gly	His	Arg	Gly	Lys	Ile	Met	Lys	Lys	Asp
			100					105					110		
Val	Leu	Ala	Leu	Leu	Pro	Glu	Asn	Ile	Glu	Asn	Asp	Ser	Ile	Lys	Ser
		115					120					125			
Pro	Ala	Gln	Ile	Glu	Lys	Val	Glu	Glu	Val	Pro	Asp	Asn	Val	Thr	Pro
	130					135					140				
Tyr	Gly	Glu	Ile	Glu	Arg	Ile	Pro	Met	Thr	Pro	Met	Arg	Lys	Val	Ile
145					150					155					160
Ala	Gln	Arg	Met	Val	Glu	Ser	Tyr	Leu	Thr	Ala	Pro	Thr	Phe	Thr	Leu
			165						170					175	
Asn	Tyr	Glu	Val	Asp	Met	Thr	Glu	Met	Leu	Ala	Leu	Arg	Lys	Arg	Val
			180					185					190		
Leu	Glu	Pro	Ile	Met	Glu	Ala	Thr	Gly	Lys	Lys	Thr	Thr	Val	Thr	Asp
		195					200					205			
Leu	Leu	Ser	Leu	Ala	Val	Val	Lys	Ser	Leu	Met	Lys	His	Pro	Tyr	Ile
	210					215					220				
Asn	Ala	Ser	Leu	Thr	Glu	Asp	Gly	Lys	Thr	Ile	Ile	Thr	His	Asn	Tyr
225					230					235					240
Val	Asn	Leu	Ala	Met	Ala	Val	Gly	Met	Asp	Asn	Gly	Leu	Met	Thr	Pro
			245						250					255	
Val	Val	Tyr	Asn	Ala	Glu	Lys	Met	Ser	Leu	Ser	Glu	Leu	Val	Val	Ala
			260					265						270	
Phe	Lys	Asp	Val	Ile	Gly	Arg	Thr	Leu	Asp	Gly	Lys	Leu	Ala	Pro	Ser
		275					280					285			
Glu	Leu	Gln	Asn	Ser	Thr	Phe	Thr	Ile	Ser	Asn	Leu	Gly	Met	Phe	Gly
	290					295					300				
Val	Gln	Ser	Phe	Gly	Pro	Ile	Ile	Asn	Gln	Pro	Asn	Ser	Ala	Ile	Leu
305					310					315					320
Gly	Val	Ser	Ser	Thr	Ile	Glu	Lys	Pro	Val	Val	Val	Asn	Gly	Glu	Ile
				325					330					335	
Val	Ile	Arg	Pro	Ile	Met	Ser	Leu	Gly	Leu	Thr	Ile	Asp	His	Arg	Val
			340					345					350		
Val	Asp	Gly	Met	Ala	Gly	Ala	Lys	Phe	Met	Lys	Asp	Leu	Lys	Glu	Leu
	355						360					365			
Ile	Glu	Thr	Pro	Ile	Ser	Met	Leu	Ile							
	370					375									

(2) INFORMATION FOR SEQ ID NO:3089:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 277 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...277

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3089:

Lys	Glu	Leu	Ala	Ile	Thr	Gly	Phe	Leu	Met	Asn	Lys	Met	Asn	Lys	Val	1	5	10	15
Met	Leu	Thr	Met	Phe	Gly	Leu	Val	Met	Leu	Pro	Leu	Leu	Phe	Ala	Cys	20	25	30	
Ser	Asn	Asn	Gln	Ser	Ala	Gly	Ile	Glu	Ala	Ile	Lys	Ser	Lys	Gly	Lys	35	40	45	
Leu	Val	Val	Ala	Leu	Asn	Pro	Asp	Phe	Ala	Pro	Phe	Glu	Tyr	Gln	Lys	50	55	60	
Val	Val	Asp	Gly	Lys	Asn	Gln	Ile	Val	Gly	Ser	Asp	Ile	Glu	Leu	Ala	65	70	75	80
Lys	Ala	Ile	Ala	Thr	Glu	Leu	Gly	Val	Glu	Leu	Glu	Leu	Ser	Pro	Met	85	90	95	
Ser	Phe	Asp	Asn	Val	Leu	Ala	Ser	Val	Gln	Ser	Gly	Lys	Ala	Asp	Leu	100	105	110	
Ala	Ile	Ser	Gly	Val	Ser	Lys	Thr	Asp	Glu	Arg	Ser	Lys	Val	Phe	Asp	115	120	125	
Phe	Ser	Thr	Pro	Tyr	Tyr	Thr	Ala	Lys	Asn	Lys	Leu	Ile	Val	Lys	Lys	130	135	140	
Ser	Asp	Leu	Ala	Thr	Tyr	Gln	Ser	Val	Asn	Asp	Leu	Ala	Gln	Lys	Lys	145	150	155	160
Val	Gly	Ala	Gln	Lys	Gly	Ser	Ile	Gln	Glu	Thr	Met	Ala	Lys	Asp	Leu	165	170	175	
Leu	Gln	Asn	Ser	Ser	Leu	Val	Ser	Leu	Pro	Lys	Asn	Gly	Asn	Leu	Ile	180	185	190	
Thr	Asp	Leu	Lys	Ser	Gly	Gln	Val	Asp	Ala	Val	Ile	Phe	Glu	Glu	Pro	195	200	205	
Val	Ala	Lys	Gly	Phe	Val	Glu	Asn	Asn	Pro	Asp	Leu	Ala	Ile	Ala	Asp	210	215	220	
Leu	Asn	Phe	Glu	Lys	Glu	Gln	Asp	Asp	Ser	Tyr	Ala	Val	Ala	Met	Lys	225	230	235	240
Lys	Asp	Ser	Lys	Glu	Leu	Lys	Glu	Ala	Val	Asp	Lys	Thr	Ile	Gln	Lys	245	250	255	
Leu	Lys	Glu	Ser	Gly	Glu	Leu	Asp	Lys	Leu	Ile	Glu	Asp	Ala	Phe	Lys	260	265	270	
Ala	Ser	Ile	Glu	Lys												275			

(2) INFORMATION FOR SEQ ID NO:3090:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 93 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...93

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3090:

Thr	Trp	Leu	Ala	Gly	Leu	Ser	Pro	Thr	Lys	Ile	Thr	Thr	Lys	Pro	Gly
1				5					10					15	
Thr	Arg	Pro	Val	Ser	Ser	Phe	Asn	Phe	Ala	Val	Phe	Ser	Ala	Asn	Cys
			20					25					30		
Pro	Cys	Asn	Leu	Ala	Ala	Lys	Ala	Phe	Pro	Ser	Ile	Ile	Cys	Val	Ile
		35					40					45			
Ser	Leu	Leu	Phe	Ser	Phe	Lys	Tyr	Leu	Pro	Leu	Tyr	Gln	Lys	Leu	Gln
	50					55				60					
Val	Pro	Ser	Asn	Thr	Ser	Phe	Leu	Gly	Tyr	Pro	Ile	Val	Ser	Asn	Tyr
65					70				75						80
Lys	Lys	Lys	Leu	Trp	Leu	Asn	Phe	Ser	Leu	Ile	Leu	Ser			
				85					90						

(2) INFORMATION FOR SEQ ID NO:3091:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 94 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...94

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3091:

Pro	Arg	Leu	Ala	Ile	Pro	Thr	Arg	Phe	Leu	Ser	Ser	Val	Pro	Lys	Ser
1				5					10					15	
Lys	Gly	Ile	Gln	Ala	Ser	Met	Ser	Arg	Lys	Gly	Asn	Ser	Gln	Asp	Asn
			20					25					30		
Gly	Met	Met	Glu	Ser	Phe	Phe	Gly	Ile	Leu	Lys	Ser	Glu	Met	Phe	Tyr
		35					40					45			
Gly	Tyr	Glu	Lys	Thr	Phe	Lys	Ser	Leu	Asn	Gln	Leu	Glu	Gln	Ala	Ile
	50					55				60					
Val	Asp	Tyr	Ile	Asp	Tyr	Tyr	Asn	Asn	Lys	Arg	Ile	Lys	Val	Lys	Leu
65					70				75						80
Lys	Gly	Leu	Ser	Leu	Val	Gln	Tyr	Arg	Thr	Lys	Ser	Phe	Gly		
				85					90						

(2) INFORMATION FOR SEQ ID NO:3092:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 438 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...438
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3092:

```

Glu Ile Met Ala Leu Pro Thr Ile Ala Ile Val Gly Arg Pro Asn Val
1      5      10      15
Gly Lys Ser Thr Leu Phe Asn Arg Ile Ala Gly Glu Arg Ile Ser Ile
      20      25      30
Val Glu Asp Val Glu Gly Val Thr Arg Asp Arg Ile Tyr Ala Thr Gly
      35      40      45
Glu Trp Leu Asn Arg Ser Phe Ser Met Ile Asp Thr Gly Gly Ile Asp
50      55      60
Asp Val Asp Ala Pro Phe Met Glu Gln Ile Lys His Gln Ala Glu Ile
65      70      75      80
Ala Met Glu Glu Ala Asp Val Ile Val Phe Val Val Ser Gly Lys Glu
      85      90      95
Gly Ile Thr Asp Ala Asp Glu Tyr Val Ala Arg Lys Leu Tyr Lys Thr
      100     105     110
His Lys Pro Val Ile Leu Ala Val Asn Lys Val Asp Asn Pro Glu Met
      115     120     125
Arg Asn Asp Ile Tyr Asp Phe Tyr Ala Leu Gly Leu Gly Glu Pro Leu
      130     135     140
Pro Ile Ser Ser Val His Gly Ile Gly Thr Gly Asp Val Leu Asp Ala
145      150     155     160
Ile Val Glu Asn Leu Pro Asn Glu Tyr Glu Glu Glu Asn Pro Asp Val
      165     170     175
Ile Lys Phe Ser Leu Ile Gly Arg Pro Asn Val Gly Lys Ser Ser Leu
      180     185     190
Ile Asn Ala Ile Leu Gly Glu Asp Arg Val Ile Ala Ser Pro Val Ala
      195     200     205
Gly Thr Thr Arg Asp Ala Ile Asp Thr His Phe Thr Asp Thr Asp Gly
210      215     220
Gln Glu Phe Thr Met Ile Asp Thr Ala Gly Met Arg Lys Ser Gly Lys
225      230     235     240
Val Tyr Glu Asn Thr Glu Lys Tyr Ser Val Met Arg Ala Met Arg Ala
      245     250     255
Ile Asp Arg Ser Asp Val Val Leu Met Val Ile Asn Ala Glu Glu Gly
      260     265     270
Ile Arg Glu Tyr Asp Lys Arg Ile Ala Gly Phe Ala His Glu Ala Gly
      275     280     285
Lys Gly Met Ile Ile Val Val Asn Lys Trp Asp Thr Leu Glu Lys Asp
290      295     300
Asn His Thr Met Lys Asn Trp Glu Glu Asp Ile Arg Glu Gln Phe Gln
305      310     315     320
Tyr Leu Pro Tyr Ala Pro Ile Ile Phe Val Ser Ala Leu Thr Lys Gln
      325     330     335

```

Arg	Leu	His	Lys	Leu	Pro	Gly	Met	Ile	Lys	Gln	Ile	Ser	Glu	Ser	Gln
			340					345					350		
Asn	Thr	Arg	Ile	Pro	Ser	Ala	Val	Leu	Asn	Asp	Val	Ile	Met	Asp	Ala
		355					360					365			
Ile	Ala	Ile	Asn	Pro	Thr	Pro	Thr	Asp	Lys	Gly	Lys	Arg	Leu	Lys	Ile
	370					375					380				
Phe	Tyr	Ala	Thr	Gln	Val	Ala	Thr	Lys	Pro	Pro	Thr	Phe	Val	Ile	Phe
385					390					395					400
Val	Asn	Glu	Glu	Glu	Leu	Met	His	Phe	Ser	Tyr	Leu	Arg	Phe	Leu	Glu
			405					410						415	
Asn	Gln	Ile	Arg	Lys	Ala	Phe	Val	Phe	Glu	Gly	Thr	Pro	Ile	His	Leu
		420					425						430		
Ile	Ala	Arg	Lys	Arg	Lys										
		435													

(2) INFORMATION FOR SEQ ID NO:3093:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 96 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...96
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3093:

Gln	Ser	Met	Ala	Arg	Lys	Glu	Thr	Met	Ala	Glu	Arg	Lys	Tyr	Cys	Lys
1			5					10					15		
Met	Lys	Lys	Asp	Ile	His	Pro	Glu	Tyr	Arg	Pro	Val	Val	Phe	Met	Asp
		20					25					30			
Thr	Thr	Thr	Gly	Tyr	Gln	Phe	Leu	Ser	Gly	Ser	Thr	Lys	Arg	Ser	Asn
		35				40					45				
Glu	Thr	Val	Glu	Phe	Glu	Gly	Glu	Thr	Tyr	Pro	Leu	Ile	Arg	Val	Glu
	50				55				60						
Ile	Ser	Ser	Asp	Ser	His	Pro	Phe	Tyr	Thr	Gly	Arg	Gln	Lys	Phe	Thr
65				70				75						80	
Gln	Ala	Asp	Gly	Arg	Val	Asp	Arg	Phe	Asn	Lys	Lys	Tyr	Gly	Leu	Lys
			85				90							95	

(2) INFORMATION FOR SEQ ID NO:3094:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 273 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3094:

Glu	Ser	Met	Ala	Lys	Glu	Arg	Val	Asp	Val	Leu	Ala	Tyr	Lys	Gln	Gly
1				5					10					15	
Leu	Phe	Glu	Thr	Arg	Glu	Gln	Ala	Lys	Arg	Gly	Val	Met	Ala	Gly	Leu
			20					25					30		
Val	Val	Ala	Val	Leu	Asn	Gly	Glu	Arg	Phe	Asp	Lys	Pro	Gly	Glu	Lys
		35				40					45				
Ile	Pro	Asp	Asp	Thr	Glu	Leu	Lys	Leu	Lys	Gly	Glu	Lys	Leu	Lys	Tyr
50					55					60					
Val	Ser	Arg	Gly	Gly	Leu	Lys	Leu	Glu	Lys	Ala	Leu	Gln	Val	Phe	Asp
65				70					75					80	
Leu	Ser	Val	Asp	Gly	Ala	Thr	Thr	Ile	Asp	Ile	Gly	Ala	Ser	Thr	Gly
			85					90						95	
Gly	Phe	Thr	Asp	Val	Met	Leu	Gln	Asn	Ser	Ala	Lys	Leu	Val	Phe	Ala
		100						105					110		
Val	Asp	Val	Gly	Thr	Asn	Gln	Leu	Ala	Trp	Lys	Leu	Arg	Gln	Asp	Pro
	115					120						125			
Arg	Val	Val	Ser	Met	Glu	Gln	Phe	Asn	Phe	Arg	Tyr	Ala	Glu	Lys	Thr
	130					135					140				
Asp	Phe	Glu	Gln	Glu	Pro	Ser	Phe	Ala	Ser	Ile	Asp	Val	Ser	Phe	Ile
145				150					155					160	
Ser	Leu	Ser	Leu	Ile	Leu	Pro	Ala	Leu	His	Arg	Val	Leu	Ala	Asp	Gln
			165					170					175		
Gly	Gln	Val	Val	Ala	Leu	Val	Lys	Pro	Gln	Phe	Glu	Ala	Gly	Arg	Glu
		180					185					190			
Gln	Ile	Gly	Lys	Asn	Gly	Ile	Ile	Arg	Asp	Ala	Lys	Val	His	Gln	Asn
	195					200					205				
Val	Leu	Glu	Ser	Val	Thr	Ala	Met	Ala	Val	Glu	Val	Gly	Phe	Ser	Val
	210				215					220					
Leu	Gly	Leu	Asp	Phe	Ser	Pro	Ile	Gln	Gly	Gly	His	Gly	Asn	Ile	Glu
225			230						235					240	
Phe	Leu	Ala	Tyr	Leu	Lys	Lys	Glu	Lys	Ser	Ala	Ser	Asn	Gln	Ile	Leu
		245					250							255	
Ala	Glu	Ile	Lys	Glu	Ala	Val	Glu	Arg	Ala	His	Ser	Gln	Phe	Lys	Asn
		260					265					270			
Glu															

(2) INFORMATION FOR SEQ ID NO:3095:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 162 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3095:

```
Lys Lys Met Ala Ser Leu Tyr Glu Leu Thr Gly Gln Phe Leu Thr Ile
 1          5          10          15
Tyr Gln Leu Asp Ile Asp Asp Glu Thr Lys Ala Asp Thr Leu Glu Ala
 20          25          30
Ile Asp Trp Gln Glu Gln Phe Glu Gln Lys Ala Glu Gly Tyr Ala His
 35          40          45
Val Ile Lys Asn Leu Glu Ala Asp Val Ala Met Tyr Lys Ala Glu Glu
 50          55          60
Glu Ser Phe Lys Ala Lys Lys Gln Val Ala Gln Lys Lys Leu Asp Tyr
 65          70          75          80
Val Lys Asp Asn Ile Met Ala Ala Met Asn Val Thr Gly Gln Thr Glu
 85          90          95
Val Lys Ser Gly Ala Leu Ile Ile Lys Ile Ala Lys Asn Pro Glu Ser
 100         105         110
Val Lys Val Asn Glu Asp Asp Leu Pro Lys Lys Tyr Phe Thr Lys Lys
 115         120         125
Val Thr Leu Ala Pro Asp Lys Lys Thr Leu Lys Glu Leu Leu Lys Ser
 130         135         140
Gly Lys Lys Val Lys Gly Ala Glu Leu Val Arg Thr Glu Lys Leu Val
145         150         155         160
Ile Lys
```

(2) INFORMATION FOR SEQ ID NO:3096:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 166 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...166

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3096:

```
Met Lys Thr Ala Phe Ile Ile Ile Asp Val Gln Asn Val Leu Val Glu
 1          5          10          15
```

Thr	Gly	Phe	Gln	Thr	Lys	Ser	Leu	Leu	Glu	Lys	Ile	Ser	Tyr	Leu	Gln
			20					25					30		
Asn	Gln	Ala	Arg	Ser	Lys	Asn	Ile	Glu	Ile	Ile	Tyr	Val	Gln	His	Ile
		35					40					45			
Glu	Asn	Ser	Glu	Ala	Gln	Thr	Ser	Glu	Asp	Trp	Gln	Leu	Ser	Ala	Leu
	50					55					60				
Leu	Asn	Arg	Lys	Pro	Ala	Glu	Lys	Val	Phe	Gln	Lys	Lys	Tyr	Asn	Ser
65					70					75					80
Ile	Phe	Lys	Glu	Thr	Gly	Leu	Lys	Glu	Tyr	Leu	Asp	Lys	Gln	Gly	Ile
				85					90					95	
Glu	Lys	Leu	Val	Leu	Cys	Gly	Met	Gln	Thr	Glu	Tyr	Cys	Val	Asp	Thr
			100					105					110		
Ser	Val	Lys	Val	Ala	Phe	Glu	Tyr	Gly	Tyr	Gln	Leu	Ile	Val	Pro	Glu
		115					120					125			
Gly	Ala	Val	Thr	Thr	Phe	Asp	Gly	Asp	Asp	Ile	Pro	Ala	Glu	Thr	Ile
	130					135					140				
Asn	Glu	Phe	Tyr	Glu	Asp	Ile	Trp	Glu	Glu	Arg	Phe	Ala	Asp	Val	Leu
145					150					155					160
Asp	Tyr	Lys	His	Ile	Phe										
				165											

(2) INFORMATION FOR SEQ ID NO:3097:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 84 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...84

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3097:

Gln	Pro	Ala	Ala	Ser	Phe	Leu	Val	Cys	Thr	Leu	Ile	Phe	Ile	Glu	Tyr
1				5					10					15	
Tyr	Leu	Ile	Ser	Ser	Pro	Phe	Glu	Arg	Ala	Trp	Phe	Asp	Ile	Cys	Phe
			20					25				30			
Asp	Gln	Pro	Ala	Ser	Pro	Ser	Leu	His	Lys	His	His	Arg	Arg	Leu	Pro
		35					40					45			
Ser	His	Pro	Val	Leu	Glu	Ser	Ser	Ile	Phe	Gln	Tyr	His	Phe	Leu	Leu
	50					55					60				
His	Pro	Lys	Gln	Ile	Asn	Arg	Leu	Leu	Gly	Gly	Lys	Tyr	Lys	Val	Arg
65					70					75					80
Trp	Leu	Arg	Ser												

(2) INFORMATION FOR SEQ ID NO:3098:

(i) SEQUENCE CHARACTERISTICS:

```
(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
      (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:
      (A) NAME/KEY: misc_feature
      (B) LOCATION 1...615
```

Ser 1	Thr	Ala	Ala	Tyr 5	Ser	Lys	Tyr	Thr	Thr 10	Trp	Ala	Leu	Ala	Val 15	Ala
Asn	Cys	Ala	Lys 20	Tyr	Asn	Ile	Arg	Arg 25	Ser	Lys	Met	Lys	Thr 30	Val	Gln
Phe	Phe	Trp 35	His	Tyr	Phe	Lys	Val 40	Tyr	Lys	Phe	Ser	Phe 45	Val	Val	Val
Ile	Leu 50	Met	Ile	Val	Leu	Ala 55	Thr	Phe	Ala	Gln	Ala 60	Leu	Phe	Pro	Val
Phe 65	Ser	Gly	Gln	Ala 70	Val	Thr	Gln	Leu	Ala 75	Asn	Leu	Val	Gln	Ala 80	Tyr
Gln	Asn	Gly	Asn 85	Pro	Glu	Leu	Val 90	Trp	Gln	Ser	Leu	Ser	Gly 95	Ile	Met
Val	Asn	Leu 100	Gly	Leu	Leu	Val	Leu 105	Val	Leu	Phe	Ile	Ser	Ser 110	Val	Ile
Tyr	Met	Cys 115	Leu	Met	Thr	Arg	Val 120	Ile	Ala	Glu	Ser	Thr 125	Asn	Glu	Met
Arg	Lys 130	Gly	Leu	Phe	Gly	Lys 135	Leu	Ala	Gln	Leu	Thr 140	Val	Ser	Phe	Phe
Asp 145	Arg	Arg	Gln	Asp 150	Gly	Asp	Ile	Leu	Ser	His 155	Phe	Thr	Ser	Asp	Leu 160
Asp	Asn	Ile	Leu 165	Gln	Ala	Phe	Asn 170	Glu	Ser	Leu	Ile	Gln	Val	Met	Ser
Asn	Ile	Val 180	Leu	Tyr	Ile	Gly	Leu 185	Ile	Leu	Val	Met	Phe	Ser 190	Arg	Asn
Val	Thr	Leu 195	Ala	Leu	Ile	Thr	Ile 200	Ala	Ser	Thr	Pro	Leu	Ala 205	Phe	Leu
Met	Leu 210	Ile	Phe	Ile	Val	Lys 215	Met	Ala	Arg	Lys	Tyr 220	Thr	Asn	Leu	Gln
Gln 225	Lys	Glu	Val	Gly	Lys 230	Leu	Asn	Ala	Tyr	Met	Asp 235	Glu	Ser	Ile	Ser
Gly	Gln	Lys	Ala 245	Val	Ile	Val	Gln 250	Gly	Ile	Gln	Glu	Asp	Met	Met	Ala
Gly	Phe	Leu 260	Glu	Gln	Asn	Glu	Arg 265	Val	Arg	Lys	Ala	Thr	Phe 270	Lys	Gly
Arg	Met	Phe 275	Ser	Gly	Ile	Leu	Phe 280	Pro	Val	Met	Asn	Gly	Met	Ser	Leu
Ile	Asn 290	Thr	Ala	Ile	Val	Ile 295	Phe	Ala	Gly	Ser	Ala 300	Val	Leu	Leu	Asn
Asp 305	Lys	Ser	Ile	Glu	Thr 310	Ser	Thr	Ala	Leu	Gly 315	Leu	Ile	Val	Met	Phe 320

Ala	Gln	Phe	Ser	Gln	Gln	Tyr	Tyr	Gln	Pro	Ile	Ile	Gln	Val	Ala	Ala	325	330	335
Ser	Trp	Gly	Ser	Leu	Gln	Leu	Ala	Phe	Thr	Gly	Ala	Glu	Arg	Ile	Gln	340	345	350
Glu	Met	Phe	Asp	Ala	Glu	Glu	Glu	Ile	Arg	Pro	Glu	Lys	Ala	Pro	Thr	355	360	365
Phe	Thr	Lys	Leu	Gln	Glu	Ser	Val	Glu	Ile	Ser	His	Ile	Asp	Phe	Ser	370	375	380
Tyr	Leu	Pro	Asp	Lys	Pro	Ile	Leu	Lys	Asp	Val	Ser	Ile	Ser	Ala	Pro	385	390	395
Lys	Gly	Gln	Met	Thr	Ala	Val	Val	Gly	Pro	Thr	Gly	Ser	Gly	Lys	Thr	405	410	415
Thr	Ile	Met	Asn	Leu	Ile	Asn	Arg	Phe	Tyr	Asp	Val	Asp	Ala	Gly	Gly	420	425	430
Ile	Tyr	Phe	Asp	Gly	Lys	Asp	Ile	Arg	Gly	Tyr	Asp	Leu	Asp	Ser	Leu	435	440	445
Arg	Ser	Lys	Val	Gly	Ile	Val	Leu	Gln	Asp	Ser	Val	Leu	Phe	Ser	Gly	450	455	460
Thr	Ile	Arg	Asp	Asn	Ile	Arg	Phe	Gly	Val	Pro	Asp	Ala	Ser	Gln	Glu	465	470	475
Met	Val	Glu	Val	Ala	Ala	Lys	Ala	Thr	His	Ile	His	Asp	Tyr	Ile	Glu	485	490	495
Ser	Leu	Pro	Asp	Lys	Tyr	Asp	Thr	Leu	Ile	Asp	Asp	Asp	Gln	Ser	Ile	500	505	510
Phe	Ser	Ala	Gly	Gln	Lys	Gln	Leu	Ile	Ser	Ile	Ala	Arg	Thr	Leu	Met	515	520	525
Thr	Asp	Pro	Glu	Val	Leu	Ile	Leu	Asp	Glu	Ala	Thr	Ser	Asn	Val	Asp	530	535	540
Thr	Val	Thr	Glu	Ser	Lys	Ile	Gln	His	Ala	Met	Glu	Val	Val	Val	Ala	545	550	555
Gly	Arg	Thr	Ser	Phe	Val	Ile	Ala	His	Arg	Leu	Lys	Thr	Ile	Leu	Asn	565	570	575
Ala	Asp	Gln	Ile	Ile	Val	Leu	Lys	Asp	Gly	Glu	Val	Ile	Glu	Arg	Gly	580	585	590
Asn	His	His	Glu	Leu	Leu	Lys	Leu	Gly	Gly	Phe	Tyr	Ser	Glu	Leu	Tyr	595	600	605
His	Asn	Gln	Phe	Val	Phe	Glu										610		615

(2) INFORMATION FOR SEQ ID NO:3099:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 69 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...69

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3099:

```
Asn Ser Gln Ala Glu Asp Ile Gln Thr Leu Lys Ile Lys Phe Ser Met
1      5      10      15
Val Gly Phe Gly Glu Gly Leu Leu Lys Gly Trp Gln Ala Ile Asp Thr
      20      25      30
Lys Ile Ala Asp Ile Leu Leu Lys Ser Ile Asn Ile Arg Leu Thr Glu
      35      40      45
Val Ser Ile Gln Ile Ser Ser Lys Lys Ile Asp Gln Ile Leu Leu Thr
      50      55      60
Lys Thr Val Thr Phe
65
```

(2) INFORMATION FOR SEQ ID NO:3100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3100:

```
Val Ile Lys Ala Leu Ile Val Gly Val Ala Ile Asn Gly Ile Ser Ile
1      5      10      15
Ile Gly Phe Lys Thr Val Gly Asn Val Asn Arg Ile Ala Val Leu Ile
      20      25      30
Leu Lys Ile Asp Gly Ile Ile Ala Ser Leu Pro Asn Val Leu Phe Ala
      35      40      45
Arg Leu Leu Leu Asn Arg Lys Arg Gln Ile Ala Arg Pro Ile Val Ala
      50      55      60
Pro Pro Pro Pro Ile Asn Thr Asn Lys Ser Leu Asn Gly Asn Val Ile
      65      70      75      80
Met Cys Trp Ser Val Cys Pro Ala Ala Thr Ala Ser Trp Phe Ser Val
      85      90      95
Val Asn Cys Asn Gln Thr Gly Ser Thr Lys Ala Phe Lys Thr Cys Pro
      100      105      110
Pro Leu Thr Pro Gln Asn Gln Lys Asn Glu Phe Thr Ile Thr His Arg
      115      120      125
Ile Ile Pro Gly Ser Val Pro Ala Ile Asn Leu Ser Gly Val Pro Thr
      130      135      140
Ile Ala Pro Arg Asn Pro Leu Arg Pro Pro Ala Thr Pro Ala Ala Ser
      145      150      155      160
Arg Pro Phe Lys Thr Lys Ala His Lys Thr Lys Val Val Lys Pro Gly
      165      170      175
Lys Arg Ala Glu Asn Asp Leu Leu Thr Thr Ser Gly Thr Pro Leu Gly
      180      185      190
```

Ile Phe Ile Val Ile Pro Arg Trp Ile Asn Ile Arg
 195 200

(2) INFORMATION FOR SEQ ID NO:3101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3101:

Glu	Val	Glu	Ala	Tyr	Leu	Leu	Asp	Lys	Leu	Lys	His	Pro	Lys	Val	Val	1	5	10	15
Ala	Leu	Gly	Glu	Ile	Gly	Leu	Asp	Tyr	His	Trp	Met	Thr	Ala	Pro	Lys	20	25	30	
Glu	Val	Gln	Glu	Gln	Val	Phe	Arg	Arg	Gln	Ile	Gln	Leu	Ser	Lys	Asp	35	40	45	
Leu	Asp	Leu	Pro	Phe	Val	Val	His	Thr	Arg	Asp	Ala	Leu	Glu	Asp	Thr	50	55	60	
Tyr	Glu	Ile	Ile	Lys	Ser	Glu	Gly	Val	Gly	Pro	Arg	Gly	Gly	Ile	Met	65	70	75	80
His	Ser	Phe	Ser	Gly	Thr	Leu	Glu	Trp	Ala	Glu	Lys	Phe	Val	Asp	Leu	85	90	95	
Gly	Met	Thr	Ile	Ser	Phe	Ser	Gly	Val	Val	Thr	Phe	Lys	Lys	Ala	Thr	100	105	110	
Asp	Leu	Gln	Glu	Ala	Ala	Lys	Glu	Leu	Pro	Leu	Asp	Lys	Met	Leu	Val	115	120	125	
Glu	Thr	Asp	Ala	Pro	Tyr	Leu	Ala	Pro	Val	Pro	Lys	Arg	Gly	Arg	Glu	130	135	140	
Asn	Lys	Thr	Ala	Tyr	Thr	Arg	Tyr	Val	Val	Asp	Phe	Ile	Ala	Asp	Leu	145	150	155	160
Arg	Gly	Met	Thr	Thr	Glu	Glu	Leu	Ala	Val	Ala	Thr	Thr	Ala	Asn	Ala	165	170	175	
Glu	Arg	Ile	Phe	Gly	Leu	Asp	Ser	Lys	180	185									

(2) INFORMATION FOR SEQ ID NO:3102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...166

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3102:

Ile	Lys	Glu	Ala	Asp	Met	Asn	Leu	Lys	Gln	Ala	Leu	Ile	Asp	Asn	Asp
1				5					10					15	
Ser	Ile	Arg	Leu	Gly	Leu	Glu	Ala	Asn	Asn	Trp	Lys	Glu	Ala	Val	Lys
			20					25					30		
Val	Ala	Val	Asp	Pro	Leu	Ile	Glu	Ser	Gly	Ala	Ile	Leu	Pro	Glu	Tyr
			35				40					45			
Tyr	Asp	Ala	Ile	Ile	Glu	Ser	Thr	Glu	Glu	Tyr	Gly	Pro	Tyr	Tyr	Ile
	50					55					60				
Leu	Met	Pro	Gly	Met	Ala	Met	Pro	His	Ala	Arg	Pro	Glu	Ala	Gly	Val
65					70					75					80
Gln	Ser	Asp	Ala	Phe	Ser	Leu	Ile	Thr	Leu	Gln	Asn	Pro	Val	Val	Phe
				85					90					95	
Ser	Asp	Gly	Lys	Glu	Val	Ser	Val	Leu	Leu	Ala	Leu	Ala	Ala	Thr	Ser
			100					105					110		
Ser	Lys	Ile	His	Thr	Ser	Val	Ala	Ile	Pro	Gln	Ile	Ile	Ala	Leu	Phe
			115				120					125			
Glu	Leu	Glu	Asp	Ser	Ile	Ala	Arg	Leu	Gln	Ala	Cys	Gln	Thr	Lys	Glu
	130					135					140				
Asp	Val	Leu	Ala	Met	Ile	Glu	Glu	Ser	Lys	Asp	Ser	Pro	Tyr	Leu	Glu
145					150					155					160
Gly	Leu	Asp	Leu	Glu	Ser										
				165											

(2) INFORMATION FOR SEQ ID NO:3103:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 295 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...295

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3103:

Asn	Met	Arg	Ala	Lys	Glu	Leu	Gln	Asp	Trp	Phe	Pro	Glu	Ala	Arg	Ile
1				5					10					15	
Ser	Asp	Gln	Pro	Val	Glu	Lys	Glu	Gly	Tyr	Leu	Thr	Leu	Pro	Leu	Ala

				20					25				30		
Ser	Gln	Gln	Trp	Ile	Leu	Leu	Glu	Glu	Ala	Gly	Leu	Ser	Glu	Arg	Glu
		35					40					45			
Lys	Gln	Leu	Val	Ala	Leu	Leu	Thr	Gln	Gln	Glu	Gln	Ala	Arg	Ser	Leu
	50					55					60				
Asn	Pro	Trp	Tyr	Ser	Tyr	Leu	Val	Glu	Gly	Lys	Gly	Gln	Ala	Pro	Gln
65					70					75					80
Val	Phe	Lys	Lys	Ile	Gln	Leu	Val	Tyr	Cys	His	Leu	Ser	Tyr	Phe	Gln
				85					90					95	
Gln	Glu	Asn	Leu	Ala	Ser	Trp	Leu	Asp	Met	Met	Arg	Thr	Leu	Phe	Pro
			100					105					110		
Asn	Cys	Gln	Thr	Val	Leu	Gln	Val	Gly	Ala	Gln	Asp	Tyr	Val	Phe	Val
		115					120					125			
Leu	Gln	Gln	Asp	Lys	Tyr	Thr	Ser	Val	Arg	Asp	Ile	Leu	Ser	Asp	Thr
	130					135					140				
Ile	Glu	Ala	Val	Glu	Tyr	Asp	Phe	Gly	Leu	Arg	Leu	Ser	Ile	Met	Leu
145					150					155					160
Gly	Gln	Val	Trp	Ser	Gln	Thr	Gly	His	Gln	Ala	Leu	Ser	Asp	Leu	Ile
				165					170					175	
Lys	Ala	Glu	Arg	Asp	Leu	Phe	Lys	Thr	Trp	Trp	Arg	Gln	Gly	His	Gln
			180					185					190		
Gly	Val	His	Thr	Phe	Ser	Gln	Leu	Tyr	Leu	Trp	Ser	Met	Gly	Glu	Arg
		195					200					205			
Leu	Val	Asp	Leu	Lys	Pro	Ile	Lys	Glu	Cys	Leu	His	Gln	Met	Ile	Leu
	210					215					220				
Asp	Gln	Asp	Gln	Ile	Gln	Glu	Ile	Ile	Leu	Ser	Leu	Trp	Glu	Asn	Ser
225					230					235					240
Ala	Val	Leu	Thr	Lys	Thr	Ala	Gln	Gln	Leu	Tyr	Leu	His	Arg	Asn	Ser
				245					250					255	
Leu	Gln	Tyr	Lys	Ile	Asp	Lys	Trp	Glu	Glu	Leu	Thr	Gly	Leu	Gln	Leu
			260					265					270		
Lys	Glu	Leu	Thr	Asp	Leu	Thr	Leu	Cys	Tyr	Gln	Leu	Ile	Leu	Gly	Ser
		275					280					285			
Leu	Ser	Thr	Ile	Val	Gly	Leu									
	290					295									

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEO ID NO:3104:

Lys	Lys	Arg	Ala	Phe	Met	Thr	Tyr	Glu	Tyr	Lys	Ser	His	Ile	Tyr	Leu
1				5					10					15	
Ala	Glu	Thr	Ala	Leu	Asn	Val	Lys	Asp	Leu	Ala	Ser	Gln	Thr	Ala	Phe
			20					25					30		
Tyr	Gln	Gln	Val	Ile	Gly	Leu	Glu	Ile	Leu	Ser	Gln	Thr	Glu	Thr	Glu
		35					40					45			
Ser	Ile	Leu	Gly	Leu	Gly	Gly	Lys	Val	Leu	Val	Gln	Leu	Ile	Gln	Ala
	50					55					60				
Gln	Glu	Ser	Gly	Glu	Val	Arg	Glu	Tyr	Tyr	Gly	Leu	Tyr	His	Leu	Ala
65					70					75					80
Ile	Leu	Leu	Pro	Thr	Arg	Lys	Ala	Leu	Ala	Asp	Val	Leu	Lys	His	Leu
				85					90					95	
Thr	Asp	Leu	Gln	Ile	Pro	Leu	Val	Gly	Gly	Ala	Asp	His	Gly	Tyr	Ser
		100						105					110		
Glu	Ala	Ile	Tyr	Leu	Glu	Asp	Leu	Glu	Gly	Asn	Gly	Ile	Glu	Leu	Tyr
		115					120					125			
Arg	Asp	Lys	Pro	Phe	Ser	Thr	Trp								
	130					135									

(2) INFORMATION FOR SEQ ID NO:3105:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 132 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...132

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3105:

Arg	Ala	Gly	Ala	Pro	Asp	Asn	Ile	Ser	Thr	Pro	Ser	Ser	Ser	Pro	Val
1				5					10					15	
Leu	Leu	Pro	Thr	Ser	Pro	Val	Pro	Thr	Leu	Ala	Arg	Gly	Ala	Arg	Pro
			20					25					30		
Ala	Ala	Pro	Pro	Ser	Ala	Ala	Gly	Arg	Ser	Leu	Pro	Arg	Ser	Ala	Ala
		35					40					45			
Thr	Lys	Arg	Ser	Ser	Arg	Pro	Pro	His	Thr	His	Pro	Pro	Pro	Pro	Arg
	50				55					60					
Pro	Thr	Pro	Thr	Arg	His	Asn	Pro	Glu	Arg	Ala	Thr	Gln	Pro	Ser	Thr
65				70						75					80
Asp	Ser	Lys	Ala	Thr	Ser	His	Pro	Arg	Pro	Ala	Arg	Asp	Pro	Arg	Ala
			85					90					95		
Pro	Ala	Pro	Arg	Pro	Pro	Ala	Pro	His	Arg	Glu	Arg	Lys	Pro	Ser	His
		100					105					110			
Pro	Asp	Pro	Pro	Thr	His	His	Arg	Gly	Pro	Ala	Ser	Pro	Lys	Lys	Phe
		115					120					125			
Gln	Gln	Ser	Gln												
	130														

(2) INFORMATION FOR SEQ ID NO:3106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...372

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3106:

Ser	Phe	His	Leu	Asp	Arg	Glu	Glu	Ile	His	Met	Arg	Ile	Phe	Ala	Ser
1			5					10					15		
Pro	Ser	Arg	Tyr	Ile	Gln	Gly	Glu	Asn	Ala	Leu	Phe	Glu	Asn	Ala	Lys
			20					25					30		
Ser	Ile	Leu	Asp	Leu	Gly	Asn	Tyr	Pro	Ile	Leu	Leu	Cys	Asp	Gln	Leu
		35					40					45			
Val	Tyr	Asp	Ile	Val	Gly	Lys	Arg	Phe	Glu	Asp	Tyr	Leu	His	Arg	Tyr
	50					55				60					
Gly	Phe	His	Ile	Val	Leu	Ala	Leu	Phe	Asn	Gly	Glu	Ala	Ser	Asp	Asn
65				70					75						80
Glu	Ile	Asn	Arg	Val	Val	Ala	Leu	Ala	Glu	Lys	Glu	Asn	Cys	Asp	Ser
			85						90					95	
Ile	Ile	Gly	Leu	Gly	Gly	Gly	Lys	Thr	Ile	Asp	Ser	Ala	Lys	Ala	Ile
			100					105					110		
Ala	Asp	Leu	Ile	Glu	Lys	Pro	Val	Ile	Ile	Ala	Pro	Thr	Ile	Ala	Ser
	115						120					125			
Thr	Asp	Ala	Pro	Val	Ser	Ala	Leu	Ser	Val	Ile	Tyr	Thr	Asp	Glu	Gly
	130					135					140				
Ala	Phe	Asp	His	Tyr	Leu	Phe	Tyr	Ser	Lys	Asn	Pro	Asp	Leu	Val	Leu
145					150					155					160
Val	Asp	Thr	Lys	Val	Ile	Ser	Gln	Ala	Pro	Lys	Arg	Leu	Leu	Ala	Ser
			165						170					175	
Gly	Ile	Ala	Asp	Gly	Leu	Ala	Thr	Trp	Val	Glu	Ala	Arg	Ala	Val	Met
			180					185					190		
Gln	Ala	Asn	Gly	Lys	Thr	Met	Leu	Gly	Gln	Gln	Gln	Thr	Leu	Ala	Gly
		195					200					205			
Val	Ala	Ile	Ala	Lys	Lys	Cys	Glu	Glu	Thr	Leu	Phe	Ala	Asp	Gly	Leu
	210					215					220				
Gln	Ala	Met	Ala	Ala	Cys	Glu	Ala	Lys	Val	Val	Thr	Pro	Ala	Leu	Glu
225					230					235					240
Asn	Ile	Val	Glu	Ala	Asn	Thr	Leu	Leu	Ser	Gly	Leu	Gly	Phe	Glu	Ser
			245						250					255	
Gly	Gly	Leu	Ala	Ala	Ala	His	Ala	Ile	His	Asn	Gly	Phe	Thr	Ala	Leu
		260					265						270		
Thr	Gly	Asp	Ile	His	His	Leu	Thr	His	Gly	Glu	Lys	Val	Ala	Tyr	Gly
		275					280						285		

Thr	Leu	Val	Gln	Leu	Leu	Leu	Glu	Asn	Arg	Pro	Lys	Glu	Glu	Leu	Asp
290						295					300				
Lys	Tyr	Ile	Glu	Phe	Tyr	Lys	Lys	Ile	Gly	Met	Pro	Thr	Thr	Leu	Lys
305					310					315					320
Glu	Met	His	Leu	Asp	Gln	Val	Gly	Tyr	Asp	Asp	Leu	Ile	Lys	Val	Gly
			325						330					335	
Lys	Gln	Ala	Thr	Met	Glu	Gly	Glu	Thr	Ile	His	Gln	Met	Pro	Phe	Lys
			340						345					350	
Ile	Ser	Pro	Ser	Asp	Val	Ala	Gln	Ala	Ile	Ile	Ala	Val	Asp	Ala	Tyr
		355					360						365		
Val	Asn	Ser	Lys												
370															

(2) INFORMATION FOR SEQ ID NO:3107:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 62 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...62
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3107:

Ile	Thr	His	Leu	Gly	Gly	Asn	Phe	Met	Lys	Lys	Lys	Ile	Leu	Ile	Ile
1				5					10					15	
Phe	Ile	Leu	Tyr	Leu	Ile	Met	Ser	Ile	Phe	Leu	Tyr	Pro	Leu	Arg	Glu
		20					25						30		
Ser	Ile	Trp	Tyr	Gln	Leu	Phe	Tyr	Thr	Ile	Ala	Tyr	Val	Ile	Ala	Val
		35					40					45			
Met	Ile	Tyr	Phe	Ala	Leu	Thr	Lys	Lys	Lys	Gly	Ala	Lys	Lys		
50						55					60				

(2) INFORMATION FOR SEQ ID NO:3108:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 123 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...123

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3108:

Gly	Trp	Thr	Xaa	Val	Val	Arg	Trp	Trp	Val	Gly	Val	Ala	Trp	Phe	Ser
1				5					10					15	
Leu	Pro	Val	Gly	Gly	Xaa	Gly	Ser	Arg	Gly	Gly	Gly	Pro	Gly	Val	Pro
			20					25					30		
Cys	Gly	Ala	Gly	Val	Ala	Arg	Arg	Leu	Ala	Val	Cys	Ala	Gly	Leu	Arg
			35				40					45			
Gly	Ala	Leu	Trp	Val	Val	Ala	Gly	Gly	Arg	Gly	Pro	Gly	Arg	Gly	Gly
			50			55					60				
Val	Arg	Val	Trp	Trp	Pro	Ala	Ala	Pro	Phe	Gly	Cys	Arg	Gly	Ser	Gly
65					70					75				80	
Glu	Ala	Ala	Ala	Gly	Cys	Ala	Gly	Gly	Cys	Gly	Gly	Ser	Arg	Pro	Ser
				85					90					95	
Arg	Gln	Ser	Gly	Asp	Gly	Gly	Gly	Gly	Glu	Glu	Tyr	Arg	Thr	Arg	Gly
			100					105					110		
Trp	Arg	Ala	Tyr	Val	Val	Arg	Arg	Pro	Arg	Pro					
			115				120								

(2) INFORMATION FOR SEQ ID NO:3109:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 363 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...363

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3109:

Asp	Cys	Asn	Phe	Leu	Thr	Gly	Met	Ile	Leu	Ser	Leu	Thr	Val	His	Thr
1				5					10					15	
Tyr	Phe	Ile	Ile	Phe	Ser	Ala	Glu	Asn	Tyr	Tyr	Arg	Lys	Val	Thr	Lys
			20					25					30		
Arg	Ile	Lys	Ser	Leu	Phe	Ile	Phe	Lys	Ala	Trp	Leu	Ile	Leu	Glu	Lys
			35				40					45			
Cys	Gly	Ile	Ile	Phe	Leu	Met	Glu	Lys	Ile	Val	Ile	Thr	Ala	Thr	Ala
			50			55				60					
Glu	Ser	Ile	Glu	Gln	Val	Glu	Gln	Leu	Leu	Glu	Ala	Gly	Val	Asp	Arg
65				70						75				80	
Ile	Tyr	Val	Gly	Glu	Lys	Asp	Phe	Gly	Leu	Arg	Leu	Pro	Thr	Thr	Phe
			85					90					95		
Ser	Tyr	Asp	Gln	Leu	Arg	Glu	Ile	Ala	Lys	Leu	Val	His	Asp	Ala	Gly
			100					105					110		

Lys	Glu	Leu	Ile	Val	Ala	Val	Asn	Ala	Leu	Met	His	Gln	Asp	Met	Met
		115					120					125			
Asp	Arg	Ile	Lys	Pro	Phe	Leu	Asp	Phe	Leu	Glu	Glu	Ile	Lys	Thr	Asp
	130					135					140				
Tyr	Ile	Thr	Ile	Gly	Asp	Ala	Gly	Val	Phe	Tyr	Val	Val	Asn	Arg	Asp
145				150					155						160
Gly	Tyr	Ser	Phe	Lys	Thr	Ile	Tyr	Asp	Ala	Ser	Thr	Met	Val	Thr	Ser
				165					170					175	
Ser	Arg	Gln	Ile	Asn	Phe	Trp	Gly	Gln	Lys	Ala	Gly	Ala	Ser	Glu	Ala
			180				185						190		
Val	Leu	Ala	Arg	Glu	Ile	Pro	Ser	Ala	Glu	Leu	Phe	Lys	Met	Pro	Glu
		195				200						205			
Ile	Leu	Glu	Ile	Pro	Ala	Glu	Val	Leu	Val	Tyr	Gly	Ala	Ser	Val	Ile
	210					215					220				
His	His	Ser	Lys	Arg	Pro	Leu	Leu	Gln	Asn	Tyr	Tyr	Asn	Phe	Thr	His
225				230						235					240
Ile	Asp	Asp	Glu	Lys	Thr	His	Lys	Arg	Asp	Leu	Phe	Leu	Ala	Glu	Pro
			245						250					255	
Ser	Asp	Pro	Glu	Ser	His	Tyr	Ser	Ile	Phe	Glu	Asp	Asn	His	Gly	Thr
			260				265						270		
His	Ile	Phe	Ala	Asn	Asn	Asp	Leu	Asp	Leu	Met	Ile	Lys	Leu	Thr	Glu
		275				280						285			
Leu	Val	Glu	His	Gly	Phe	Thr	Arg	Trp	Lys	Leu	Glu	Gly	Leu	Tyr	Thr
	290					295					300				
Pro	Gly	Gln	Asn	Phe	Val	Glu	Ile	Ala	Lys	Leu	Phe	Ile	Gln	Ala	Arg
305				310						315					320
Asn	Leu	Ile	Gln	Glu	Gly	Asn	Phe	Ser	His	Asp	Gln	Val	Phe	Leu	Leu
			325						330					335	
Asp	Glu	Glu	Val	Arg	Lys	Leu	His	Pro	Lys	Asn	Arg	Phe	Leu	Asp	Thr
			340					345					350		
Gly	Phe	Tyr	Asp	Tyr	Asp	Pro	Asp	Met	Val	Arg					
		355					360								

(2) INFORMATION FOR SEQ ID NO:3110:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 86 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...86

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3110:

Phe	Cys	Phe	Phe	Tyr	Leu	Tyr	Ser	Met	Lys	Ile	Lys	Glu	Gln	Thr	Arg
1				5					10					15	
Lys	Leu	Ala	Ala	Gly	Cys	Ser	Lys	His	Cys	Phe	Glu	Val	Val	Asp	Arg
		20						25					30		

Thr	Asp	Glu	Val	Ser	Ser	Lys	His	Val	Phe	Glu	Val	Val	Asp	Glu	Thr
		35					40					45			
Asp	Glu	Val	Ser	Ser	Lys	His	Cys	Phe	Glu	Val	Val	Asp	Glu	Thr	Asp
	50					55					60				
Glu	Val	Ser	Asn	His	Thr	Tyr	Gly	Arg	Ala	Thr	Leu	Thr	Trp	Phe	Glu
65					70					75					80
Glu	Ile	Phe	Glu	Glu	Tyr										
					85										

(2) INFORMATION FOR SEQ ID NO:3111:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 73 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...73
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3111:

Lys	Leu	Asn	Phe	Met	Lys	Ala	Ile	Phe	Phe	Ile	Ile	Leu	Phe	Ala	Phe
1				5					10					15	
Gln	Thr	Tyr	Leu	Ile	Tyr	Leu	Ser	Ile	Ser	Ile	Ser	Asp	Lys	Lys	Gln
			20					25					30		
Lys	Thr	Ile	Glu	Leu	Thr	Ser	Leu	Asn	Cys	Phe	Val	Ile	Leu	Phe	Leu
			35					40				45			
Ile	Tyr	Asp	Lys	Leu	Ile	Phe	Leu	Phe	Ile	Ala	Tyr	Val	Phe	Leu	Ile
	50					55					60				
Ile	Phe	Ile	Leu	Asn	Leu	Phe	Arg	Asn							
65					70										

(2) INFORMATION FOR SEQ ID NO:3112:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 343 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...343

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3112:

Ile	Lys	Asn	Leu	Glu	Asn	Leu	Arg	Ile	Glu	Lys	Arg	Thr	Asn	Leu	Met
1			5						10					15	
Ala	Lys	Asp	Ile	Arg	Val	Leu	Leu	Tyr	Tyr	Leu	Tyr	Thr	Pro	Ile	Glu
		20						25					30		
Asn	Ala	Glu	Gln	Phe	Ala	Ala	Asp	His	Leu	Ala	Phe	Cys	Lys	Ser	Ile
		35					40					45			
Gly	Leu	Lys	Gly	Arg	Ile	Leu	Val	Ala	Asp	Glu	Gly	Ile	Asn	Gly	Thr
	50					55					60				
Val	Ser	Gly	Asp	Tyr	Glu	Thr	Thr	Gln	Lys	Tyr	Met	Asp	Tyr	Val	His
65					70					75					80
Ser	Leu	Pro	Gly	Met	Glu	Asp	Leu	Trp	Phe	Lys	Ile	Asp	Glu	Glu	Ser
			85						90					95	
Glu	Gln	Ala	Phe	Lys	Lys	Met	Phe	Val	Arg	Tyr	Lys	Lys	Glu	Ile	Val
		100						105					110		
His	Leu	Gly	Leu	Glu	Asp	Asn	Asp	Phe	Asp	Asn	Asp	Ile	Asn	Pro	Leu
	115						120					125			
Glu	Thr	Thr	Gly	Ala	Tyr	Leu	Ser	Pro	Lys	Glu	Phe	Lys	Glu	Ala	Leu
	130					135					140				
Leu	Asp	Lys	Asp	Thr	Val	Val	Leu	Asp	Thr	Arg	Asn	Asp	Tyr	Glu	Tyr
145					150					155					160
Asp	Leu	Glu	His	Phe	Arg	Gly	Ala	Ile	Arg	Pro	Asp	Ile	Arg	Asn	Phe
			165						170					175	
Arg	Glu	Leu	Pro	Gln	Trp	Val	Arg	Asp	Asn	Lys	Glu	Lys	Phe	Met	Asp
		180						185					190		
Lys	Arg	Val	Val	Val	Tyr	Cys	Thr	Gly	Gly	Val	Arg	Cys	Glu	Lys	Phe
	195						200					205			
Ser	Gly	Trp	Met	Val	Arg	Glu	Gly	Tyr	Lys	Asp	Val	Gly	Gln	Leu	His
	210					215					220				
Gly	Gly	Ile	Ala	Thr	Tyr	Gly	Lys	Asp	Pro	Glu	Val	Gln	Gly	Glu	Leu
225					230					235					240
Trp	Asp	Gly	Lys	Met	Tyr	Val	Phe	Asp	Glu	Arg	Ile	Ala	Val	Asp	Val
			245						250					255	
Asn	His	Val	Asn	Pro	Thr	Ile	Val	Gly	Lys	Asp	Trp	Phe	Asp	Gly	Thr
		260						265					270		
Pro	Cys	Glu	Arg	Tyr	Val	Asn	Cys	Gly	Asn	Pro	Phe	Cys	Asn	Arg	Arg
	275						280					285			
Ile	Leu	Thr	Ser	Glu	Glu	Asn	Glu	Asp	Lys	Tyr	Leu	Arg	Gly	Cys	Ser
	290					295					300				
His	Glu	Cys	Arg	Val	His	Pro	Arg	Asn	Arg	Tyr	Val	Ser	Lys	Asn	Glu
305					310					315					320
Leu	Thr	Gln	Ala	Glu	Val	Ile	Glu	Arg	Leu	Ala	Ala	Ile	Gly	Glu	Ser
			325						330					335	
Leu	Asp	Gln	Ala	Ala	Thr	Val									
			340												

(2) INFORMATION FOR SEQ ID NO:3113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...327

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3113:

```
Phe His Phe Tyr Tyr Gly Gly Phe Leu Tyr Tyr Leu Thr Asn Pro Ile
1      5      10      15
Val Thr Phe Leu Asn Lys Val Cys Lys Leu Asn Arg Leu Leu Gly Ile
      20      25      30
Leu Ile Thr Leu Cys Thr Leu Val Trp Gly Met Val Ile Gly Val Val
      35      40      45
Tyr Leu Leu Pro Ile Leu Ile Asn Gln Leu Ser Ser Leu Ile Ile Ser
      50      55      60
Ser Gln Thr Ile Tyr Ser Arg Val Gln Asp Leu Ile Ile Asp Leu Ser
      65      70      75      80
Asn Tyr Pro Ala Leu Gln Asn Leu Asp Val Glu Ala Thr Ile Gln Gln
      85      90      95
Leu Asn Leu Ser Tyr Val Asp Ile Leu Gln Asn Ile Leu Asn Ser Val
      100     105     110
Ser Asn Ser Val Gly Ser Val Leu Ser Ala Leu Ile Ser Thr Val Leu
      115     120     125
Ile Leu Ile Met Thr Pro Val Phe Leu Val Tyr Phe Leu Leu Asp Gly
      130     135     140
His Lys Phe Leu Pro Met Leu Glu Arg Thr Ile Leu Lys Arg Asp Arg
      145     150     155     160
Leu His Ile Ala Gly Leu Leu Lys Asn Leu Asn Ala Thr Ile Ala Arg
      165     170     175
Tyr Ile Ser Gly Val Ser Ile Asp Ala Ile Ile Ile Gly Cys Leu Ala
      180     185     190
Tyr Ile Gly Tyr Ser Ile Ile Gly Leu Lys Tyr Ala Leu Val Phe Ala
      195     200     205
Ile Phe Ser Gly Val Ala Asn Leu Ile Pro Tyr Val Gly Pro Ser Ile
      210     215     220
Gly Leu Ile Pro Met Ile Ile Ala Asn Ile Phe Thr Asp Pro His Arg
      225     230     235     240
Leu Leu Ile Ala Val Ile Tyr Met Leu Val Val Gln Gln Val Asp Gly
      245     250     255
Asn Ile Leu Tyr Pro Arg Ile Val Gly Ser Val Met Lys Val His Pro
      260     265     270
Ile Thr Ile Leu Val Leu Leu Leu Leu Ser Ser Asn Ile Tyr Gly Val
      275     280     285
Val Gly Met Ile Val Ala Val Pro Thr Tyr Ser Ile Leu Lys Glu Ile
      290     295     300
Ser Lys Phe Leu Ser Arg Leu Tyr Glu Asn His Lys Ile Met Lys Glu
      305     310     315     320
Arg Glu Arg Glu Leu Ala Lys
      325
```

(2) INFORMATION FOR SEQ ID NO:3114:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3114:

Lys	Ser	Phe	Tyr	Gly	Leu	Ser	Thr	Ile	Asp	Ser	Val	Tyr	Ser	Tyr	Ala
1				5					10					15	
Met	Gln	His	Leu	Thr	Ser	Gln	Asn	Tyr	Pro	Asp	Ile	Ile	Phe	Val	Ser
			20					25					30		
Gly	Asp	Glu	Lys	Val	Gln	Gly	Leu	Ile	Arg	Ala	Cys	Tyr	Glu	Lys	Gly
	35					40						45			
Ile	Leu	Ile	Pro	Asp	Asp	Ile	Ser	Ile	Ile	Gly	Phe	Asn	Asn	Ile	Pro
	50					55					60				
Ile	Ser	Gln	Tyr	Tyr	Thr	Pro	Ala	Leu	Ser	Thr	Ile	Ala	Pro	Asn	Tyr
65					70					75					80
Val	Lys	Leu	Ala	Lys	Glu	Met	Ile	Glu	Gly	Val	Leu	Ala	Ile	Ile	Lys
			85						90					95	
Gly	Glu	Ser	Val	Thr	Ser	Val	Glu	Val	Ser	Pro	Lys	Phe	Val	Arg	Arg
			100					105						110	
Gln	Ile	Phe													
			115												

(2) INFORMATION FOR SEQ ID NO:3115:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3115:

Thr	Lys	Phe	Tyr	Arg	Arg	Lys	Thr	Met	Asp	Trp	Tyr	Asp	Tyr	Met	Ile
1						5			10					15	
Gln	Ala	Ser	Lys	Gln	Ser	Gln	Phe	Asn	Ala	Ser	His	Trp	Phe	Arg	Tyr

		20					25				30				
Leu	Arg	Lys	Val	Ile	Phe	Glu	Asp	Tyr	Ser	Tyr	Leu	Thr	Asn	Gln	Asp
		35					40					45			
Val	Glu	Lys	Leu	Leu	Asp	Ser	Lys	Glu	Leu	Thr	Arg	Phe	Gln	Lys	Ile
	50					55					60				
Ser	Leu	Lys	Tyr	Ala	Phe	Gln	Glu	His	Thr	Pro	Thr	His	Lys	Tyr	Val
65					70					75					80
Ile	Ser	Leu	Asn	Lys	Pro	Ala	Lys	Leu	Thr	Asn	Val	Gln	Lys	Leu	Met
			85						90					95	
Glu	Lys	Tyr	Lys	His	Gly										
			100												

(2) INFORMATION FOR SEQ ID NO:3116:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 229 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...229

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3116:

Lys	His	Phe	Leu	Phe	His	Ser	Ser	Lys	Glu	Glu	Val	Tyr	Arg	Met	Asn
1				5					10					15	
Glu	Ile	Ile	Thr	Leu	Lys	Asn	Ile	Glu	Leu	Lys	Leu	Lys	Lys	Thr	Cys
			20					25					30		
Val	Phe	Gln	Asn	Leu	Asn	Phe	Ser	Cys	Lys	Gln	Gly	Glu	Ile	Ile	Gly
		35				40					45				
Ile	Thr	Gly	Ala	Asn	Gly	Ser	Gly	Lys	Ser	Val	Leu	Phe	Lys	Leu	Ile
	50				55					60					
Ala	Gly	Leu	Tyr	Ser	Pro	Ser	Tyr	Gly	Glu	Val	Leu	Ile	Asn	Gly	Glu
65				70					75						80
Asn	Ile	Val	Pro	Glu	Arg	Lys	Ile	Pro	Ala	Asn	Leu	Gly	Ala	Leu	Ile
			85					90						95	
Glu	Glu	Pro	Gly	Phe	Ile	Asn	Tyr	Tyr	Ser	Gly	Phe	Lys	Asn	Leu	Gln
		100					105						110		
Tyr	Leu	Ala	Ser	Ile	Arg	Gly	Val	Val	Gly	Asn	Gln	Glu	Ile	Asn	Asp
	115					120					125				
Thr	Leu	Lys	Ile	Val	Gly	Leu	Tyr	Glu	Gln	Lys	Asp	Gln	Lys	Val	Lys
	130				135						140				
Thr	Tyr	Ser	Leu	Gly	Met	Arg	Lys	Lys	Leu	Gly	Ile	Ala	Gln	Ala	Ile
145				150					155						160
Met	Glu	Asn	Pro	Ser	Ile	Leu	Leu	Leu	Asp	Glu	Pro	Met	Asn	Ala	Leu
		165						170					175		
Asp	Lys	Ser	Ser	Val	Glu	Asn	Met	Arg	Thr	Leu	Phe	Arg	Lys	Leu	Ser
		180					185					190			
Ser	Glu	Lys	Gly	Thr	Thr	Ile	Leu	Ile	Ala	Ser	His	Ser	Glu	Glu	Asp

	195		200		205
Ile	Arg	Ile	Leu	Cys	Asp
	210		215		220
Thr	Leu	Cys	Ser	Asp	
225					

(2) INFORMATION FOR SEQ ID NO:3117:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 155 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...155
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3117:

Ile	Ile	Leu	Tyr	Thr	Arg	Lys	Gln	Glu	Val	His	Ser	Val	Leu	Ala	Ser
1				5					10					15	
Lys	Lys	Ser	Val	Lys	Leu	Phe	Tyr	Ser	Met	Leu	Leu	Leu	Ile	Asn	Val
		20						25					30		
Leu	Gly	Ala	Val	Leu	Val	Leu	Ser	Asp	Asn	Leu	Phe	Ile	Lys	Asn	Thr
	35					40					45				
Leu	Gln	Gln	Glu	Leu	Val	Asp	Phe	Leu	Leu	Pro	Ser	Phe	Phe	Phe	Leu
	50				55				60						
Phe	Gly	Leu	Asp	Leu	Leu	Ile	Phe	Leu	Pro	Leu	Lys	Lys	Tyr	Val	Arg
65			70						75					80	
Asp	Phe	Leu	Ala	Met	Leu	Asp	Arg	Lys	Lys	Thr	Val	Leu	Val	Thr	Ile
		85						90					95		
Leu	Ala	Thr	Leu	Leu	Phe	Leu	Arg	Asn	Pro	Met	Thr	Ile	Val	Ser	Leu
		100						105					110		
Leu	Ile	Tyr	Ile	Gly	Leu	Gly	Leu	Phe	Phe	Ala	Ala	Tyr	Leu	Val	Pro
	115					120						125			
Asn	Ser	Val	Lys	Lys	Glu	Val	Ser	Phe	Tyr	Gly	His	Ile	Phe	Arg	Asp
	130				135						140				
Leu	Val	Leu	Val	Ile	Val	Thr	Leu	Ile	Phe	Phe					
145					150					155					

(2) INFORMATION FOR SEQ ID NO:3118:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 205 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3118:

Val	Ile	Leu	Tyr	Tyr	Lys	Tyr	Leu	Gly	Phe	Ser	Leu	Glu	Lys	Ile	Ala
1				5					10					15	
Glu	Leu	Leu	Lys	Glu	Glu	Arg	Thr	Asp	Leu	Leu	Pro	His	Leu	Thr	Arg
			20					25					30		
Gln	Leu	Asp	Tyr	Leu	Thr	Arg	Glu	Arg	Gln	His	Leu	Asp	Thr	Leu	Ile
		35					40					45			
Ser	Thr	Leu	Gln	Lys	Thr	Ile	Gln	Glu	Gln	Lys	Gly	Glu	Arg	Lys	Met
	50					55					60				
Thr	Ile	Glu	Glu	Lys	Phe	Thr	Gly	Phe	Ser	Tyr	Gln	Asp	Asn	Gln	Lys
65					70				75					80	
Tyr	His	Gln	Glu	Ala	Val	Glu	Lys	Tyr	Gly	Gln	Glu	Val	Met	Gly	Gln
				85					90					95	
Ala	Leu	Glu	Arg	Gln	Lys	Gly	His	Glu	Asp	Glu	Ala	Thr	Ala	Ala	Phe
			100					105					110		
Asn	Gln	Val	Phe	Gln	Thr	Leu	Ala	Gln	Asn	Leu	Gln	Val	Gly	Leu	Pro
		115					120					125			
Ala	Thr	Ala	Thr	Glu	Asn	Gln	Glu	Gln	Ala	Ala	Lys	Leu	Leu	Gln	Ala
	130					135					140				
Ile	Arg	Thr	Tyr	Gly	Phe	Asp	Cys	Ser	Ile	Glu	Val	Phe	Gly	His	Ile
145					150				155					160	
Gly	Lys	Gly	Tyr	Val	Tyr	Asn	Pro	Asn	Phe	Lys	Glu	Asn	Ile	Asp	Lys
				165					170					175	
Phe	Gly	Ser	Gly	Thr	Ala	Gln	Tyr	Thr	Ser	Asp	Ala	Ile	Ala	Gly	Leu
			180					185					190		
Arg	Ser	Asp	Lys	Cys	Arg	Ile	Asn	Arg	Leu	Gly	Ile	Ser			
		195					200					205			

(2) INFORMATION FOR SEQ ID NO:3119:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...65

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3119:

```

Leu Tyr Leu Tyr Thr Phe Leu Lys Leu Phe Glu Gln Ile Phe His Lys
1      5      10      15
Asn Glu Ser Phe Ser Tyr Gln Pro Ile His Asp Ile Phe Leu Leu Asn
      20      25      30
Ile Met Glu Ser His Ser Val Lys Glu Leu Gln Val Ala Leu Ser Arg
      35      40      45
Glu His Val Val His Gln Thr Ile His His Asn Ile Ser Asn Gln Leu
      50      55      60
Arg
65

```

(2) INFORMATION FOR SEQ ID NO:3120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...62

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3120:

```

Leu Lys Leu Tyr Arg Val Gln Asn Ser Ala Met Asn Ser Ile Trp Val
1      5      10      15
Leu Thr Ser Lys Lys Lys Leu Val Cys Val Ala Leu Ile Pro Leu Gln
      20      25      30
Pro Ser Leu Thr Gln Lys Ser Ser Ser Gln Leu Leu Ala His Gln Gln
      35      40      45
Val Met Ser Thr Val Val Lys Ala Arg Leu Glu Met Glu Pro
      50      55      60

```

(2) INFORMATION FOR SEQ ID NO:3121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

(B) LOCATION 1...315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3121:

Asp	Tyr	Ile	Tyr	Leu	His	Thr	Thr	Lys	Cys	Lys	His	Phe	Cys	Leu	Lys
1				5					10					15	
Leu	Arg	Ile	Lys	Ser	Met	Lys	Lys	Ala	Met	Val	Ile	Ile	Asn	Pro	Thr
			20					25					30		
Ser	Gly	Gly	Glu	Lys	Ala	Leu	Asp	Tyr	Lys	Glu	Lys	Leu	Glu	Asn	Lys
		35					40					45			
Ala	Lys	Glu	Tyr	Phe	Glu	Tyr	Val	Glu	Thr	Lys	Ile	Thr	Glu	Lys	Ala
	50					55					60				
Leu	Asp	Ala	Thr	His	Phe	Ala	Glu	Glu	Ala	Ser	Arg	Glu	Gln	Tyr	Asp
65				70						75				80	
Ala	Val	Val	Val	Phe	Gly	Gly	Asp	Gly	Thr	Val	Asn	Glu	Val	Ile	Ser
				85					90					95	
Gly	Ile	Asp	Glu	Arg	Asp	Tyr	Ile	Pro	Lys	Leu	Gly	Ile	Ile	Pro	Gly
		100						105					110		
Gly	Thr	Gly	Asn	Leu	Ile	Thr	Lys	Leu	Leu	Glu	Ile	Asn	Gln	Asp	Ile
	115						120					125			
Asp	Gly	Ala	Ile	Asp	Glu	Leu	Asp	Phe	Asp	Leu	Thr	Asn	Lys	Ile	Asp
	130					135					140				
Ile	Gly	Lys	Ala	Asn	Asp	Asn	Tyr	Phe	Gly	Tyr	Ile	Phe	Ser	Ile	Gly
145				150						155				160	
Ser	Leu	Pro	Glu	Ala	Ile	His	Asn	Val	Glu	Ile	Glu	Asp	Lys	Thr	Lys
				165					170					175	
Phe	Gly	Ile	Leu	Thr	Tyr	Ala	Val	Asn	Thr	Met	Lys	Ser	Val	Met	Thr
		180						185					190		
Asp	Gln	Val	Phe	Asn	Ile	Lys	Val	Glu	Thr	Glu	Asn	Gly	Asn	Tyr	Val
	195						200					205			
Gly	Glu	Ala	Ser	His	Val	Leu	Val	Leu	Leu	Thr	Asn	Tyr	Phe	Ala	Asp
	210					215					220				
Lys	Lys	Ile	Phe	Glu	Glu	Asn	Lys	Asp	Gly	Tyr	Ala	Asn	Ile	Leu	Ile
225					230					235				240	
Leu	Lys	Asp	Ala	Ser	Ile	Phe	Ser	Lys	Leu	Ser	Val	Ile	Pro	Asp	Leu
			245						250					255	
Leu	Lys	Gly	Asp	Val	Ile	Ala	Asn	Asp	Asn	Ile	Glu	Tyr	Ile	Lys	Ala
		260						265					270		
Arg	Asn	Ile	Lys	Ile	Ser	Ser	Asp	Ser	Glu	Leu	Glu	Ser	Asp	Val	Asp
	275						280					285			
Gly	Asp	Lys	Ser	Asp	Asn	Leu	Pro	Val	Glu	Ile	Lys	Val	Leu	Ala	Gln
	290					295					300				
Arg	Val	Glu	Val	Phe	Ser	Lys	Pro	Lys	Glu	Asp					
305					310					315					

(2) INFORMATION FOR SEQ ID NO:3122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...65

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3122:

```
Pro Pro Phe Leu Lys Asn Ser Lys Phe Trp Val Ile Asp Glu Thr Asp
1      5      10      15
Glu Arg Leu Gly Pro Phe Asn Thr Phe Glu Glu Ala Tyr Gln Ser Leu
      20      25      30
Leu Phe Tyr Leu Lys Met Thr Glu Asp Glu Tyr Gln Ser Asn Tyr Thr
      35      40      45
Ala Gln Glu Leu Val Tyr Ile Tyr Lys Glu Glu Lys Lys Pro Cys Arg
      50      55      60
Arg
65
```

(2) INFORMATION FOR SEQ ID NO:3123:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 381 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...381

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3123:

```
Asn Met Ile Tyr Phe Asp Asn Ser Ala Thr Thr Arg Pro Tyr Pro Glu
1      5      10      15
Ala Leu Glu Thr Tyr Met Gln Val Ala Ser Lys Ile Leu Gly Asn Pro
      20      25      30
Ser Ser Leu His Arg Leu Gly Asp Gln Ala Thr Arg Ile Leu Asp Ala
      35      40      45
Ser Arg Gln Gln Ile Ala Asp Leu Ile Gly Lys Lys Ser Asp Glu Ile
      50      55      60
Phe Phe Thr Ser Gly Gly Thr Glu Gly Asp Asn Trp Ile Ile Lys Gly
65      70      75      80
Val Ala Phe Glu Lys Ala Gln Phe Gly Lys His Ile Ile Val Ser Ala
      85      90      95
Ile Glu His Pro Ala Val Lys Glu Ser Ala Leu Trp Leu Lys Ala Gln
      100     105     110
Gly Phe Glu Val Asp Phe Ala Pro Val Asp Asn Lys Gly Phe Val Asp
      115     120     125
Val Glu Ala Leu Glu Asp Leu Ile Arg Pro Asp Thr Thr Leu Val Ser
      130     135     140
```

```

Ile Met Ala Val Asn Asn Glu Ile Gly Ser Val Gln Pro Ile Glu Ala
145                      150                      155                      160
Ile Ser Lys Leu Leu Ala Asp Lys Pro Thr Ile Ser Phe His Val Asp
                      165                      170                      175
Ala Val Gln Ala Leu Ala Lys Ile Pro Thr Glu Lys Tyr Leu Thr Glu
                      180                      185                      190
Arg Val Asp Phe Ala Thr Phe Ser Gly His Lys Phe His Gly Ile Arg
                      195                      200                      205
Gly Val Gly Phe Ile Tyr Ile Lys Ser Gly Lys Lys Ile Thr Pro Leu
210                      215                      220
Leu Thr Gly Gly Gly Gln Glu Arg Asp Tyr Arg Ser Thr Thr Glu Asn
225                      230                      235                      240
Val Ala Gly Ile Ala Ala Thr Ala Lys Ala Leu Arg Leu Ser Met Glu
                      245                      250                      255
Lys Leu Asp Ile Phe Arg Ser Lys Thr Gly Gln Met Lys Ala Val Ile
260                      265                      270
Arg Gln Ala Leu Leu Asp Tyr Pro Asp Ile Phe Val Phe Ser Asp Glu
275                      280                      285
Glu Asp Phe Ala Pro His Ile Leu Thr Phe Gly Ile Lys Gly Val Arg
290                      295                      300
Gly Glu Val Ile Val His Ala Phe Glu Asp Tyr Asp Ile Phe Ile Ser
305                      310                      315                      320
Thr Thr Ser Ala Cys Ser Ser Lys Ala Gly Lys Pro Ala Gly Thr Leu
                      325                      330                      335
Ile Ala Met Gly Val Asp Lys Asp Lys Ala Gln Ser Ala Val Arg Leu
340                      345                      350
Ser Leu Asp Leu Glu Asn Asp Met Ser Gln Val Glu Gln Phe Leu Thr
355                      360                      365
Lys Leu Lys Leu Ile Tyr Asn Gln Thr Arg Lys Val Arg
370                      375                      380

```

(2) INFORMATION FOR SEQ ID NO:3124:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 370 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...370

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3124:

```

Lys Arg Asn Phe His Ile Phe Thr Phe Val Ser Arg Tyr Arg Ala Ser
1                      5                      10                      15
Ile Ser Thr Ser Thr Cys Lys Arg Met Cys Glu Ile Glu Arg Thr Gly
20                      25                      30
Lys Gly Met Asn Ala Asp Asp Thr Val Thr Ile Tyr Asp Val Ala Arg
35                      40                      45

```


Glu	Ala	Gly	Val	Ser	Met	Ala	Thr	Val	Ser	Arg	Val	Val	Asn	Gly	Asn
50						55					60				
Lys	Asn	Val	Lys	Glu	Asn	Thr	Arg	Lys	Lys	Val	Leu	Glu	Val	Ile	Asp
65					70					75					80
Arg	Leu	Asp	Tyr	Arg	Pro	Asn	Ala	Val	Ala	Arg	Gly	Leu	Ala	Ser	Lys
				85					90					95	
Lys	Thr	Thr	Thr	Val	Gly	Val	Val	Ile	Pro	Asn	Ile	Thr	Asn	Gly	Tyr
			100					105					110		
Phe	Ser	Ser	Leu	Ala	Lys	Gly	Ile	Asp	Asp	Ile	Ala	Glu	Met	Tyr	Lys
		115					120					125			
Tyr	Asn	Ile	Val	Leu	Ala	Asn	Ser	Asp	Glu	Asp	Asn	Glu	Lys	Glu	Val
	130					135					140				
Ser	Val	Val	Asn	Thr	Leu	Phe	Ser	Lys	Gln	Val	Asp	Gly	Ile	Ile	Tyr
145					150				155						160
Met	Gly	Tyr	His	Leu	Thr	Asp	Lys	Ile	Arg	Ser	Glu	Phe	Ser	Arg	Ser
			165						170					175	
Arg	Thr	Pro	Ile	Val	Leu	Ala	Gly	Thr	Val	Asp	Val	Glu	His	Gln	Leu
			180					185					190		
Pro	Ser	Val	Asn	Ile	Asp	Tyr	Lys	Gln	Ala	Thr	Ile	Asp	Ala	Val	Ser
	195						200					205			
Tyr	Leu	Ala	Lys	Glu	Asn	Glu	Arg	Ile	Ala	Phe	Val	Ser	Gly	Pro	Leu
	210					215					220				
Val	Asp	Asp	Ile	Asn	Gly	Lys	Val	Arg	Leu	Val	Gly	Tyr	Lys	Glu	Thr
225					230				235						240
Leu	Lys	Lys	Ala	Gly	Ile	Thr	Tyr	Ser	Glu	Gly	Leu	Val	Phe	Glu	Ser
			245						250					255	
Lys	Tyr	Ser	Tyr	Asp	Asp	Gly	Tyr	Ala	Leu	Ala	Glu	Arg	Leu	Ile	Ser
			260					265					270		
Ser	Asn	Ala	Thr	Ala	Ala	Val	Val	Thr	Gly	Asp	Glu	Leu	Ala	Ala	Gly
		275					280					285			
Val	Leu	Asn	Gly	Leu	Ala	Asp	Lys	Gly	Val	Ser	Val	Pro	Glu	Asp	Phe
	290					295					300				
Glu	Ile	Ile	Thr	Ser	Asp	Asp	Ser	Gln	Ile	Ser	Arg	Phe	Thr	Arg	Pro
305					310					315					320
Asn	Leu	Thr	Thr	Ile	Ala	Gln	Pro	Leu	Tyr	Asp	Leu	Gly	Ala	Ile	Ser
			325						330					335	
Met	Arg	Met	Leu	Thr	Lys	Ile	Met	His	Lys	Glu	Glu	Leu	Glu	Glu	Arg
			340					345					350		
Glu	Val	Leu	Leu	Pro	His	Gly	Leu	Thr	Glu	Arg	Ser	Ser	Thr	Arg	Lys
		355					360					365			
Arg	Lys														
															370

(2) INFORMATION FOR SEQ ID NO:3125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...71

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3125:

```
Gln Arg Phe Leu Tyr Val Arg Glu Tyr Arg Thr Tyr Glu Glu Ile Ala
1          5          10          15
Ala Asp Phe Gly Ile His Glu Ser Asn Leu Leu Arg Arg Ser Gln Trp
          20          25          30
Val Glu Val Thr Leu Val Gln Ser Gly Val Thr Ile Ser Lys Thr His
          35          40          45
Leu Ser Ala Glu Asn Thr Val Ile Val Asp Ala Thr Glu Val Lys Ile
          50          55          60
Asn Arg Pro Lys Lys Ile Asn
65          70
```

(2) INFORMATION FOR SEQ ID NO:3126:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 132 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...132

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3126:

```
Gln Arg Asn Phe Ala Tyr Asn Leu Ser Thr Ser Pro Asn Leu Glu Gln
1          5          10          15
Val Lys Ala Met Leu Asn Gln Ala Phe Thr Glu Lys His Tyr Glu Asn
          20          25          30
Thr Ile Leu His Ser Asp Gln Gly Trp Gln Tyr Gln His Asp Phe Tyr
          35          40          45
His Arg Phe Leu Glu Ser Lys Gly Ile Gln Pro Ser Met Ser Arg Lys
          50          55          60
Gly Asn Ser Pro Asp Asn Gly Met Met Glu Ser Phe Phe Gly Ile Leu
65          70          75          80
Lys Ser Glu Met Phe Tyr Gly Tyr Glu Lys Asn Phe Arg Ser Leu Glu
          85          90          95
Asn Leu Glu Gln Ala Ile Val Asp Tyr Ile Asp Tyr Tyr Asn Asn Lys
          100          105          110
Arg Ile Lys Val Lys Leu Lys Gly Leu Ser Pro Val Gln Tyr Arg Thr
          115          120          125
Lys Ser Phe Gly
130
```

(2) INFORMATION FOR SEQ ID NO:3127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...129

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3127:

Ala	Ile	Phe	Leu	Thr	Val	Leu	Lys	Thr	Met	Val	Lys	Gln	Leu	Val	Gln
1			5					10					15		
Gln	Pro	Arg	Asn	Asn	Thr	Gly	Ser	Lys	Tyr	Pro	Tyr	Thr	Ile	Asp	Val
		20					25					30			
Thr	Gly	Glu	Val	Gly	Asp	Leu	Lys	Gln	Gly	Phe	Ser	Val	Asn	Ile	Glu
	35					40					45				
Val	Lys	Ser	Lys	Thr	Lys	Ala	Ile	Leu	Val	Pro	Val	Ser	Ser	Leu	Val
	50					55				60					
Met	Asp	Asp	Ser	Lys	Asn	Tyr	Val	Trp	Ile	Val	Asp	Glu	Gln	Gln	Lys
65					70					75				80	
Ala	Lys	Lys	Val	Glu	Val	Ser	Leu	Gly	Asn	Ala	Asp	Ala	Glu	Asn	Gln
			85					90					95		
Glu	Ile	Thr	Ser	Gly	Leu	Thr	Asn	Gly	Ala	Lys	Val	Ile	Ser	Asn	Pro
			100					105				110			
Thr	Ser	Ser	Leu	Glu	Glu	Gly	Lys	Glu	Val	Lys	Ala	Asp	Glu	Ala	Thr
			115				120					125			
Asn															

(2) INFORMATION FOR SEQ ID NO:3128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...223

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3128:

Trp	Pro	Phe	Leu	Leu	Ser	Thr	Trp	Ala	Thr	Arg	Leu	Ser	Arg	Trp	Ile
1			5						10					15	
Leu	Arg	Arg	Ile	Ala	Arg	Pro	Leu	Ala	Trp	Arg	Lys	Ser	Leu	Trp	His
			20					25					30		
Leu	Ile	Thr	Met	Trp	Thr	Pro	Ser	Val	Ser	Trp	Gln	Thr	Val	Ala	Met
		35					40					45			
Ser	Ser	Leu	Met	Ser	Leu	Lys	Met	Ser	Thr	Leu	Thr	Val	Trp	Met	Pro
	50					55					60				
Leu	Ser	Arg	Met	Thr	Thr	Pro	Ser	Arg	Asn	Arg	Phe	Cys	Arg	Ile	Ser
65					70				75					80	
Gln	Asn	Arg	Ile	Leu	Glu	Lys	Asp	Phe	Leu	Ser	Asn	Lys	Ala	Gln	Val
			85					90						95	
Thr	Val	Ala	Pro	Tyr	Lys	Val	Val	Thr	Ser	Ser	Leu	Asp	Leu	Ala	Asp
		100						105					110		
Ile	Asp	Met	Ser	Lys	Asn	Tyr	Val	Leu	Lys	Thr	Ala	Thr	Gly	Gly	Tyr
	115					120						125			
Asp	Gly	His	Gly	Gln	Lys	Val	Ile	Arg	Ser	Glu	Ala	Asp	Leu	Glu	Ala
	130					135					140				
Ala	Tyr	Ala	Leu	Ala	Asp	Ser	Asp	Ser	Cys	Val	Leu	Glu	Glu	Phe	Val
145					150					155					160
Asn	Phe	Asp	Leu	Glu	Ile	Ser	Val	Ile	Val	Ser	Gly	Asn	Gly	Lys	Glu
			165					170						175	
Val	Thr	Phe	Phe	Pro	Val	Gln	Glu	Asn	Ile	His	Arg	Asn	Asn	Ile	Leu
		180						185					190		
Ser	Lys	Thr	Ile	Val	Pro	Ala	Arg	Ile	Ser	Glu	Ser	Leu	Val	Asp	Asn
	195					200						205			
His	Lys	Thr	Met	Ala	Val	Glu	Ser	Gln	Asn	Lys	Thr	Gln	Leu	Val	
	210					215					220				

(2) INFORMATION FOR SEQ ID NO:3129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...283

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3129:

Lys	Gly	Asn	Phe	Met	Ile	Ile	Lys	Arg	Ile	Leu	Asn	His	Asn	Ala	Val
1			5						10					15	
Ile	Ala	Gln	Ser	Lys	Lys	Asp	Ile	Asp	Ile	Leu	Leu	Phe	Gly	Arg	Gly
		20						25					30		
Ile	Ala	Phe	Gly	Arg	Lys	Thr	Gly	Asp	Lys	Val	Asn	Pro	Ile	Asp	Ile
		35				40						45			

Glu	Lys	Ser	Phe	Phe	Leu	Lys	Asn	Arg	Asp	Asn	Met	Thr	Arg	Phe	Thr
50						55				60					
Glu	Met	Phe	Ile	Asn	Val	Pro	Leu	Glu	Leu	Val	Tyr	Ile	Thr	Glu	Lys
65					70					75				80	
Ile	Ile	Asn	Leu	Gly	Lys	Ile	Thr	Leu	Gly	Asn	Asn	Phe	Asp	Glu	Ile
			85						90					95	
Ile	Tyr	Ile	Asn	Leu	Thr	Asp	His	Ile	Ser	Ser	Ser	Ile	Glu	Arg	Tyr
			100					105					110		
Lys	Glu	Gly	Ile	Ile	Ile	Ser	Asn	Pro	Leu	Arg	Trp	Glu	Ile	Ser	Lys
		115					120					125			
Tyr	Tyr	Lys	Glu	Glu	Phe	Glu	Leu	Gly	Lys	Arg	Ala	Leu	Gln	Ile	Ile
		130					135				140				
Lys	Lys	Glu	Leu	Gly	Ile	Glu	Leu	Pro	Ile	Asp	Glu	Ala	Ala	Phe	Ile
145					150					155				160	
Ala	Leu	His	Phe	Val	Asn	Ala	Asn	Leu	Glu	Asn	Asn	Phe	Gln	Glu	Ser
				165					170					175	
Tyr	Lys	Ile	Thr	Glu	Ile	Ile	Met	Gly	Ile	Glu	Lys	Ile	Ile	Gln	Asp
			180					185					190		
Phe	Tyr	Cys	Thr	Glu	Phe	Asn	Gln	Asp	Ser	Ile	Asp	Tyr	Tyr	Arg	Phe
		195					200					205			
Ile	Thr	His	Ile	Lys	Leu	Phe	Ala	His	Arg	Leu	Val	Glu	Asn	Thr	Thr
		210					215					220			
Tyr	Cys	Asp	Asp	Asp	Asp	Glu	Asp	Leu	Leu	Ala	Leu	Met	Lys	Asn	Lys
225					230					235				240	
Tyr	Pro	Arg	Glu	Tyr	Glu	Cys	Gly	Glu	Gln	Val	Ala	Met	Phe	Ile	Gln
				245					250					255	
Thr	Glu	Tyr	Asn	Tyr	Leu	Leu	Thr	Ser	Ser	Glu	Leu	Val	Tyr	Leu	Met
			260					265					270		
Ala	Asn	Ile	Arg	Arg	Leu	Thr	Lys	Asn	Leu	Asp					
		275					280								

(2) INFORMATION FOR SEQ ID NO:3130:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 452 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...452
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3130:

Phe	Phe	Ser	Tyr	Cys	Phe	Asn	Pro	Phe	Ile	Cys	Gly	Lys	Ile	Arg	Leu
1				5					10					15	
Leu	Ser	Leu	Lys	Arg	Ile	Pro	Met	Lys	Leu	Gln	Lys	Pro	Lys	Gly	Thr
			20					25					30		
Gln	Asp	Ile	Leu	Pro	Ala	Glu	Ser	Ala	Lys	Trp	Gln	Tyr	Val	Glu	Gly
		35					40					45			

Phe	Ala	Arg	Glu	Ile	Phe	Lys	Arg	Tyr	Asn	Tyr	Ala	Glu	Val	Arg	Thr
50					55					60					
Pro	Ile	Phe	Glu	His	Tyr	Glu	Val	Ile	Ser	Arg	Ser	Val	Gly	Asp	Thr
65					70					75					80
Thr	Asp	Ile	Val	Thr	Lys	Glu	Met	Tyr	Asp	Phe	Tyr	Asp	Lys	Gly	Asp
				85					90					95	
Arg	His	Ile	Thr	Leu	Arg	Pro	Glu	Gly	Thr	Ala	Pro	Val	Val	Arg	Ser
			100					105					110		
Tyr	Val	Glu	Asn	Lys	Leu	Phe	Ala	Pro	Glu	Val	Gln	Lys	Pro	Ser	Lys
		115				120						125			
Phe	Tyr	Tyr	Met	Gly	Pro	Met	Phe	Arg	Tyr	Glu	Arg	Pro	Gln	Ala	Gly
	130					135					140				
Arg	Leu	Arg	Gln	Phe	His	Gln	Ile	Gly	Val	Glu	Cys	Phe	Gly	Ser	Ser
145					150					155					160
Asn	Pro	Ala	Thr	Asp	Val	Glu	Thr	Ile	Ser	Met	Ala	Ala	Tyr	Phe	Leu
			165						170					175	
Lys	Glu	Ile	Gly	Ile	Gln	Gly	Val	Lys	Leu	His	Leu	Asn	Thr	Leu	Gly
			180					185					190		
Asn	Pro	Glu	Ser	Arg	Ala	Ala	Tyr	Arg	Gln	Ala	Leu	Ile	Asp	Tyr	Leu
	195						200					205			
Thr	Pro	Leu	Lys	Glu	Thr	Leu	Ser	Lys	Asp	Ser	Gln	Arg	Arg	Leu	Glu
	210					215					220				
Glu	Asn	Pro	Leu	Arg	Val	Leu	Asp	Ser	Lys	Glu	Lys	Glu	Asp	Lys	Val
225					230					235					240
Ala	Val	Glu	Asn	Ala	Pro	Ser	Ile	Leu	Asp	Phe	Leu	Asp	Glu	Glu	Ser
			245						250					255	
Gln	Thr	His	Phe	Asp	Ala	Val	Arg	Gln	Met	Leu	Glu	Asn	Leu	Gly	Val
		260						265					270		
Asp	Tyr	Ile	Ile	Asp	Thr	Asn	Met	Val	Arg	Gly	Leu	Asp	Tyr	Tyr	Asn
	275					280					285				
His	Thr	Ile	Phe	Glu	Phe	Ile	Thr	Glu	Ile	Glu	Gly	Asn	Asp	Leu	Thr
	290					295					300				
Val	Cys	Ala	Gly	Gly	Arg	Tyr	Asp	Gly	Leu	Val	Ala	Tyr	Phe	Gly	Gly
305					310					315					320
Pro	Glu	Thr	Ala	Gly	Phe	Gly	Phe	Gly	Leu	Gly	Val	Glu	Arg	Leu	Leu
			325					330						335	
Leu	Ile	Leu	Glu	Lys	Gln	Gly	Val	Ala	Leu	Pro	Ile	Glu	Asn	Ala	Leu
		340						345					350		
Asp	Val	Tyr	Ile	Ala	Val	Leu	Gly	Asp	Gly	Ala	Asn	Val	Lys	Ala	Leu
	355						360					365			
Glu	Leu	Val	Gln	Ala	Leu	Arg	Gln	Gln	Gly	Phe	Lys	Ala	Glu	Arg	Asp
	370					375					380				
Tyr	Leu	Asn	Arg	Lys	Leu	Lys	Ala	Gln	Phe	Lys	Ser	Ala	Asp	Val	Phe
385					390					395					400
Ala	Ala	Lys	Thr	Leu	Ile	Thr	Leu	Gly	Glu	Ser	Glu	Val	Glu	Ser	Gly
			405						410					415	
Gln	Val	Thr	Val	Lys	Asn	Asn	Gln	Thr	Arg	Glu	Glu	Val	Gln	Val	Ser
		420						425					430		
Leu	Glu	Thr	Ile	Ser	Gln	Asn	Phe	Ser	Glu	Ile	Phe	Glu	Lys	Leu	Gly
	435						440					445			
Phe	Tyr	Thr	Gln												
	450														

(2) INFORMATION FOR SEQ ID NO:3131:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 244 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...244

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3131:

Asn	Asn	Ser	Tyr	Leu	Leu	Glu	Arg	Trp	Arg	Asp	Met	Arg	Trp	Leu	Phe
1				5					10					15	
Arg	Leu	Ile	Gly	Ala	Phe	Phe	Ser	Phe	Val	Trp	Arg	Leu	Phe	Trp	Arg
			20					25					30		
Leu	Val	Trp	Ile	Val	Val	Leu	Leu	Cys	Val	Leu	Ala	Phe	Gly	Leu	Leu
		35					40					45			
Trp	Tyr	Leu	Asn	Gly	Asp	Phe	Gln	Gly	Ala	Leu	Lys	Gln	Ala	Glu	Arg
	50					55					60				
Ser	Val	Lys	Ile	Gly	Gln	Gln	Ser	Ile	Asp	Gln	Trp	Glu	Lys	Thr	Gly
65					70					75					80
Gln	Leu	Pro	Lys	Leu	Ser	Gln	Thr	Asp	Ser	His	Gln	His	Ser	Glu	Gly
				85					90					95	
Arg	Trp	Pro	Gln	Ala	Ser	Ala	Arg	Ile	Tyr	Leu	Asp	Pro	Gln	Met	Asp
			100					105					110		
Ser	Arg	Phe	Gln	Glu	Ala	Tyr	Leu	Glu	Ala	Ile	Gln	Asn	Trp	Asn	Gln
		115					120					125			
Thr	Gly	Ala	Phe	Asn	Phe	Glu	Leu	Val	Thr	Glu	Ser	Ser	Lys	Ala	Asp
	130					135					140				
Ile	Thr	Ala	Thr	Glu	Met	Asn	Asp	Gly	Gly	Thr	Pro	Val	Ala	Gly	Glu
145					150					155					160
Ala	Glu	Ser	Gln	Thr	Asn	Leu	Leu	Thr	Gly	Gln	Phe	Leu	Ser	Val	Thr
			165						170					175	
Val	Arg	Leu	Asn	His	Tyr	Tyr	Leu	Ser	Asn	Pro	Tyr	Tyr	Gly	Tyr	Ser
		180						185					190		
Tyr	Glu	Arg	Leu	Val	His	Thr	Ala	Glu	His	Glu	Leu	Gly	His	Ala	Ile
		195					200					205			
Gly	Leu	Asp	His	Thr	Asp	Glu	Lys	Ser	Val	Met	Gln	Pro	Ala	Gly	Ser
	210					215					220				
Phe	Tyr	Gly	Ile	Gln	Glu	Glu	Asp	Val	Ala	Asn	Leu	Arg	Lys	Ile	Tyr
225					230					235					240
Glu	Thr	Ser	Glu												

(2) INFORMATION FOR SEQ ID NO:3132:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 93 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...93
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3132:

Leu	Arg	Phe	Leu	His	Ser	Ile	Asn	Phe	Leu	Glu	Leu	Val	Val	Val	Thr
1				5					10					15	
Arg	Val	Thr	Arg	Gln	Leu	Leu	Ile	Phe	His	Met	Ile	Asp	Asn	Ile	Asp
			20					25					30		
Asn	Val	Ile	Glu	Glu	Trp	Asn	Ile	Val	Arg	Asn	Glu	Asn	Lys	Gly	Ile
		35				40					45				
Leu	Ile	Val	Leu	Glu	Ile	Ala	Leu	Glu	Pro	Ile	Asn	Met	Leu	Ser	Ile
	50				55					60					
Gln	Val	Val	Gly	Arg	Leu	Val	Gln	Gln	Gln	Asn	Ile	Arg	Leu	Phe	Lys
65				70					75						80
Glu	Lys	Phe	Cys	Gln	Lys	His	Leu	Gly	Ser	Leu	Pro	Thr			
			85					90							

(2) INFORMATION FOR SEQ ID NO:3133:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 269 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...269
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3133:

Thr	Glu	Ser	Tyr	Asn	Lys	Arg	Val	Ile	Lys	Ala	Asn	Thr	Met	Thr	Gly
1				5				10					15		
Phe	Ile	His	Phe	Lys	Asp	Leu	Asp	Gly	Ala	Ser	Val	Gly	Asn	Ser	His
			20					25					30		
Pro	Ser	Thr	Ser	Pro	Gly	Gly	Thr	His	Tyr	Phe	Lys	Thr	Lys	Ser	Ala
		35			40						45				
Ile	Lys	Thr	Glu	Pro	Leu	Ala	Ser	Gly	Thr	Val	Ile	Asp	Tyr	Tyr	Tyr
	50			55				60							
Pro	Gly	Glu	Lys	Val	His	Tyr	Asp	Gln	Ile	Leu	Glu	Lys	Asp	Gly	Tyr
65				70				75							80

Lys	Trp	Leu	Ser	Tyr	Thr	Ala	Tyr	Asn	Gly	Ser	Tyr	Arg	Tyr	Val	Gln
				85					90					95	
Leu	Glu	Ala	Val	Asn	Lys	Asn	Pro	Leu	Gly	Asn	Ser	Val	Leu	Ser	Ser
			100					105					110		
Thr	Gly	Gly	Thr	His	Tyr	Phe	Lys	Thr	Lys	Ser	Ala	Ile	Lys	Thr	Glu
		115					120					125			
Pro	Leu	Val	Ser	Ala	Thr	Val	Ile	Asp	Tyr	Tyr	Tyr	Pro	Gly	Glu	Lys
		130				135					140				
Val	His	Tyr	Asp	Gln	Ile	Leu	Glu	Lys	Asp	Gly	Tyr	Lys	Trp	Leu	Ser
145					150					155					160
Tyr	Thr	Ala	Tyr	Asn	Gly	Ser	Arg	Arg	Tyr	Ile	Gln	Leu	Glu	Gly	Val
				165					170					175	
Thr	Ser	Ser	Gln	Asn	Tyr	Gln	Asn	Gln	Ser	Gly	Asn	Ile	Ser	Ser	Tyr
			180					185					190		
Gly	Ser	Asn	Asn	Ser	Ser	Thr	Val	Gly	Trp	Lys	Lys	Ile	Asn	Gly	Ser
		195					200					205			
Trp	Tyr	His	Phe	Lys	Ser	Asn	Gly	Ser	Lys	Ser	Thr	Gly	Trp	Leu	Lys
	210					215					220				
Asp	Gly	Ser	Ser	Trp	Tyr	Tyr	Leu	Lys	Leu	Ser	Gly	Glu	Met	Gln	Thr
225					230					235					240
Gly	Trp	Leu	Lys	Glu	Asn	Gly	Ser	Trp	Tyr	Tyr	Leu	Gly	Ser	Ser	Gly
			245						250					255	
Ala	Met	Gln	Thr	Gly	Ser	Thr	Ser	Ile	Val	Arg	Arg	Ala			
			260					265							

(2) INFORMATION FOR SEQ ID NO:3134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3134:

Met	Asn	Thr	Tyr	Glu	Gly	Asn	Leu	Val	Ala	Asn	Asn	Ile	Lys	Ile	Gly
1				5					10					15	
Ile	Val	Val	Ala	Arg	Phe	Asn	Glu	Phe	Ile	Thr	Ser	Lys	Leu	Leu	Ser
			20					25					30		
Gly	Ala	Leu	Asp	Asn	Leu	Lys	Arg	Glu	Asn	Val	Asn	Glu	Lys	Asp	Ile
		35				40					45				
Glu	Val	Ala	Trp	Val	Pro	Gly	Ala	Phe	Glu	Ile	Pro	Leu	Ile	Ala	Ser
		50				55					60				
Lys	Met	Ala	Lys	Ser	Lys	Lys	Tyr	Asp	Ala	Ile	Ile	Cys	Leu	Gly	Ala
65					70				75					80	
Val	Ile	Arg	Gly	Asn	Thr	Ser	His	Tyr	Asp	Tyr	Val	Cys	Ser	Glu	Val

				85					90					95					
Ser	Lys	Gly	Ile	Ala	Gln	Ile	Ser	Leu	Asn	Ser	Glu	Ile	Pro	Val	Met				
				100					105					110					
Phe	Gly	Val	Leu	Thr	Thr	Asp	Thr	Ile	Glu	Gln	Ala	Ile	Glu	Arg	Ala				
				115				120					125						
Gly	Thr	Lys	Ala	Gly	Asn	Lys	Gly	Ser	Glu	Cys	Ala	Gln	Gly	Ala	Ile				
				130			135				140								
Glu	Met	Val	Asn	Leu	Ile	Arg	Thr	Leu	Asp	Ala									
145						150				155									

(2) INFORMATION FOR SEQ ID NO:3135:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 98 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...98
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3135:

Val	Ser	Thr	Tyr	Pro	Phe	Leu	Lys	Glu	Lys	Ser	Glu	Asp	Ile	Trp	Pro				
1				5					10					15					
Ser	Ser	Asp	Phe	Phe	Tyr	Phe	Pro	Gln	Phe	His	Val	Ile	His	Leu	Asp				
			20					25					30						
Asp	Glu	Gln	Ile	Ser	Cys	Ser	Phe	Leu	Tyr	Gly	Ile	Asp	Lys	Met	Pro				
			35				40					45							
Gln	Val	Ala	Arg	Thr	Leu	Asp	Leu	Pro	Arg	Leu	Thr	Asp	Leu	Leu	Leu				
			50			55					60								
Ser	Glu	Gly	Asp	Ser	Phe	Asp	Pro	Asn	Gly	Ser	Phe	Pro	Leu	Gln	Ile				
65					70					75				80					
Phe	Pro	Phe	Leu	Leu	Asn	Ser	Val	Leu	Val	Ala	Glu	Leu	Leu	Ala	Leu				
				85					90					95					
Ala	Phe																		

(2) INFORMATION FOR SEQ ID NO:3136:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 320 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...320

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3136:

Met	Glu	Thr	Tyr	Tyr	Lys	Ala	Ile	Asn	Trp	Asn	Ala	Ile	Glu	Asp	Val
1				5				10					15		
Ile	Asp	Lys	Ser	Thr	Trp	Glu	Lys	Leu	Thr	Glu	Gln	Phe	Trp	Leu	Asp
		20					25					30			
Thr	Arg	Ile	Pro	Leu	Ser	Asn	Asp	Leu	Asp	Asp	Trp	Arg	Lys	Leu	Ser
		35				40					45				
Asn	Lys	Glu	Lys	Asp	Leu	Val	Gly	Lys	Val	Phe	Gly	Gly	Leu	Thr	Leu
	50					55				60					
Leu	Asp	Thr	Met	Gln	Ser	Glu	Thr	Gly	Val	Gln	Ala	Leu	Arg	Ala	Asp
65				70				75						80	
Ile	Arg	Thr	Pro	His	Glu	Glu	Ala	Val	Phe	Asn	Asn	Ile	Gln	Phe	Met
			85					90					95		
Glu	Ser	Val	His	Ala	Lys	Ser	Tyr	Ser	Ser	Ile	Phe	Ser	Thr	Leu	Asn
		100					105						110		
Thr	Lys	Ala	Glu	Ile	Glu	Glu	Ile	Phe	Glu	Trp	Thr	Asn	Thr	Asn	Pro
	115					120						125			
Tyr	Leu	Gln	Lys	Lys	Ala	Glu	Ile	Val	Asn	Glu	Ile	Tyr	Leu	Asn	Gly
	130					135					140				
Ser	Pro	Leu	Glu	Lys	Lys	Val	Ala	Ser	Val	Phe	Leu	Glu	Thr	Phe	Leu
145				150						155					160
Phe	Tyr	Ser	Gly	Phe	Phe	Thr	Pro	Leu	Tyr	Tyr	Leu	Gly	Asn	Asn	Lys
			165					170					175		
Leu	Ala	Asn	Val	Ala	Glu	Ile	Ile	Lys	Leu	Ile	Ile	Arg	Asp	Glu	Ser
		180						185					190		
Val	His	Gly	Thr	Tyr	Ile	Gly	Tyr	Lys	Phe	Gln	Leu	Gly	Phe	Asn	Glu
	195					200						205			
Leu	Pro	Glu	Glu	Glu	Gln	Glu	Lys	Leu	Lys	Glu	Trp	Met	Tyr	Asp	Leu
	210					215					220				
Leu	Tyr	Thr	Leu	Tyr	Glu	Asn	Glu	Glu	Gly	Tyr	Thr	Glu	Ser	Leu	Tyr
225				230						235					240
Asp	Gly	Val	Gly	Trp	Thr	Glu	Glu	Val	Lys	Thr	Phe	Leu	Arg	Tyr	Asn
			245						250					255	
Ala	Asn	Lys	Ala	Leu	Met	Asn	Met	Gly	Gln	Asp	Pro	Leu	Phe	Pro	Asp
		260						265					270		
Ser	Ala	Glu	Asp	Val	Asn	Pro	Ile	Val	Met	Asn	Gly	Ile	Ser	Thr	Gly
	275					280						285			
Thr	Ser	Asn	His	Asp	Phe	Phe	Ser	Gln	Val	Gly	Asn	Gly	Tyr	Leu	Leu
	290					295					300				
Gly	Glu	Val	Glu	Ala	Met	Gln	Asp	Asp	Asp	Tyr	Asn	Tyr	Gly	Leu	Asp
305					310					315					320

(2) INFORMATION FOR SEQ ID NO:3137:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...96

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3137:

Trp	Arg	Thr	Tyr	Val	Leu	Lys	Ile	Arg	Tyr	His	Lys	Gln	Phe	Lys	Lys
1				5					10					15	
Asp	Phe	Lys	Leu	Ala	Met	Lys	Arg	Gly	Leu	Lys	Ala	Glu	Leu	Leu	Glu
			20					25					30		
Glu	Val	Leu	Asn	Phe	Leu	Val	Gln	Glu	Lys	Glu	His	Pro	Ala	Arg	Tyr
			35				40					45			
Arg	Asp	His	Ser	Leu	Thr	Ala	Ser	Lys	His	Phe	Gln	Gly	Val	Arg	Glu
	50					55					60				
Cys	His	Thr	Gln	Pro	Asp	Trp	Leu	Leu	Val	Tyr	Lys	Val	Asp	Lys	Ser
65					70					75					80
Glu	Leu	Ile	Leu	Asn	Leu	Leu	Arg	Thr	Gly	Ser	His	Ser	Asp	Leu	Phe
				85					90					95	

(2) INFORMATION FOR SEQ ID NO:3138:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 331 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...331

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3138:

Val	Phe	Leu	Leu	Thr	Tyr	Pro	Phe	Tyr	Phe	Ile	Arg	Leu	Phe	Glu	Arg
1				5					10					15	
Leu	Leu	Tyr	Arg	Leu	Gln	Thr	Ser	Tyr	Tyr	Ala	Tyr	Tyr	Ala	Asn	Phe
			20					25					30		
Glu	Ser	Lys	Leu	Pro	Tyr	Phe	Thr	Tyr	Ile	Leu	Ser	Thr	Phe	Thr	Val
			35				40					45			
Tyr	Ala	Met	Cys	Met	Tyr	Leu	Ala	Thr	Lys	Pro	Lys	Lys	Leu	Gln	Ala
	50					55					60				
Thr	Ala	Val	Leu	Val	Ser	Phe	Ile	Ala	Ala	Asn	Thr	Ile	His	Leu	Ala
65					70					75					80
Ile	Gly	Thr	Arg	Asn	Pro	Phe	Ile	Leu	Ser	Ile	Leu	Phe	Ala	Phe	Val
				85					90					95	

Tyr	Tyr	Phe	Met	Arg	Glu	Gln	Thr	Glu	Lys	Gly	Lys	Trp	Ile	Gly	Phe	100	105	110
Lys	Glu	Lys	Leu	Ala	Ile	Phe	Val	Gly	Ser	Pro	Ile	Leu	Met	Leu	Ala	115	120	125
Met	Gly	Val	Leu	Asn	Tyr	Val	Arg	Asp	Asn	Val	Gln	Val	Ser	His	Thr	130	135	140
Gly	Phe	Trp	Asp	Ile	Leu	Leu	Asp	Phe	Ile	Tyr	Lys	Gln	Gly	Thr	Ser	145	150	155
Phe	Gly	Val	Leu	Ala	Arg	Gly	Phe	Leu	Phe	Asn	Ser	Ser	Leu	Pro	Tyr	165	170	175
Arg	Asp	Phe	Arg	Asn	Phe	Thr	Phe	Gly	Pro	Val	Leu	Asp	Tyr	Phe	Ala	180	185	190
Arg	Gly	Ser	Leu	Gly	Ala	Ile	Phe	Gly	Gly	Lys	Ala	Phe	Glu	His	Thr	195	200	205
Thr	Asn	Ser	Val	Glu	Leu	Ala	Ile	Asp	Ser	Asn	Ser	Tyr	Ala	His	Asn	210	215	220
Ile	Ser	Tyr	Leu	Val	Leu	Asn	Lys	Glu	Tyr	Leu	Lys	Gly	His	Gly	Ile	225	230	235
Glu	Ser	Ser	Tyr	Ile	Met	Glu	Leu	Tyr	Thr	Asp	Tyr	Gly	Met	Ile	Gly	245	250	255
Val	Phe	Leu	Leu	Ser	Phe	Leu	Leu	Gly	Val	Leu	Tyr	Ile	Ala	Met	Leu	260	265	270
Gln	Val	Ala	Tyr	Arg	Ser	Arg	Thr	Ile	Leu	Phe	Ala	Leu	Ser	Ile	Leu	275	280	285
Ile	Leu	Asn	Asn	Leu	Phe	Phe	Met	Pro	Arg	Ser	Ser	Phe	Ser	Glu	Ser	290	295	300
Phe	Phe	Asn	Leu	Phe	Thr	Met	Gln	Phe	Trp	Gly	Ile	Val	Leu	Val	Ile	305	310	315
Ile	Phe	Val	Ala	Lys	Met	Leu	Thr	Lys	Glu	Asn						325	330	

(2) INFORMATION FOR SEQ ID NO:3139:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 125 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...125
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3139:

Glu	Leu	Leu	Leu	Asp	Pro	Leu	Tyr	Arg	Leu	His	Val	Ser	Val	Ile	Phe	1	5	10	15
Leu	Glu	Arg	Glu	Gln	Ala	Ile	Ser	Thr	Glu	Xaa	Tyr	Leu	Ala	His	Leu	20	25	30	

Phe	Leu	His	Phe	His	Lys	Asn	Gln	Asp	His	Ile	Thr	Ser	Leu	Leu	Phe
	35					40						45			
Ser	Lys	Asn	Asp	Tyr	Phe	Leu	Arg	Gln	Leu	His	Lys	Glu	Leu	Glu	His
	50				55						60				
His	Val	Tyr	Ser	Val	Leu	Ala	Asp	Asn	Leu	Lys	Glu	Ala	His	Pro	Asn
65				70					75					80	
Met	Pro	Thr	Ser	Tyr	Leu	Gln	His	Leu	Val	Val	Ser	Asn	Phe	Ile	Glu
			85					90						95	
Thr	Leu	Thr	Trp	Trp	Leu	Lys	Lys	Gly	Gln	Asp	Phe	Thr	Gly	Gln	Glu
			100					105					110		
Val	Val	Gln	Phe	Tyr	Leu	Asp	Leu	Leu	Ile	Pro	Lys	Asn			
		115					120					125			

(2) INFORMATION FOR SEQ ID NO:3140:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 68 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...68
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3140:

Asn	Gly	Tyr	Tyr	Lys	Lys	Trp	Ser	Glu	Ile	Asp	Asp	Asp	Thr	Phe	Arg
1				5				10						15	
Lys	Ser	Phe	Tyr	Val	Ser	Ser	Ala	Leu	Pro	Cys	Cys	Val	Leu	Ser	Lys
		20					25					30			
Leu	Arg	Leu	Ala	Ser	Glu	Phe	Asp	Phe	His	Leu	Leu	Glu	Met	Lys	Leu
	35					40					45				
Met	Arg	Asp	Ile	Ser	Arg	His	Leu	Ser	Gln	Asp	Ile	Met	Glu	Asn	Asp
	50				55					60					
Lys	Lys	Ser	Ser												
65															

(2) INFORMATION FOR SEQ ID NO:3141:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 456 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...456

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3141:

Lys	Ile	Tyr	Tyr	Glu	Arg	Ala	Leu	Ile	Met	Leu	Leu	Asn	Phe	Leu	Phe
1				5					10					15	
Ile	Phe	Ile	Phe	Leu	Leu	Ile	Ile	Ile	Thr	Phe	Ile	Leu	Phe	Glu	Gly
			20					25					30		
Asp	Leu	Phe	Gln	Pro	Ala	Val	Ile	Leu	Thr	Leu	Ala	Tyr	Phe	Ile	Ser
		35					40					45			
Ile	Ala	Ser	Ala	Leu	Val	Asn	Arg	Asn	Val	Trp	Gly	Thr	Glu	Leu	His
	50					55					60				
Phe	Lys	Thr	Phe	Gly	Leu	Ile	Leu	Leu	Gly	Val	Ala	Thr	Phe	Ile	Ile
65					70					75					80
Val	Ser	Leu	Leu	Thr	Lys	Leu	Ser	Tyr	Lys	Pro	Lys	Val	Glu	Gly	Ile
				85					90					95	
Ser	Tyr	Lys	Glu	Leu	Lys	Glu	Ile	Asn	Pro	Ser	Lys	Ile	Ile	Tyr	Gly
			100					105					110		
Ile	Leu	Leu	Ile	Leu	Asn	Leu	Val	Met	Leu	Phe	Leu	Tyr	Ile	His	Glu
		115					120					125			
Ile	Gln	Lys	Val	Val	Leu	Phe	Ser	Gly	Arg	Gly	Phe	Ser	Asn	Ile	Thr
	130					135					140				
Asp	Leu	Ile	Ser	Asn	Tyr	Arg	Tyr	Leu	Ser	Tyr	Tyr	Ser	Asn	Glu	Val
145					150					155					160
Glu	Asp	Arg	Val	Ser	Gly	Met	Ile	Asn	Gln	Leu	Ala	Lys	Ile	Ile	Pro
				165					170					175	
Ala	Thr	Thr	Phe	Val	Ser	Leu	Tyr	Ile	Phe	Ile	Asn	Asn	Tyr	Phe	Ile
			180					185					190		
Thr	Lys	Gln	Ile	Lys	Lys	Asn	Phe	Ile	Tyr	Leu	Ile	Pro	Ile	Ala	Ile
		195				200						205			
Phe	Phe	Val	Tyr	Ala	Ile	Ile	Ser	Gly	Gly	Arg	Leu	Pro	Leu	Ile	Arg
	210					215					220				
Leu	Val	Ile	Gly	Thr	Leu	Leu	Ile	Leu	Tyr	Ile	Tyr	Ser	Val	Tyr	Gly
225					230					235					240
Ser	His	Lys	Ser	Gln	Leu	Thr	Arg	Ser	Phe	Lys	Met	Ile	Thr	Arg	Ser
				245					250					255	
Leu	Phe	Ala	Phe	Leu	Met	Leu	Ile	Val	Leu	Phe	Phe	Leu	Leu	Lys	Phe
		260						265					270		
Val	Leu	Gly	Arg	Ser	Ser	Gln	Glu	Asp	Phe	Ile	Ser	Tyr	Ile	Thr	Arg
		275					280					285			
Tyr	Met	Gly	Gly	Ser	Ile	Gln	Leu	Phe	Asp	Leu	Phe	Val	Ile	Asp	Pro
	290					295					300				
Ile	Arg	Arg	Asn	Lys	Glu	Leu	Gly	Ala	Glu	Thr	Phe	Ser	Gly	Ile	Tyr
305					310					315					320
Glu	Met	Leu	Ala	Lys	Leu	Gly	Phe	Asp	Asn	Asn	Ile	Ile	Lys	Gly	Leu
				325					330					335	
Glu	Trp	Arg	Ile	Ser	Pro	Asn	Tyr	Tyr	Ser	Leu	Gly	Asn	Val	Tyr	Thr
			340					345					350		
Ala	Ile	Arg	Arg	Tyr	Tyr	Ser	Asp	Phe	Gly	Val	Ile	Gly	Ile	Val	Ile
		355					360					365			
Cys	Gln	Ser	Phe	Thr	Ala	Trp	Leu	Tyr	Thr	Leu	Gly	Tyr	Glu	Lys	Ile
	370					375					380				
Arg	His	His	Ser	Leu	Val	Thr	Asn	Gly	Gln	Arg	Phe	Arg	Leu	Ile	Leu
385					390					395					400

Leu	Ala	Ala	Ser	Phe	Tyr	Pro	Leu	Phe	Leu	Asn	Ser	Ile	Glu	Asp	Val
				405					410					415	
Phe	Tyr	Ile	Ser	Met	Val	Thr	Ile	Gly	Tyr	Gly	Ile	Gln	Ile	Val	Ile
			420					425					430		
Phe	Tyr	Leu	Val	Phe	Trp	Val	Leu	Leu	Lys	Val	Gln	Val	Asp	Phe	Asn
		435					440					445			
Lys	Gly	Lys	Leu	Arg	Ile	Asn	Arg								
	450					455									

(2) INFORMATION FOR SEQ ID NO:3142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...292

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3142:

Ser	Leu	His	Tyr	Asp	Cys	Asp	Ser	Gly	Arg	Phe	Ser	Leu	Phe	Ser	Leu
1				5					10					15	
Asp	Trp	Ser	His	Pro	Met	Ile	Arg	Phe	Leu	Val	Leu	Ala	Gly	Tyr	Phe
			20					25					30		
Glu	Leu	Thr	Ile	Tyr	Leu	His	Leu	Ser	Gly	Lys	Leu	Asn	Gln	Tyr	Ile
		35					40					45			
Asn	Met	His	Tyr	Ser	Tyr	Leu	Ala	Tyr	Ile	Ser	Met	Val	Leu	Ser	Phe
	50					55				60					
Ile	Leu	Ala	Ile	Val	Gln	Leu	Tyr	Ile	Trp	Met	Lys	Gln	Val	Lys	Thr
65				70				75						80	
His	Ser	His	Leu	Asn	Ser	Arg	Leu	Ala	Lys	Met	Thr	Ser	Ile	Ser	Leu
			85					90					95		
Leu	Ala	Ile	Pro	Leu	Val	Ile	Gly	Leu	Thr	Phe	Pro	Thr	Val	Ser	Leu
			100					105					110		
Asp	Ser	Gln	Thr	Val	Ser	Ala	Lys	Gly	Tyr	His	Phe	Pro	Leu	Ser	Glu
		115					120					125			
Gly	Thr	Asp	Leu	Ala	Ile	Gln	Thr	Ser	Glu	Gly	Thr	Thr	Ser	Gln	Tyr
	130					135					140				
Leu	Lys	Pro	Asp	Thr	Ser	Ser	Tyr	Phe	Ser	Lys	Ser	Ala	Tyr	Glu	Lys
145					150				155					160	
Glu	Met	Arg	Thr	Ala	Ala	Asp	Lys	Tyr	Leu	Ser	Gln	Asp	Ser	Ile	Gln
			165					170					175		
Ile	Thr	Asn	Glu	Asn	Tyr	Met	Glu	Val	Met	Glu	Ala	Ile	Tyr	Asp	Tyr
		180					185					190			
Pro	Asp	Glu	Phe	Glu	Gly	Lys	Thr	Ile	Gln	Phe	Thr	Gly	Phe	Val	Tyr
	195					200						205			
Asn	Asp	Pro	Ser	His	Ala	Asn	Ser	Gln	Phe	Leu	Phe	Arg	Phe	Gly	Ile
	210					215						220			


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Ile His Cys Ile Ala Asp Ser Gly Val Tyr Gly Leu Leu Thr Lys Gly
225                230                235                240
Asn Thr Arg Gln Tyr Glu Asn Asn Thr Trp Ile Thr Ala Lys Gly Lys
                245                250                255
Leu Val Asn His Tyr His Lys Glu Leu Lys Gln Asn Leu Pro Thr Leu
                260                265                270
Glu Ile Asp Ser Phe Thr Lys Val Asp Lys Pro Glu Asn Pro Tyr Val
                275                280                285
Tyr Arg Ala Phe
290

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(2) INFORMATION FOR SEQ ID NO:3143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...458

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3143:

```

Arg Thr His Tyr Pro Ser Trp Ile Arg Leu Leu His Arg Arg Ile Gln
1                5                10                15
Met Lys Phe Arg Lys Leu Ala Cys Thr Val Leu Ala Gly Ala Ala Val
                20                25                30
Leu Gly Leu Ala Ala Cys Gly Asn Ser Gly Gly Ser Lys Asp Ala Ala
35                40                45
Lys Ser Gly Gly Asp Gly Ala Lys Thr Glu Ile Thr Trp Trp Ala Phe
50                55                60
Pro Val Phe Thr Gln Glu Lys Thr Gly Asp Gly Val Gly Thr Tyr Glu
65                70                75                80
Lys Ser Ile Ile Glu Ala Phe Glu Lys Ala Asn Pro Asp Ile Lys Val
                85                90                95
Lys Leu Glu Thr Ile Asp Phe Lys Ser Gly Pro Glu Lys Ile Thr Thr
100               105               110
Ala Ile Glu Ala Gly Thr Ala Pro Asp Val Leu Phe Asp Ala Pro Gly
115               120               125
Arg Ile Ile Gln Tyr Gly Lys Asn Gly Lys Leu Ala Glu Leu Asn Asp
130               135               140
Leu Phe Thr Asp Glu Phe Val Lys Asp Val Asn Asn Glu Asn Ile Val
145               150               155               160
Gln Ala Ser Lys Ala Gly Asp Lys Ala Tyr Met Tyr Pro Ile Ser Ser
165               170               175
Ala Pro Phe Tyr Met Ala Met Asn Lys Lys Met Leu Glu Asp Ala Gly
180               185               190
Val Ala Asn Leu Val Lys Glu Gly Trp Thr Thr Asp Asp Phe Glu Lys
195               200               205

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Val	Leu	Lys	Ala	Leu	Lys	Asp	Lys	Gly	Tyr	Thr	Pro	Gly	Ser	Leu	Phe
210						215					220				
Ser	Ser	Gly	Gln	Gly	Gly	Asp	Gln	Gly	Thr	Arg	Ala	Phe	Ile	Ser	Asn
225					230					235					240
Leu	Tyr	Ser	Gly	Ser	Val	Thr	Asp	Glu	Lys	Val	Ser	Lys	Tyr	Thr	Thr
			245						250					255	
Asp	Asp	Pro	Lys	Phe	Val	Lys	Gly	Leu	Glu	Lys	Ala	Thr	Ser	Trp	Ile
			260					265					270		
Lys	Asp	Asn	Leu	Ile	Asn	Asn	Gly	Ser	Gln	Phe	Asp	Gly	Gly	Ala	Asp
		275					280					285			
Ile	Gln	Asn	Phe	Ala	Asn	Gly	Gln	Thr	Ser	Tyr	Thr	Ile	Leu	Trp	Ala
	290					295					300				
Pro	Ala	Gln	Asn	Gly	Ile	Gln	Ala	Lys	Leu	Leu	Glu	Ala	Ser	Lys	Val
305					310					315					320
Glu	Val	Val	Glu	Val	Pro	Phe	Pro	Ser	Asp	Glu	Gly	Lys	Pro	Ala	Leu
			325						330					335	
Glu	Tyr	Leu	Val	Asn	Gly	Phe	Ala	Val	Phe	Asn	Asn	Lys	Asp	Asp	Lys
		340						345					350		
Lys	Val	Ala	Ala	Ser	Lys	Lys	Phe	Ile	Gln	Phe	Ile	Ala	Asp	Asp	Lys
		355					360					365			
Glu	Trp	Gly	Pro	Lys	Asp	Val	Val	Arg	Thr	Gly	Ala	Phe	Pro	Val	Arg
	370					375					380				
Thr	Ser	Phe	Gly	Lys	Leu	Tyr	Glu	Asp	Lys	Arg	Met	Glu	Thr	Ile	Ser
385					390					395					400
Gly	Trp	Thr	Gln	Tyr	Tyr	Ser	Pro	Tyr	Tyr	Asn	Thr	Ile	Asp	Gly	Phe
			405						410					415	
Ala	Glu	Met	Arg	Thr	Leu	Trp	Phe	Pro	Met	Leu	Gln	Ser	Val	Ser	Asn
			420					425					430		
Gly	Asp	Glu	Lys	Pro	Ala	Asp	Ala	Leu	Lys	Ala	Phe	Thr	Glu	Lys	Ala
		435					440					445			
Asn	Glu	Thr	Ile	Lys	Lys	Ala	Met	Lys	Gln						
	450					455									

(2) INFORMATION FOR SEQ ID NO:3144:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 202 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...202
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3144:

Val	Gly	Leu	Leu	Glu	Cys	Pro	Thr	Phe	Leu	Leu	Lys	Lys	Glu	Phe	Phe
1				5					10					15	
Met	Leu	Lys	Lys	Trp	Gln	Leu	Lys	Asp	Val	Ile	Leu	Leu	Ala	Phe	Leu
			20					25					30		

Ser	Ile	Phe	Phe	Gly	Gly	Val	Phe	Val	Gly	Ser	Gly	Tyr	Val	Tyr	Asn
		35					40					45			
Ile	Leu	Ser	Leu	Leu	Leu	Thr	Pro	Leu	Gly	Leu	Gln	Ala	Phe	Ala	Asn
	50					55					60				
Glu	Ile	Leu	Phe	Gly	Leu	Trp	Cys	Met	Ala	Ala	Pro	Ile	Ala	Ala	Ile
65					70					75					80
Phe	Val	Pro	Arg	Val	Gly	Ser	Ala	Thr	Ile	Gly	Glu	Val	Leu	Ala	Ala
				85					90					95	
Leu	Ala	Glu	Val	Leu	Tyr	Gly	Ser	Gln	Phe	Gly	Leu	Gly	Ala	Leu	Leu
			100					105					110		
Ser	Gly	Leu	Val	Gln	Gly	Leu	Gly	Ser	Glu	Phe	Gly	Phe	Ile	Val	Thr
	115					120						125			
Lys	Asn	Arg	Tyr	Glu	Ser	Trp	Leu	Ser	Leu	Thr	Ala	Asn	Ser	Ile	Gly
	130					135					140				
Val	Thr	Leu	Val	Ser	Phe	Val	Tyr	Glu	Tyr	Ile	Lys	Leu	Gly	Tyr	Tyr
145					150					155					160
Ala	Phe	Ser	Leu	Pro	Phe	Val	Leu	Ser	Leu	Leu	Val	Val	Arg	Phe	Ile
				165					170					175	
Ser	Val	Tyr	Phe	Phe	Cys	Thr	Ile	Leu	Val	Arg	Ala	Ile	Val	Lys	Leu
			180					185					190		
Tyr	His	Gln	Phe	Ala	Thr	Gly	Gly	Lys	Ala						
		195					200								

(2) INFORMATION FOR SEQ ID NO:3145:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 224 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...224

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3145:

Arg	Asp	Asn	Tyr	Tyr	Asn	Pro	Val	Ile	Val	Gln	Pro	Leu	Val	Leu	Ile
1				5					10					15	
Gly	Ala	Pro	Asp	Val	Lys	Glu	Met	Pro	Lys	Asp	Trp	Thr	Glu	Leu	Gly
			20					25					30		
Ser	Lys	Tyr	Lys	Gly	Lys	Tyr	Ser	Ile	Tyr	Gly	Leu	Gln	Gly	Gly	Thr
		35					40					45			
Gly	Arg	Ala	Ile	Leu	Ala	Ser	Ile	Leu	Val	Arg	Tyr	Leu	Asp	Glu	Lys
	50					55				60					
Gly	Asp	Leu	Gly	Val	Ser	Glu	Lys	Gly	Trp	Glu	Val	Ala	Lys	Glu	Tyr
65					70					75					80
Phe	Ala	Asn	Ala	Tyr	Thr	Leu	Gln	Lys	Gly	Glu	Ser	Ser	Val	Val	Lys
				85					90					95	
Ala	Leu	Asp	Lys	Glu	Ser	Pro	Ile	Gln	Tyr	Gly	Met	Ile	Trp	Gly	Ser
			100					105					110		

Gly	Ala	Leu	Ile	Gly	Gln	Lys	Glu	Gln	Asn	Val	Glu	Phe	Lys	Val	Met
		115					120					125			
Thr	Pro	Glu	Ile	Gly	Val	Pro	Phe	Val	Thr	Glu	Gln	Thr	Met	Val	Leu
		130					135				140				
Ser	Thr	Ser	Lys	Lys	Gln	Ala	Leu	Ala	Lys	Glu	Phe	Ile	Asp	Trp	Phe
145					150					155					160
Gly	Gln	Ser	Glu	Ile	Gln	Val	Glu	Tyr	Ser	Lys	Lys	Phe	Gly	Ser	Ile
				165					170					175	
Pro	Ala	Asn	Lys	Asp	Ala	Leu	Lys	Glu	Leu	Pro	Glu	Asp	Thr	Lys	Lys
			180					185					190		
Phe	Val	Asp	Gln	Val	Lys	Pro	Gln	Asn	Ile	Asp	Trp	Glu	Ala	Val	Gly
		195					200					205			
Lys	His	Leu	Asp	Glu	Trp	Val	Glu	Lys	Ala	Glu	Leu	Glu	Tyr	Val	Lys
	210					215					220				

(2) INFORMATION FOR SEQ ID NO:3146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...87

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3146:

Asn	Met	Asn	Tyr	Phe	Arg	Lys	Arg	Arg	Glu	Arg	Gln	Ala	Lys	Ser	Asn
1				5					10					15	
Ser	Gly	Ile	Tyr	Cys	Pro	Ala	Ala	Asn	Arg	Ser	Lys	Ile	Gln	Tyr	Glu
		20					25					30			
Thr	Lys	Glu	Lys	Ala	Asp	His	Ala	Val	Gln	Tyr	Asp	Asn	Gly	Gly	Leu
		35				40					45				
Val	Arg	Ser	Tyr	Tyr	Cys	Arg	Thr	Cys	Ala	Cys	Trp	His	Thr	Thr	Ser
		50				55				60					
Lys	Ser	Asn	Lys	Pro	Pro	Leu	Ser	Leu	Lys	Asn	Tyr	Gly	Leu	Lys	Leu
65				70					75						80
Phe	Gly	Leu	Asp	Lys	Ser	Glu									
				85											

(2) INFORMATION FOR SEQ ID NO:3147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...284

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3147:

Gln	His	Leu	Leu	His	His	Gln	Lys	Val	Gly	Lys	Ser	Lys	Met	Thr	Asn
1				5					10					15	
Ser	Asn	Tyr	Lys	Leu	Thr	Lys	Glu	Asp	Phe	Asn	Gln	Ile	Asn	Lys	Arg
			20					25					30		
Ser	Leu	Phe	Thr	Phe	Gln	Leu	Gly	Trp	Asn	Tyr	Glu	Arg	Met	Gln	Ala
		35					40					45			
Ser	Gly	Tyr	Leu	Tyr	Met	Ile	Leu	Pro	Gln	Leu	Arg	Lys	Met	Tyr	Gly
	50				55						60				
Asp	Gly	Thr	Pro	Glu	Leu	Lys	Glu	Met	Met	Lys	Val	His	Thr	Gln	Phe
65					70					75				80	
Phe	Asn	Thr	Ser	Pro	Phe	Phe	His	Thr	Ile	Ile	Ala	Gly	Phe	Asp	Leu
				85					90					95	
Ala	Met	Glu	Glu	Lys	Asp	Gly	Val	Gly	Ser	Lys	Asp	Ala	Val	Asn	Gly
			100					105					110		
Ile	Lys	Thr	Gly	Leu	Met	Gly	Pro	Phe	Ala	Pro	Leu	Gly	Asp	Thr	Ile
		115				120						125			
Phe	Gly	Ser	Leu	Val	Pro	Ala	Ile	Met	Gly	Ser	Val	Ala	Ala	Thr	Met
	130					135					140				
Ala	Ile	Ala	Gly	Gln	Pro	Trp	Gly	Ile	Phe	Leu	Trp	Ile	Ala	Val	Ala
145					150					155				160	
Val	Ala	Tyr	Asp	Ile	Phe	Arg	Trp	Lys	Gln	Leu	Glu	Phe	Ala	Tyr	Lys
			165						170					175	
Glu	Gly	Val	Asn	Leu	Ile	Asn	Asn	Met	Gln	Ser	Thr	Leu	Thr	Ala	Leu
			180					185					190		
Ile	Asp	Ala	Ala	Ser	Val	Leu	Gly	Val	Phe	Met	Met	Gly	Ala	Leu	Val
	195					200						205			
Ala	Thr	Val	Ile	Asn	Phe	Glu	Ile	Ser	Tyr	Lys	Leu	Pro	Ile	Gly	Glu
	210				215					220					
Lys	Met	Ile	Asp	Phe	Gln	Asp	Ile	Leu	Asn	Gln	Ile	Phe	Pro	Arg	Leu
225					230					235				240	
Leu	Pro	Ala	Ile	Phe	Thr	Ala	Phe	Ile	Phe	Trp	Leu	Leu	Gly	Lys	Lys
			245						250					255	
Gly	Met	Asn	Ser	Thr	Lys	Ala	Ile	Gly	Ile	Ile	Ile	Val	Leu	Ala	Leu
		260						265					270		
Ala	Leu	Ser	Ala	Leu	Gly	His	Phe	Ala	Leu	Gly	Met				
	275						280								

(2) INFORMATION FOR SEQ ID NO:3148:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 510 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...510

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3148:

Lys	Leu	Leu	Leu	Ser	Leu	Thr	Ile	Arg	Lys	Lys	Asn	Ala	Phe	Ser	Ser
1				5					10					15	
Phe	Gly	Leu	Arg	Phe	Ile	Ile	Arg	Val	Ser	Lys	Ser	Gly	Gly	Lys	Lys
			20					25					30		
Met	Thr	Thr	Phe	Lys	Asp	Gly	Phe	Leu	Trp	Gly	Gly	Ala	Val	Ala	Ala
			35				40					45			
His	Gln	Leu	Glu	Gly	Gly	Trp	Gln	Glu	Gly	Gly	Lys	Gly	Ile	Ser	Val
	50					55					60				
Ala	Asp	Val	Met	Thr	Ala	Gly	Arg	His	Gly	Val	Ala	Arg	Glu	Ile	Thr
65					70					75				80	
Leu	Gly	Val	Leu	Glu	Gly	Lys	Tyr	Tyr	Pro	Asn	His	Glu	Ala	Ile	Asp
			85						90					95	
Phe	Tyr	His	Arg	Tyr	Lys	Glu	Asp	Ile	Ala	Leu	Phe	Ala	Glu	Met	Gly
			100					105					110		
Phe	Lys	Cys	Phe	Arg	Thr	Ser	Ile	Ala	Trp	Thr	Arg	Ile	Phe	Pro	Lys
		115					120					125			
Gly	Asp	Glu	Leu	Glu	Pro	Asn	Glu	Glu	Gly	Leu	Gln	Phe	Tyr	Asp	Asn
	130					135					140				
Leu	Phe	Asp	Glu	Cys	Leu	Lys	Asn	Gly	Ile	Glu	Pro	Val	Ile	Thr	Leu
145					150					155				160	
Ser	His	Phe	Glu	Met	Pro	Tyr	His	Leu	Val	Thr	Glu	Tyr	Gly	Gly	Trp
			165						170				175		
Lys	Asn	Arg	Lys	Leu	Ile	Asp	Phe	Phe	Ala	Arg	Phe	Ala	Glu	Val	Ile
			180					185					190		
Phe	Lys	Arg	Tyr	Lys	Asp	Lys	Val	Lys	Tyr	Trp	Met	Thr	Phe	Asn	Glu
	195						200					205			
Ile	Asn	Asn	Gln	Ala	Asn	Tyr	Gln	Glu	Asp	Phe	Ala	Pro	Phe	Thr	Asn
	210					215					220				
Ser	Gly	Ile	Val	Tyr	Glu	Gly	Asp	Asn	Arg	Glu	Ala	Ile	Met	Tyr	
225					230				235				240		
Gln	Ala	Ala	His	Tyr	Glu	Leu	Val	Ala	Ser	Ala	Arg	Ala	Val	Lys	Ile
			245						250				255		
Gly	His	Glu	Ile	Asn	Pro	Asp	Phe	Gln	Ile	Gly	Cys	Met	Ile	Ala	Met
		260						265					270		
Cys	Pro	Ile	Tyr	Pro	Ala	Thr	Cys	Asn	Pro	Lys	Asp	Ile	Leu	Met	Ala
	275						280					285			
Met	Lys	Ala	Met	Gln	Lys	Arg	Tyr	Tyr	Phe	Ala	Asp	Val	His	Val	Leu
	290					295					300				
Gly	Lys	Tyr	Pro	Glu	His	Ile	Phe	Lys	Tyr	Trp	Glu	Arg	Lys	Gly	Ile
305				310					315					320	
Ser	Val	Asp	Phe	Thr	Ala	Gln	Asp	Lys	Glu	Asp	Leu	Leu	Gly	Gly	Thr
			325						330				335		
Val	Asp	Tyr	Ile	Gly	Phe	Ser	Tyr	Tyr	Met	Ser	Phe	Ala	Ile	Asp	Ser
	340						345					350			
His	Arg	Glu	Asn	Asn	Pro	Tyr	Phe	Asp	Tyr	Leu	Glu	Thr	Glu	Asp	Leu
		355					360					365			

Val	Lys	Asn	Asn	Tyr	Val	Lys	Ala	Ser	Glu	Trp	Glu	Trp	Gln	Ile	Asp
370						375					380				
Pro	Glu	Gly	Leu	Arg	Tyr	Ala	Leu	Asn	Trp	Phe	Thr	Asp	His	Tyr	His
385					390					395					400
Leu	Pro	Leu	Phe	Ile	Val	Glu	Asn	Gly	Phe	Gly	Ala	Ile	Asp	Lys	Val
				405					410					415	
Ala	Ala	Asp	Gly	Met	Val	His	Asp	Asp	Tyr	Arg	Ile	Glu	Tyr	Leu	Gly
			420					425					430		
Ala	His	Ile	Arg	Glu	Met	Lys	Lys	Ala	Val	Val	Glu	Asp	Gly	Val	Asp
		435					440					445			
Leu	Met	Gly	Tyr	Thr	Pro	Trp	Gly	Cys	Ile	Asp	Leu	Val	Ser	Ala	Gly
	450					455					460				
Thr	Gly	Glu	Met	Arg	Lys	Arg	Tyr	Gly	Phe	Ile	Tyr	Val	Asp	Lys	Asp
465					470					475					480
Asp	Asn	Gly	Lys	Gly	Ser	Tyr	Asn	Arg	Ser	Pro	Lys	Lys	Ser	Phe	Gly
			485					490						495	
Trp	Tyr	Lys	Glu	Val	Ile	Ser	Ser	Asn	Gly	Glu	Ser	Val	Glu		
			500					505					510		

(2) INFORMATION FOR SEQ ID NO:3149:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...65

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3149:

Lys	Thr	Leu	Leu	Lys	Lys	Lys	His	Asn	Lys	Met	Lys	Arg	Gln	Asn	Leu
1				5				10						15	
Ala	Ser	Arg	Lys	Arg	Lys	Lys	Lys	Ile	Arg	Lys	Gln	Gln	Leu	Arg	Thr
			20				25						30		
Leu	Leu	His	Leu	Leu	Gln	Val	Asn	Leu	Pro	Leu	Lys	Met	Lys	Asn	Ser
		35				40					45				
Pro	Ile	Leu	Gln	Leu	Gln	Lys	Ile	Ile	Leu	Asn	Glu	Asn	Gln	Arg	Thr
	50					55					60				
Asn															
65															

(2) INFORMATION FOR SEQ ID NO:3150:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 311 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...311
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3150:

```

Thr Arg Cys Tyr Ser Leu Glu Cys Phe Arg Lys Thr Val Leu Lys Pro
1      5      10      15
Leu Thr Phe Ser Asn Asn Lys Ala Gly Phe Glu Leu Leu Asp Leu Ser
      20      25      30
Phe Arg Gln Leu Asn Gln Asp Cys Leu Ile Ala Leu Lys Leu Leu Ser
      35      40      45
Asp Pro Asn Arg Glu Gln Phe Gln His Asp Asn Arg Gln Val Glu Leu
      50      55      60
Lys Ile Leu Ala Arg His Ile His Arg Leu Lys Lys Lys Gln Ser Asp
      65      70      75      80
Trp Lys Val Gln Tyr Thr Arg Cys Leu Asp Ile Ile Phe Pro Glu Leu
      85      90      95
Asp Lys Ile Val Gly Lys His Ser Glu Tyr Thr Tyr Gln Leu Leu Thr
      100     105     110
Arg Tyr Pro Asn Pro Gln Lys Arg Leu Glu Ala Gly Phe Asp Lys Leu
      115     120     125
Ile Glu Ile Lys Arg Leu Thr Ala Ser Lys Ile Gln Asp Ile Leu Ser
      130     135     140
Val Ala Pro Arg Ser Ile Gly Thr Thr Ser Pro Ala Arg Glu Phe Glu
      145     150     155     160
Ile Ile Glu Ile Ile Lys His Tyr Lys Arg Leu Ile Asp Lys Ala Glu
      165     170     175
Thr Cys Val Asn Asp Leu Met Ala Glu Phe Asn Ser Val Ile Thr Thr
      180     185     190
Val Thr Gly Ile Gly Gly Arg Leu Gly Ala Val Ile Leu Ala Glu Ile
      195     200     205
Arg Asn Ile His Ala Phe Asp Asn Pro Ala Gln Leu Gln Ala Phe Ala
      210     215     220
Gly Leu Asp Ser Ser Ile Tyr Gln Ser Gly Gln Ile Asp Leu Ala Gly
      225     230     235     240
Arg Met Ile Lys Arg Gly Ser Pro His Leu Arg Trp Ala Leu Ile Gln
      245     250     255
Ala Ala Lys Ala Cys Ala Arg Phe Ser Pro Ala Phe Lys Val Tyr Leu
      260     265     270
Lys Thr Lys Leu Glu Gln Gly Lys His Tyr Asn Val Ala Ile Ile His
      275     280     285
Leu Ala Lys Lys Leu Ile Arg Thr Leu Phe Tyr Ile Leu Lys Lys Ser
      290     295     300
Cys His Leu Thr Asn Lys Lys
      305     310

```

(2) INFORMATION FOR SEQ ID NO:3151:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...69

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3151:

Cys	Asn	Arg	Tyr	Gln	Lys	Ser	Lys	Lys	Glu	Phe	Leu	Asp	Gly	Tyr	Gln
1				5					10					15	
Asn	Lys	Lys	Gly	Gly	Asn	Tyr	Glu	Lys	Val	Phe	Lys	Asn	Ile	Glu	Arg
			20					25					30		
Gln	Leu	Asp	Leu	Ser	Leu	Asp	Gly	Phe	Ala	Arg	Gly	Thr	Leu	Val	Asp
		35					40					45			
Ser	Ile	Leu	Leu	His	Ser	Ser	Ile	Trp	Glu	Arg	Gly	Cys	Leu	Gln	Arg
	50					55					60				
Leu	Pro	His	Asp	Gln											
65															

(2) INFORMATION FOR SEQ ID NO:3152:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 95 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...95

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3152:

Ser	Gln	Leu	Leu	Phe	Ile	Tyr	Lys	Ile	Leu	Pro	Val	Gln	Arg	Gln	Gly
1				5					10					15	
Leu	Ser	Arg	Leu	Leu	Phe	Tyr	Phe	Val	His	Pro	Cys	Phe	Phe	Phe	Leu
			20					25					30		
Gly	Leu	Gly	Val	Gly	Ser	Trp	Leu	Tyr	Ile	Ala	Lys	Ile	Arg	Ser	Tyr
		35				40					45				
Arg	Asn	Ile	Leu	Leu	Ser	Ser	Ser	Thr	Gln	Ile	Ile	Ser	Leu	Ala	
	50					55				60					

Pro	Leu	Tyr	Gly	Asn	Ser	Lys	Glu	Asp	Trp	Ser	Ile	Leu	Ser	Lys	Thr
65				70					75						80
Ala	Cys	Thr	Gly	Leu	Thr	Lys	Ser	Asp	Arg	His	Lys	Tyr	Arg	Gln	
			85					90						95	

(2) INFORMATION FOR SEQ ID NO:3153:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 188 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...188

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3153:

Trp	Arg	Leu	Leu	Pro	Phe	Glu	Lys	Ala	Leu	Val	Ile	Met	Asp	Arg	Gly
1				5					10					15	
Tyr	Glu	Ser	Tyr	Asn	Leu	Met	Ala	His	Phe	Gln	Glu	Lys	Gly	Trp	Leu
			20				25						30		
Tyr	Ile	Ile	Arg	Ile	Arg	Asp	Gly	Lys	Gln	Ser	Met	Pro	Ser	Ser	Phe
		35				40					45				
Asn	Leu	Pro	Asn	Thr	Glu	Cys	Phe	Asp	Gln	Lys	Val	Ser	Leu	Lys	Leu
	50				55				60						
Ser	Arg	Lys	Gln	Thr	Asn	Gln	Leu	Lys	Lys	Leu	Tyr	Arg	Asp	Phe	Pro
65				70					75					80	
Asn	Asp	Tyr	His	Phe	Ile	Pro	His	Asn	Ser	Ile	Phe	Asp	Phe	Leu	Pro
			85					90					95		
Glu	Thr	Ser	Arg	Lys	Gln	Asp	Pro	Val	Thr	Leu	Tyr	Glu	Leu	Pro	Phe
		100					105					110			
Arg	Met	Val	Arg	Leu	Glu	Val	Glu	Gly	Lys	Tyr	Glu	Thr	Leu	Val	
	115				120						125				
Thr	Asn	Thr	Asp	Tyr	Ser	Val	Gln	Glu	Leu	Lys	Asn	Leu	Tyr	Ala	Ser
	130				135						140				
Arg	Trp	Gly	Ile	Glu	Thr	Ser	Phe	Arg	Asp	Leu	Lys	Tyr	Ser	Ile	Gly
145				150					155					160	
Leu	Val	Asn	Phe	His	Ala	Lys	Lys	Lys	Gly	Gly	Ile	Ser	Lys	Lys	Ser
			165				170							175	
Leu	Leu	Ala	Leu	Gln	Ile	Leu	Thr	Phe	Val	Val	Gly				
		180					185								

(2) INFORMATION FOR SEQ ID NO:3154:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 227 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...227
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3154:

```

Trp Arg Leu Leu Pro Phe Glu Lys Ala Leu Val Ile Met Asp Arg Gly
1      5      10      15
Tyr Glu Ser Tyr Asn Leu Met Ala His Phe Gln Glu Lys Gly Trp Leu
20      25      30
Tyr Ile Ile Arg Ile Arg Asp Gly Lys Gln Ser Met Pro Ser Ser Phe
35      40      45
Asn Leu Pro Asn Thr Glu Cys Phe Asp Gln Lys Val Ser Leu Lys Leu
50      55      60
Ser Arg Lys Gln Thr Asn Gln Leu Lys Lys Leu Tyr Arg Asp Phe Pro
65      70      75      80
Asn Asp Tyr His Phe Ile Pro His Asn Ser Ile Phe Asp Phe Leu Pro
85      90      95
Glu Thr Ser Arg Lys Gln Asp Pro Val Thr Leu Tyr Glu Leu Pro Phe
100     105     110
Arg Met Val Arg Leu Glu Val Glu Glu Gly Lys Tyr Glu Thr Leu Val
115     120     125
Thr Asn Thr Asp Tyr Ser Val Gln Glu Leu Lys Asn Leu Tyr Ala Ser
130     135     140
Arg Trp Gly Ile Glu Thr Ser Phe Arg Asp Leu Lys Tyr Ser Ile Gly
145     150     155     160
Leu Val Asn Phe His Ala Lys Lys Lys Gly Gly Ile Leu Gln Glu Ile
165     170     175
Phe Ala Arg Phe Thr Asn Phe Asn Phe Cys Arg Trp Val Thr Ser Gln
180     185     190
Val Ala Ile Asp Ser Ser His Lys Lys Gln Arg Tyr Lys Val Cys Phe
195     200     205
Ser Asp Ala Ala Tyr Ala Cys Arg Leu Phe Phe Asn Gly Ser Leu Ser
210     215     220
Ser Leu Gln
225

```

(2) INFORMATION FOR SEQ ID NO:3155:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 262 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...262

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3155:

Trp	Arg	Leu	Leu	Pro	Phe	Glu	Lys	Ala	Leu	Val	Ile	Met	Asp	Arg	Gly
1				5					10					15	
Tyr	Glu	Ser	Tyr	Asn	Leu	Met	Ala	His	Phe	Gln	Glu	Lys	Gly	Trp	Leu
			20				25						30		
Tyr	Ile	Ile	Arg	Ile	Arg	Asp	Gly	Lys	Gln	Ser	Met	Pro	Ser	Ser	Phe
			35				40					45			
Asn	Leu	Pro	Asn	Thr	Glu	Cys	Phe	Asp	Gln	Lys	Val	Ser	Leu	Lys	Leu
	50					55					60				
Ser	Arg	Lys	Gln	Thr	Asn	Gln	Leu	Lys	Lys	Leu	Tyr	Arg	Asp	Phe	Pro
65				70						75					80
Asn	Asp	Tyr	His	Phe	Ile	Pro	His	Asn	Ser	Ile	Phe	Asp	Phe	Leu	Pro
			85						90					95	
Glu	Thr	Ser	Arg	Lys	Gln	Asp	Pro	Val	Thr	Leu	Tyr	Glu	Leu	Pro	Phe
			100					105					110		
Arg	Met	Val	Arg	Leu	Glu	Val	Glu	Gly	Lys	Tyr	Glu	Thr	Leu	Val	
		115				120					125				
Thr	Asn	Thr	Asp	Tyr	Ser	Val	Gln	Glu	Leu	Lys	Asn	Leu	Tyr	Ala	Ser
	130					135					140				
Arg	Trp	Gly	Ile	Glu	Thr	Ser	Phe	Arg	Asp	Leu	Lys	Tyr	Ser	Ile	Gly
145				150						155					160
Leu	Val	Asn	Phe	His	Ala	Lys	Lys	Lys	Gly	Gly	Ile	Leu	Gln	Glu	Ile
			165						170					175	
Phe	Ala	Arg	Phe	Thr	Asn	Phe	Asn	Phe	Cys	Arg	Trp	Val	Thr	Ser	Gln
		180				185						190			
Val	Ala	Ile	Asp	Ser	Ser	His	Lys	Lys	Gln	Arg	Tyr	Lys	Val	Cys	Phe
	195					200						205			
Ser	Asp	Ala	Ala	Tyr	Ala	Cys	Arg	Leu	Phe	Phe	Asn	Gly	Ser	Leu	Ser
	210					215					220				
Ser	Leu	Gln	Leu	Lys	Asn	Tyr	Leu	Lys	Lys	Gln	Leu	Ser	Ile	Ile	Arg
225				230						235					240
Pro	Asn	Arg	Lys	Tyr	Ser	Arg	Lys	Ile	Lys	Ala	Gln	Ser	Val	Val	Asp
			245						250					255	
Phe	Ile	Tyr	Arg	Val	Thr										
			260												

(2) INFORMATION FOR SEQ ID NO:3156:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 262 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(A) NAME/KEY: misc_feature
(B) LOCATION 1...358

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3157:

Lys	Glu	Ser	Tyr	Ile	Met	Asn	Lys	Arg	Val	Gln	Ala	Phe	Leu	Ala	Lys	1	5	10	15
Met	Gln	Glu	Lys	Glu	Leu	Asp	Gly	Val	Ile	Ile	Asn	Asn	Leu	Lys	Asn	20	25	30	
Val	Tyr	Tyr	Leu	Thr	Gly	Phe	Trp	Gly	Ser	Asn	Gly	Thr	Val	Phe	Ile	35	40	45	
Ser	Arg	Asp	Arg	Gln	Val	Leu	Val	Thr	Asp	Ser	Arg	Tyr	Ile	Ile	Ala	50	55	60	
Ala	Lys	Gln	Glu	Thr	Ser	Gly	Phe	Glu	Ile	Val	Ala	Asp	Arg	Asp	Glu	65	70	75	80
Leu	Ala	Val	Ile	Ala	Gly	Ile	Val	Lys	Asp	Met	Gly	Leu	Thr	Arg	Ile	85	90	95	
Gly	Phe	Glu	Asp	Glu	Ile	Ser	Val	Ser	Tyr	Tyr	His	Arg	Met	Gln	Ala	100	105	110	
Ala	Phe	Ala	Gly	Leu	Asp	Leu	Phe	Pro	Gln	Thr	Gln	Phe	Val	Glu	Gly	115	120	125	
Leu	Arg	Met	Ile	Lys	Asp	Glu	Ala	Glu	Ile	Ala	Ala	Ile	Arg	Lys	Ala	130	135	140	
Cys	Ser	Ile	Ser	Asp	Gln	Ala	Phe	Arg	Asp	Ala	Leu	Asp	Phe	Ile	Lys	145	150	155	160
Pro	Gly	Lys	Thr	Glu	Ile	Glu	Ile	Ala	Asn	Phe	Leu	Asp	Phe	Arg	Met	165	170	175	
Arg	Glu	Leu	Gly	Ala	Ser	Gly	Leu	Ser	Phe	Asp	Thr	Ile	Leu	Ala	Ser	180	185	190	
Gly	Ile	Asn	Ser	Ser	Lys	Pro	His	Ala	His	Pro	Met	His	Lys	Pro	Val	195	200	205	
Glu	Leu	Gly	Glu	Ala	Ile	Thr	Met	Asp	Phe	Gly	Cys	Leu	Tyr	Asp	His	210	215	220	
Tyr	Val	Ser	Asp	Met	Thr	Arg	Thr	Ile	Tyr	Leu	Gly	His	Val	Ser	Asp	225	230	235	240
Glu	Gln	Ala	Glu	Ile	Tyr	Asn	Thr	Val	Leu	Lys	Ala	Asn	Gln	Ala	Leu	245	250	255	
Ile	Asp	Gln	Ala	Lys	Ala	Gly	Leu	Gly	Phe	Arg	Asp	Phe	Asp	Lys	Ile	260	265	270	
Pro	Arg	Asp	Ile	Ile	Ile	Glu	Ala	Gly	Tyr	Gly	Asp	Tyr	Phe	Thr	His	275	280	285	
Gly	Ile	Gly	His	Gly	Ile	Gly	Leu	Asp	Ile	His	Glu	Glu	Pro	Tyr	Phe	290	295	300	
Ser	Gln	Thr	Ser	Thr	Glu	Thr	Ile	Lys	Thr	Gly	Met	Ala	Leu	Thr	Asp	305	310	315	320
Glu	Pro	Gly	Ile	Tyr	Ile	Glu	Gly	Lys	Tyr	Gly	Val	Arg	Ile	Glu	Asp	325	330	335	
Asp	Ile	Leu	Ile	Thr	Glu	Thr	Gly	Cys	Glu	Leu	Leu	Thr	Leu	Ala	Pro	340	345	350	
Lys	Glu	Leu	Ile	Val	Ile											355			

(2) INFORMATION FOR SEQ ID NO:3158:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 350 amino acids
 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...350

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3158:

Tyr	Gln	Gly	Tyr	Ser	Lys	Glu	Gln	Ile	Glu	Leu	Leu	Val	Ser	Leu	Pro
1				5					10					15	
Ser	Phe	Gly	Ile	Met	Met	Met	Leu	Leu	Leu	Asn	Gly	Phe	Leu	Glu	Lys
			20					25					30		
Ile	Phe	Pro	Glu	Arg	Leu	Gln	Ile	Ser	Leu	Gly	Leu	Leu	Ile	Leu	Ser
		35				40						45			
Leu	Ser	Gly	Thr	Ala	Pro	Phe	Trp	Tyr	Gln	Ala	Tyr	Pro	Phe	Val	Phe
	50					55					60				
Gly	Thr	Arg	Leu	Leu	Phe	Gly	Leu	Gly	Leu	Gly	Met	Ile	Asn	Ala	Lys
65					70				75						80
Ala	Ile	Ser	Ile	Ile	Ser	Glu	Arg	Tyr	Gln	Gly	Lys	Arg	Arg	Ile	Gln
				85					90					95	
Met	Leu	Gly	Leu	Arg	Ala	Ser	Ala	Glu	Val	Val	Gly	Ala	Ser	Ile	Ile
			100					105					110		
Thr	Leu	Ala	Val	Gly	Gln	Leu	Leu	Ala	Phe	Gly	Trp	Thr	Ala	Ile	Phe
		115				120						125			
Leu	Ala	Tyr	Ser	Ala	Gly	Phe	Leu	Val	Leu	Pro	Leu	Tyr	Leu	Leu	Phe
	130					135					140				
Val	Pro	Tyr	Gly	Lys	Ser	Lys	Lys	Glu	Val	Lys	Lys	Arg	Ala	Lys	Glu
145				150					155					160	
Ala	Ser	Arg	Leu	Thr	Arg	Glu	Met	Lys	Gly	Leu	Ile	Phe	Thr	Leu	Ala
			165					170					175		
Ile	Glu	Ala	Ala	Val	Val	Val	Cys	Thr	Asn	Thr	Ala	Ile	Thr	Ile	Arg
		180					185					190			
Ile	Pro	Ser	Leu	Met	Val	Glu	Arg	Gly	Leu	Gly	Asp	Ala	Gln	Leu	Ser
	195					200					205				
Ser	Phe	Val	Leu	Ser	Ile	Met	Gln	Leu	Ile	Gly	Ile	Val	Ala	Gly	Val
	210				215						220				
Ser	Phe	Ser	Phe	Leu	Ile	Ser	Ile	Phe	Lys	Glu	Lys	Leu	Leu	Leu	Trp
225				230					235					240	
Ser	Gly	Ile	Thr	Phe	Gly	Leu	Gly	Gln	Ile	Val	Ile	Ala	Leu	Ser	Ser
			245					250					255		
Ser	Leu	Trp	Val	Val	Val	Ala	Gly	Ser	Val	Leu	Ala	Gly	Phe	Ala	Tyr
		260				265						270			
Ser	Val	Val	Leu	Thr	Thr	Val	Phe	Gln	Leu	Val	Ser	Glu	Arg	Ile	Pro
	275					280					285				
Ala	Lys	Leu	Leu	Asn	Gln	Ala	Thr	Ser	Phe	Ala	Val	Leu	Gly	Cys	Ser
	290				295						300				
Phe	Gly	Ala	Phe	Thr	Thr	Pro	Phe	Val	Leu	Gly	Ala	Ile	Gly	Leu	Leu
305				310					315					320	
Thr	His	Asn	Gly	Met	Leu	Val	Phe	Ser	Ile	Leu	Gly	Gly	Trp	Leu	Ile
			325					330					335		

Val Ile Ser Ile Phe Val Met Tyr Leu Leu Gln Lys Arg Ala
 340 345 350

(2) INFORMATION FOR SEQ ID NO:3159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...139

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3159:

Arg	Ile	Ile	Leu	Val	Lys	Lys	Cys	His	Ala	Met	Lys	Ala	Gln	Ala	Ile
1				5					10					15	
Val	Thr	Ser	Gln	Gly	Arg	Ile	Val	Ser	Leu	Asp	Ile	Thr	Val	Asn	Tyr
			20					25					30		
Cys	His	Asp	Met	Lys	Leu	Phe	Lys	Met	Ser	Cys	Arg	Asn	Ile	Gly	Gln
			35				40					45			
Ala	Gly	Lys	Ile	Leu	Ala	Asp	Ser	Gly	Tyr	Gln	Gly	Leu	Met	Lys	Ile
			50			55				60					
Tyr	Pro	Gln	Ala	Gln	Thr	Pro	Arg	Lys	Ser	Ser	Lys	Leu	Lys	Pro	Leu
65					70				75					80	
Thr	Val	Glu	Asp	Lys	Ala	Cys	Asn	His	Ala	Leu	Ser	Lys	Glu	Arg	Ser
				85				90						95	
Lys	Val	Glu	Asn	Ile	Phe	Ala	Lys	Val	Lys	Thr	Phe	Lys	Ile	Ile	Ser
			100				105						110		
Thr	Thr	Tyr	Arg	Asn	His	Arg	Lys	Arg	Phe	Gly	Leu	Arg	Met	Asn	Leu
		115				120					125				
Ser	Ala	Gly	Ile	Ile	Asn	His	Glu	Leu	Gly	Phe					
		130				135									

(2) INFORMATION FOR SEQ ID NO:3160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 851 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...851

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3160:

Arg	Asn	Ile	Leu	Lys	Tyr	Ser	Glu	Phe	Lys	Val	Arg	Lys	Asn	Met	Ala	1	5	10	15
Asn	Ile	Leu	Lys	Thr	Ile	Ile	Glu	Asn	Asp	Lys	Gly	Glu	Ile	Arg	Arg	20	25	30	
Leu	Glu	Lys	Met	Ala	Asp	Lys	Val	Phe	Lys	Tyr	Glu	Asp	Gln	Met	Ala	35	40	45	
Ala	Leu	Thr	Asp	Asp	Gln	Leu	Lys	Ala	Lys	Thr	Val	Glu	Phe	Lys	Glu	50	55	60	
Arg	Tyr	Gln	Asn	Gly	Glu	Ser	Leu	Asp	Ser	Leu	Leu	Tyr	Glu	Ala	Phe	65	70	75	80
Ala	Val	Val	Arg	Glu	Gly	Ala	Lys	Arg	Val	Leu	Gly	Leu	Phe	Pro	Tyr	85	90	95	
Lys	Val	Gln	Val	Met	Gly	Gly	Ile	Val	Leu	His	His	Gly	Asp	Val	Pro	100	105	110	
Glu	Met	Arg	Thr	Gly	Glu	Gly	Lys	Thr	Leu	Thr	Ala	Thr	Met	Pro	Val	115	120	125	
Tyr	Leu	Asn	Ala	Leu	Ser	Gly	Lys	Gly	Val	His	Val	Val	Thr	Val	Asn	130	135	140	
Glu	Tyr	Leu	Ser	Glu	Arg	Asp	Ala	Thr	Glu	Met	Gly	Glu	Leu	Tyr	Ser	145	150	155	160
Trp	Leu	Gly	Leu	Ser	Val	Gly	Ile	Asn	Leu	Ala	Thr	Lys	Ser	Pro	Met	165	170	175	
Glu	Lys	Lys	Glu	Ala	Tyr	Glu	Cys	Asp	Ile	Thr	Tyr	Ser	Thr	Asn	Ser	180	185	190	
Glu	Ile	Gly	Phe	Asp	Tyr	Leu	Arg	Asp	Asn	Met	Val	Val	Arg	Ala	Glu	195	200	205	
Asn	Met	Val	Gln	Arg	Pro	Leu	Asn	Tyr	Ala	Leu	Val	Asp	Glu	Val	Asp	210	215	220	
Ser	Ile	Leu	Ile	Asp	Glu	Ala	Arg	Thr	Pro	Leu	Ile	Val	Ser	Gly	Ala	225	230	235	240
Asn	Ala	Val	Glu	Thr	Ser	Gln	Leu	Tyr	His	Met	Ala	Asp	His	Tyr	Val	245	250	255	
Lys	Ser	Leu	Asn	Lys	Asp	Asp	Tyr	Ile	Ile	Asp	Val	Gln	Ser	Lys	Thr	260	265	270	
Ile	Gly	Leu	Ser	Asp	Ser	Gly	Ile	Asp	Arg	Ala	Glu	Ser	Tyr	Phe	Lys	275	280	285	
Leu	Glu	Asn	Leu	Tyr	Asp	Ile	Glu	Asn	Val	Ala	Leu	Thr	His	Phe	Ile	290	295	300	
Asp	Asn	Ala	Leu	Arg	Ala	Asn	Tyr	Ile	Met	Leu	Leu	Asp	Ile	Asp	Tyr	305	310	315	320
Val	Val	Ser	Glu	Glu	Gln	Glu	Ile	Leu	Ile	Val	Asp	Gln	Phe	Thr	Gly	325	330	335	
Arg	Thr	Met	Glu	Gly	Arg	Arg	Tyr	Ser	Asp	Gly	Leu	His	Gln	Ala	Ile	340	345	350	
Glu	Ala	Lys	Glu	Gly	Val	Pro	Ile	Gln	Asp	Glu	Thr	Lys	Thr	Ser	Ala	355	360	365	
Ser	Ile	Thr	Tyr	Gln	Asn	Leu	Phe	Arg	Met	Tyr	Lys	Lys	Leu	Ser	Gly	370	375	380	
Met	Thr	Gly	Thr	Gly	Lys	Thr	Glu	Glu	Glu	Glu	Phe	Arg	Glu	Ile	Tyr	385	390	395	400
Asn	Ile	Arg	Val	Ile	Pro	Ile	Pro	Thr	Asn	Arg	Pro	Val	Gln	Arg	Ile	405	410	415	

Asp	His	Ser	Asp	Leu	Leu	Tyr	Ala	Ser	Ile	Glu	Ser	Lys	Phe	Lys	Ala
			420					425					430		
Val	Val	Glu	Asp	Val	Lys	Ala	Arg	Tyr	Gln	Lys	Gly	Gln	Pro	Val	Leu
		435					440					445			
Val	Gly	Thr	Val	Ala	Val	Glu	Thr	Ser	Asp	Tyr	Ile	Ser	Lys	Lys	Leu
	450					455					460				
Val	Ala	Ala	Gly	Val	Pro	His	Glu	Val	Leu	Asn	Ala	Lys	Asn	His	Tyr
465					470					475					480
Arg	Glu	Ala	Gln	Ile	Ile	Met	Asn	Ala	Gly	Gln	Arg	Gly	Ala	Val	Thr
			485						490					495	
Ile	Ala	Thr	Asn	Met	Ala	Gly	Arg	Gly	Thr	Asp	Ile	Lys	Leu	Gly	Glu
			500					505					510		
Gly	Val	Arg	Glu	Leu	Gly	Gly	Leu	Cys	Val	Ile	Gly	Thr	Glu	Arg	His
	515						520					525			
Glu	Ser	Arg	Arg	Ile	Asp	Asn	Gln	Leu	Arg	Gly	Arg	Ser	Gly	Arg	Gln
	530					535					540				
Gly	Asp	Pro	Gly	Glu	Ser	Gln	Phe	Tyr	Leu	Ser	Leu	Glu	Asp	Asp	Leu
545					550					555					560
Met	Lys	Arg	Phe	Gly	Ser	Glu	Arg	Leu	Lys	Gly	Ile	Phe	Glu	Arg	Leu
			565						570					575	
Asn	Met	Ser	Glu	Glu	Ala	Ile	Glu	Ser	Arg	Met	Leu	Thr	Arg	Gln	Val
			580					585					590		
Glu	Ala	Ala	Gln	Lys	Arg	Val	Glu	Gly	Asn	Asn	Tyr	Asp	Thr	Arg	Lys
	595						600					605			
Gln	Val	Leu	Gln	Tyr	Asp	Asp	Val	Met	Arg	Glu	Gln	Arg	Glu	Ile	Ile
	610					615					620				
Tyr	Thr	Gln	Arg	Tyr	Asp	Val	Ile	Thr	Ala	Asp	Arg	Asp	Leu	Ala	Pro
625					630					635					640
Glu	Ile	Gln	Ala	Met	Ile	Lys	Arg	Thr	Ile	Gly	Arg	Val	Val	Asp	Gly
			645						650					655	
His	Ala	Arg	Ala	Lys	Gln	Asp	Glu	Lys	Leu	Glu	Ala	Ile	Leu	Asn	Phe
			660					665					670		
Ala	Lys	Tyr	Asn	Leu	Leu	Pro	Glu	Asp	Ser	Ile	Thr	Met	Glu	Asp	Leu
		675					680					685			
Ser	Gly	Leu	Ser	Asp	Lys	Ala	Ile	Lys	Glu	Glu	Leu	Phe	Gln	Arg	Ala
	690					695					700				
Leu	Lys	Val	Tyr	Asp	Ser	Gln	Val	Ser	Lys	Leu	Arg	Asp	Glu	Glu	Ala
705					710					715					720
Val	Lys	Glu	Phe	Gln	Lys	Val	Leu	Ile	Leu	Arg	Val	Val	Asp	Asn	Lys
			725						730				735		
Trp	Thr	Asp	His	Ile	Asp	Ala	Leu	Asp	Gln	Leu	Arg	Asn	Ala	Val	Gly
			740					745					750		
Leu	Arg	Gly	Tyr	Ala	Gln	Asn	Asn	Pro	Val	Val	Glu	Tyr	Gln	Ala	Glu
		755					760					765			
Gly	Phe	Arg	Met	Phe	Asn	Asp	Met	Ile	Gly	Ser	Ile	Glu	Phe	Asp	Val
	770					775					780				
Thr	Arg	Leu	Met	Met	Lys	Ala	Gln	Ile	His	Glu	Gln	Glu	Arg	Pro	Gln
785					790					795					800
Ala	Glu	Arg	His	Ile	Ser	Thr	Thr	Ala	Thr	Arg	Asn	Ile	Ala	Ala	His
			805						810					815	
Gln	Ala	Ser	Met	Pro	Glu	Asp	Leu	Asp	Leu	Ser	Gln	Ile	Gly	Arg	Asn
		820						825					830		
Glu	Leu	Cys	Pro	Cys	Gly	Ser	Gly	Lys	Lys	Phe	Lys	Asn	Cys	His	Gly
		835					840					845			
Lys	Arg	Gln													
	850														

(2) INFORMATION FOR SEQ ID NO:3161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...133

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3161:

Asp	Gly	Ile	Leu	Gly	Ile	Lys	Lys	Tyr	Arg	Glu	Thr	Ser	Lys	Asp	Lys
1			5					10					15		
Val	Arg	Lys	Pro	Trp	Leu	Glu	Phe	Phe	Gly	Asn	Lys	Pro	Phe	Thr	Gln
		20					25					30			
Gln	Pro	Gln	Arg	Ala	Ile	Ser	Gln	Ala	Asn	Gln	Leu	Leu	Asp	Tyr	Lys
		35				40					45				
Ser	Trp	Ser	Glu	Glu	Asp	Arg	Lys	Met	Phe	Ser	Gln	Leu	His	Met	Arg
	50				55			60							
Glu	Glu	Gln	Val	Leu	Leu	Ala	Gln	Asp	Tyr	Ala	Leu	Glu	Thr	Ala	Arg
65				70				75						80	
Ala	Glu	Asp	Leu	Glu	Gln	Gly	Leu	Glu	Arg	Gly	Lys	Val	Glu	Gly	Arg
		85					90					95			
Ala	Glu	Arg	Lys	Leu	Phe	Ala	Phe	Leu	Asp	Ile	Val	Arg	Gln	Gly	Leu
		100				105						110			
Leu	Thr	Ser	Glu	Val	Ala	Ser	Gln	Gln	Leu	Gly	Met	Ser	Val	Ser	Glu
	115					120						125			
Phe	Glu	Ala	Leu	Leu											
	130														

(2) INFORMATION FOR SEQ ID NO:3162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...373

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3162:

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Lys Arg Asn Leu Thr Met Glu Glu Ile Leu Cys Ile Gly Cys Gly Ala
1      5      10      15
Thr Ile Gln Thr Thr Asp Lys Ala Gly Leu Gly Phe Thr Pro Gln Ser
20      25      30
Ala Leu Glu Lys Gly Leu Glu Thr Gly Glu Val Tyr Cys Gln Arg Cys
35      40      45
Phe Arg Leu Arg His Tyr Asn Glu Ile Thr Asp Val Gln Leu Thr Asn
50      55      60
Asp Asp Phe Leu Lys Leu Leu His Glu Val Gly Asp Ser Asp Ala Leu
65      70      75      80
Val Val Asn Val Ile Asp Ile Phe Asp Phe Asn Gly Ser Val Ile Pro
85      90      95
Gly Leu Pro Arg Phe Val Ser Gly Asn Asp Val Leu Leu Val Gly Asn
100      105      110
Lys Lys Asp Ile Leu Pro Lys Ser Val Lys Ser Gly Lys Ile Ser Gln
115      120      125
Trp Leu Met Lys Arg Ala His Glu Glu Gly Leu Arg Pro Val Asp Val
130      135      140
Val Leu Thr Ser Ala Gln Asn Lys His Ala Ile Lys Glu Val Ile Asp
145      150      155      160
Lys Ile Glu His Tyr Arg Lys Gly Arg Asp Val Tyr Val Val Gly Val
165      170      175
Thr Asn Val Gly Lys Ser Thr Leu Ile Asn Ala Ile Ile Gln Glu Ile
180      185      190
Thr Gly Asp Gln Asn Val Ile Thr Thr Ser Arg Phe Pro Gly Thr Thr
195      200      205
Leu Asp Lys Ile Glu Ile Pro Leu Asp Asp Gly Ser Tyr Ile Tyr Asp
210      215      220
Thr Pro Gly Ile Ile His Arg His Gln Met Ala His Tyr Leu Thr Ala
225      230      235      240
Lys Asn Leu Lys Tyr Val Ser Pro Lys Lys Glu Ile Lys Pro Lys Thr
245      250      255
Tyr Gln Leu Asn Pro Glu Gln Thr Leu Phe Leu Gly Gly Leu Gly Arg
260      265      270
Phe Asp Phe Ile Ala Gly Glu Lys Gln Gly Phe Thr Ala Phe Phe Asp
275      280      285
Asn Glu Leu Lys Leu His Arg Ser Lys Leu Glu Gly Ala Ser Ala Phe
290      295      300
Tyr Asp Lys His Leu Gly Thr Leu Leu Thr Pro Pro Asn Ser Lys Glu
305      310      315      320
Lys Glu Asp Phe Pro Arg Leu Val Gln His Val Phe Thr Ile Lys Asp
325      330      335
Lys Thr Asp Leu Val Ile Ser Gly Leu Gly Trp Ile Arg Val Thr Gly
340      345      350
Thr Ala Lys Val Ala Val Trp Ala Pro Glu Gly Val Ala Val Val Thr
355      360      365
Arg Lys Ala Ile Ile
370

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(2) INFORMATION FOR SEQ ID NO:3163:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 272 amino acids

(B) TYPE: amino acid

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...272
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3163:

Lys	Arg	Asn	Phe	Met	Ser	Ile	Lys	Leu	Ile	Ala	Val	Asp	Ile	Asp	Gly
1				5					10					15	
Thr	Leu	Val	Asn	Ser	Gln	Lys	Glu	Ile	Thr	Pro	Glu	Val	Phe	Ser	Ala
			20					25					30		
Ile	Gln	Asp	Ala	Lys	Glu	Ala	Gly	Val	Lys	Val	Val	Ile	Ala	Thr	Gly
		35					40					45			
Arg	Pro	Ile	Ala	Gly	Val	Ala	Lys	Leu	Leu	Asp	Asp	Leu	Gln	Leu	Arg
	50					55					60				
Asp	Gln	Gly	Asp	Tyr	Val	Val	Thr	Phe	Asn	Gly	Ala	Leu	Val	Gln	Glu
65					70					75					80
Thr	Ala	Thr	Gly	His	Glu	Ile	Ile	Ser	Glu	Ser	Leu	Thr	Tyr	Glu	Asp
				85					90					95	
Tyr	Leu	Asp	Met	Glu	Phe	Leu	Ser	Arg	Lys	Leu	Gly	Val	His	Met	His
			100					105					110		
Ala	Ile	Thr	Lys	Asp	Gly	Ile	Tyr	Thr	Ala	Asn	Arg	Asn	Ile	Gly	Thr
		115					120					125			
Tyr	Thr	Val	His	Glu	Ser	Thr	Leu	Val	Ser	Met	Pro	Ile	Phe	Tyr	Arg
	130					135					140				
Thr	Pro	Glu	Glu	Met	Ala	Gly	Lys	Glu	Ile	Val	Lys	Cys	Met	Phe	Ile
145				150					155					160	
Asp	Glu	Pro	Glu	Ile	Leu	Asp	Ala	Ala	Ile	Glu	Lys	Ile	Pro	Ala	Glu
				165					170					175	
Phe	Tyr	Glu	Arg	Tyr	Ser	Ile	Asn	Lys	Ser	Ala	Pro	Phe	Tyr	Leu	Glu
		180					185					190			
Leu	Leu	Thr	Lys	Asn	Val	Asp	Lys	Gly	Ser	Ala	Ile	Thr	His	Leu	Ala
	195						200					205			
Glu	Lys	Leu	Gly	Leu	Thr	Lys	Asp	Glu	Thr	Met	Ala	Ile	Gly	Asp	Glu
	210					215					220				
Glu	Asn	Asp	Arg	Ala	Met	Leu	Glu	Val	Val	Gly	Asn	Pro	Val	Val	Met
225					230					235					240
Glu	Asn	Gly	Asn	Pro	Glu	Ile	Lys	Lys	Ile	Ala	Lys	Tyr	Ile	Thr	Lys
				245					250					255	
Thr	Asn	Asp	Glu	Ser	Gly	Val	Ala	His	Ala	Ile	Arg	Thr	Trp	Val	Leu
			260				265						270		

(2) INFORMATION FOR SEQ ID NO:3164:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 64 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...64
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3164:

Val	Tyr	Leu	Tyr	Gln	Leu	Phe	Leu	Val	Leu	Phe	Leu	Leu	Leu	Gly	Gly
1				5				10						15	
Leu	Ala	Leu	Leu	Phe	Ser	Leu	Leu	Ala	Leu	Thr	Ser	His	Lys	Trp	Tyr
			20					25					30		
Tyr	Val	Arg	Phe	Gly	Lys	Arg	Val	Met	Leu	Leu	Leu	Tyr	Tyr	Leu	Phe
		35					40					45			
Ala	His	Asn	Lys	Arg	Glu	Leu	Phe	Tyr	Glu	Asn	Leu	Leu	Asn	Met	Pro
	50					55					60				

(2) INFORMATION FOR SEQ ID NO:3165:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 64 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...64
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3165:

Val	Tyr	Leu	Tyr	Gln	Pro	Phe	Leu	Val	Leu	Phe	Leu	Leu	Leu	Gly	Gly
1				5				10						15	
Leu	Ala	Leu	Leu	Phe	Ser	Leu	Leu	Ala	Leu	Thr	Ser	His	Lys	Trp	Tyr
			20					25					30		
Tyr	Val	Arg	Phe	Gly	Lys	Arg	Val	Met	Leu	Leu	Leu	Tyr	Tyr	Leu	Phe
		35					40					45			
Ala	His	Asn	Lys	Arg	Glu	Leu	Phe	Tyr	Glu	Asn	Leu	Leu	Asn	Met	Pro
	50					55					60				

(2) INFORMATION FOR SEQ ID NO:3166:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 64 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...64

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3166:

Val	Tyr	Leu	Tyr	Gln	Leu	Phe	Leu	Val	Leu	Phe	Leu	Leu	Leu	Gly	Gly
1				5				10						15	
Leu	Ala	Leu	Leu	Phe	Ser	Leu	Leu	Ala	Leu	Thr	Ser	His	Lys	Trp	Tyr
			20					25					30		
Tyr	Val	Arg	Phe	Gly	Lys	Arg	Val	Met	Leu	Leu	Leu	Tyr	Tyr	Leu	Phe
		35					40					45			
Ala	His	Asn	Lys	Arg	Glu	Leu	Phe	Tyr	Glu	Asn	Leu	Leu	Asn	Met	Pro
	50					55					60				

(2) INFORMATION FOR SEQ ID NO:3167:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...64

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3167:

Val	Tyr	Leu	Tyr	Gln	Leu	Phe	Leu	Val	Leu	Phe	Leu	Leu	Leu	Gly	Gly
1				5				10						15	
Leu	Ala	Leu	Leu	Phe	Ser	Phe	Leu	Ala	Leu	Thr	Ser	His	Lys	Trp	Tyr
			20					25					30		
Tyr	Val	Arg	Phe	Gly	Lys	Arg	Val	Met	Leu	Leu	Leu	Tyr	Tyr	Leu	Phe
		35					40					45			
Ala	His	Asn	Lys	Arg	Glu	Leu	Phe	Tyr	Glu	Asn	Leu	Leu	Asn	Met	Pro
	50					55					60				

(2) INFORMATION FOR SEQ ID NO:3168:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3168:

Phe	Asp	Leu	Tyr	Ser	Ser	Ile	His	Thr	Arg	Asp	Glu	Pro	Ile	Glu	Gln
1				5					10					15	
Val	Trp	Lys	Glu	Ile	Arg	Lys	Arg	Gly	Phe	Lys	Asn	Lys	Ala	Phe	Arg
			20					25					30		
Thr	Leu	Glu	Asp	Ile	Met	Asn	Gln	Leu	Gln	Asp	Val	Ile	Gln	Gly	Leu
		35				40					45				
Gly	Glu	Glu	Val	Ile	Lys	Ser	Ile	Val	Asn	Arg	Arg				
	50				55					60					

(2) INFORMATION FOR SEQ ID NO:3169:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 637 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...637

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3169:

His	Leu	Ile	Tyr	Thr	Leu	Ile	Leu	Met	Ile	Leu	Trp	Met	Ala	Leu	Ala
1				5					10					15	
Phe	Ala	Gly	Asp	Met	Arg	Leu	Phe	Val	Lys	Asp	Asn	Asp	Gln	Lys	Lys
			20					25					30		
Ala	Glu	Ile	Lys	Ile	Arg	Met	Pro	Glu	Lys	Ile	Lys	Glu	Thr	Lys	Ser
		35				40					45				
Glu	Tyr	Pro	Tyr	Val	Ser	Ser	Tyr	Gly	Asn	Val	Ile	Glu	Leu	Gly	Glu
	50				55					60					
Gly	Asp	Leu	Ser	Lys	Asn	Lys	Pro	Asp	Asn	Leu	Thr	Lys	Met	Glu	Ser
65				70					75					80	
Gly	Lys	Ile	Tyr	Ser	Asp	Ser	Glu	Lys	Gln	Gln	Tyr	Leu	Leu	Lys	Asp

Ser	Lys	Lys	Lys	Asp	Asn	Pro	Gln	Val	Asn	His	Ser	Gln	Leu	Asn	Glu
545					550					555					560
Ser	His	Arg	Lys	Glu	Asp	Leu	Gln	Arg	Glu	Asp	His	Ser	Gln	Lys	Ser
				565					570						575
Asp	Ser	Thr	Lys	Asp	Val	Thr	Ala	Thr	Val	Leu	Asp	Lys	Asn	Asn	Ile
			580					585					590		
Ser	Ser	Lys	Ser	Thr	Thr	Asn	Asn	Pro	Asn	Lys	Leu	Pro	Lys	Thr	Gly
		595					600					605			
Thr	Ala	Ser	Gly	Ala	Gln	Thr	Leu	Leu	Ala	Ala	Gly	Ile	Met	Phe	Ile
	610					615					620				
Val	Gly	Ile	Phe	Leu	Gly	Leu	Lys	Lys	Lys	Asn	Gln	Asp			
625					630					635					

(2) INFORMATION FOR SEQ ID NO:3170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 414 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...414

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3170:

Ser	Val	Ser	Tyr	Leu	Lys	Thr	Gly	Ile	Glu	Ser	Gly	Arg	Phe	Pro	Thr
1				5					10					15	
Gly	Ser	Ala	Cys	Leu	Leu	Ser	Val	Asn	Tyr	Ser	Leu	Asp	Phe	His	Cys
		20						25					30		
Ser	Lys	Asp	Thr	Ile	Gln	Arg	Ala	Leu	Leu	Glu	Leu	Arg	His	Glu	Gln
		35					40					45			
Tyr	Leu	Tyr	Ala	Lys	Pro	Gln	Ser	Gly	Tyr	Tyr	Val	Leu	Glu	His	Gly
	50					55					60				
Gln	His	Gln	Asp	Leu	Glu	Ile	Glu	Val	Thr	Asp	Glu	His	Ala	Ser	Ala
65				70						75					80
Tyr	Asp	Asp	Phe	Arg	Leu	Cys	Val	Asn	Glu	Thr	Leu	Ile	Gly	Arg	Glu
			85					90						95	
Asn	Tyr	Leu	Phe	Asn	Tyr	Tyr	Asp	Asn	Gln	Glu	Gly	Leu	Glu	Asp	Leu
		100						105					110		
Arg	Gln	Ser	Ile	His	Lys	Leu	Leu	Phe	Glu	Gln	Ala	Leu	Tyr	Cys	Lys
		115					120					125			
Ala	Asn	Gln	Leu	Val	Leu	Thr	Ser	Gly	Thr	Gln	Gln	Ala	Leu	Phe	Ile
	130					135					140				
Leu	Ser	Gln	Ile	Ser	Phe	Pro	Arg	Gln	Ala	Lys	Glu	Ile	Leu	Val	Glu
145				150						155					160
Gln	Pro	Thr	Tyr	His	Arg	Met	Asn	Arg	Leu	Leu	Ile	Ala	Gln	Gly	Leu
			165					170						175	
Asp	Tyr	Gln	Thr	Ile	Glu	Arg	Gly	Ile	Asp	Gly	Ile	Asp	Leu	Glu	Glu

			180					185				190			
Leu	Glu	Gly	His	Phe	Lys	Thr	Gly	Lys	Ile	Lys	Phe	Phe	Tyr	Thr	Ile
		195					200					205			
Pro	Arg	Phe	His	Tyr	Pro	Leu	Gly	His	Ser	Tyr	Ser	Glu	Gln	Asp	Lys
	210					215					220				
Arg	Ser	Ile	Leu	Asn	Leu	Ala	Ala	Lys	Tyr	Asp	Val	Tyr	Ile	Val	Glu
225				230						235					240
Asp	Asp	Tyr	Leu	Gly	Asp	Leu	Asp	Ser	Lys	Lys	Gly	Gln	Thr	Phe	His
			245						250					255	
Tyr	Leu	Asp	Thr	Glu	Glu	His	Val	Ile	Tyr	Ile	Lys	Ser	Phe	Ser	Thr
		260					265						270		
Ser	Leu	Phe	Pro	Ala	Leu	Arg	Ile	Thr	Ala	Leu	Ile	Leu	Pro	Asn	Ala
	275						280					285			
Ile	Lys	Glu	Ala	Phe	Val	Ala	Tyr	Lys	Asn	Ile	Leu	Asp	Tyr	Asp	Ser
	290					295				300					
Asn	Leu	Ile	Met	Gln	Lys	Ala	Leu	Ser	Leu	Tyr	Ile	Asp	Ser	Gln	Leu
305				310					315					320	
Phe	Glu	Lys	Asn	Arg	Leu	Ala	Arg	Leu	Thr	Asn	His	Glu	Ser	Tyr	Gln
			325						330					335	
Lys	Gln	Ile	Glu	Glu	Arg	Ile	Thr	Lys	Thr	Pro	Cys	Pro	Leu	Pro	His
		340					345					350			
Tyr	Pro	Leu	His	Asp	Gly	Leu	Leu	Leu	Asp	Leu	Arg	Gln	Tyr	Pro	Lys
		355					360					365			
Ile	Ala	Ser	Leu	Lys	His	Ser	Gln	Leu	Gly	Leu	Asp	Phe	Phe	Glu	Glu
	370					375					380				
Ala	Tyr	Leu	Ser	Thr	Cys	Pro	Tyr	Gln	Phe	Ala	Lys	Val	Ser	Leu	Asp
385				390						395					400
Asn	Leu	Glu	Asn	Val	Leu	Asn	Tyr	Leu	Lys	Ala	Glu	Leu	Glu		
			405					410							

(2) INFORMATION FOR SEQ ID NO:3171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3171:

Ser	Val	Val	Leu	Gly	Phe	Val	Gln	Lys	Ser	Ala	Gln	Val	Ser	His	Leu
1			5				10						15		
Gln	Gln	Pro	His	Arg	Ser	Ala	Ile	Lys	Ile	Thr	Arg	Ser	Ala	Thr	Ser
		20					25						30		
Arg	Ala	Asn	Pro	Ile	Ser	Cys	Val	Thr	Ile	Thr	Ile	Val	Ile	Pro	Asp
	35						40					45			

Leu	Ala	Arg	Ser	Cys	Ile	Thr	Ala	Asn	Thr	Ser	Pro	Thr	Ile	Ser	Gly
50						55					60				
Ser	Lys	Ala	Glu	Val	Gly	Ser	Ser	Lys	Ser	Lys	Thr	Ser	Gly	Thr	Ile
65					70					75					80
Ala	Asn	Pro	Arg	Ala	Met	Gln	Ser	Val	Val	Ala	His	Pro	Thr	Asp	
				85					90				95		
Ser	Val	Asp	Lys	Arg	Leu	Pro	Tyr	Leu	Ala	Asn	Gln	Leu	Phe	Pro	Lys
		100						105					110		
Ala	Leu	Gly	Leu	Ser	Ser	Gln	Gln	Leu	Pro	Cys	Phe	His	Leu		
		115					120						125		

(2) INFORMATION FOR SEQ ID NO:3172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...165

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3172:

Ile	Asn	Pro	Tyr	Lys	Ile	Arg	Asn	Ala	Lys	Leu	Ser	Ser	Ile	Arg	Arg
1				5					10					15	
Asn	Glu	Val	Ser	Phe	Ile	Phe	Gln	Ala	Tyr	Asn	Leu	Ile	Pro	Ser	Leu
			20					25					30		
Pro	Val	Ile	Glu	Asn	Ile	Ala	Leu	Pro	Leu	Arg	Leu	Ser	Gln	Lys	Lys
		35					40					45			
Leu	Thr	Ile	Lys	Asn	Val	Glu	Asn	Leu	Leu	Lys	Arg	Met	Lys	Phe	Asn
	50					55					60				
Ala	Gly	Leu	Asn	Asp	Phe	Val	Gly	Thr	Leu	Ser	Gly	Gly	Glu	Gln	Gln
65				70						75					80
Lys	Val	Ala	Ile	Ala	Arg	Ala	Phe	Ile	Ala	Asp	Ser	Asp	Ile	Ile	Phe
				85					90				95		
Ala	Asp	Glu	Pro	Thr	Gly	Ala	Leu	Asp	Ser	Val	Ser	Arg	Glu	Val	Ile
		100						105					110		
Phe	Asp	Leu	Leu	Arg	Glu	Leu	Val	Gly	Ala	Gly	Lys	Cys	Val	Ile	Met
		115					120					125			
Val	Thr	His	Asp	Ile	Glu	Leu	Ala	Ser	Lys	Thr	Asp	Arg	Ala	Leu	Ile
	130						135				140				
Leu	Lys	Asp	Gly	Lys	Ile	Phe	Lys	Glu	Leu	His	Arg	Leu	Ala	Gly	Lys
145					150					155					160
Ser	Cys	Ile	Lys	Ser											
				165											

(2) INFORMATION FOR SEQ ID NO:3173:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 157 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...157

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3173:

Ser	Met	Pro	Tyr	Lys	Arg	Gln	Arg	Ser	Phe	Ser	Met	Ala	Leu	Ser	Lys
1				5					10					15	
Leu	Asp	Ser	Leu	Tyr	Met	Ala	Val	Val	Ala	Asp	His	Ser	Lys	Asn	Pro
			20					25					30		
His	His	Gln	Gly	Lys	Leu	Glu	Asp	Ala	Glu	Gln	Thr	Ser	Leu	Asn	Asn
			35				40					45			
Pro	Thr	Cys	Gly	Asp	Val	Ile	Asn	Leu	Ser	Val	Lys	Phe	Asp	Ala	Glu
						55					60				
Asp	Arg	Leu	Glu	Asp	Ile	Ala	Phe	Leu	Asn	Ser	Gly	Cys	Thr	Ile	Ser
65					70					75				80	
Thr	Ala	Ser	Ala	Ser	Met	Met	Thr	Asp	Ala	Val	Leu	Gly	Lys	Thr	Lys
				85					90					95	
Gln	Glu	Ile	Leu	Glu	Leu	Ala	Thr	Ile	Phe	Ser	Glu	Met	Val	Gln	Gly
			100					105					110		
Gln	Lys	Asp	Glu	Arg	Gln	Gly	Gln	Leu	Gly	Asp	Ala	Ala	Phe	Leu	Ser
			115				120					125			
Gly	Val	Ala	Lys	Phe	Pro	Gln	Arg	Ile	Lys	Cys	Ala	Thr	Leu	Ala	Trp
			130				135				140				
Asn	Ala	Leu	Lys	Lys	Thr	Ile	Glu	Asn	Gln	Glu	Lys	Gln			
145						150					155				

(2) INFORMATION FOR SEQ ID NO:3174:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 287 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...287

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3174:

Leu	Ser	Ala	Tyr	Gln	Val	Val	Gly	Thr	Arg	Met	Trp	Phe	Lys	Ser	Lys
1				5					10					15	
Thr	Ala	Trp	Lys	Gln	Met	Gln	Gln	Arg	Glu	Lys	Leu	Met	Pro	Lys	
			20					25					30		
Thr	Leu	Thr	Glu	Lys	Leu	Asn	Ala	Ile	Lys	Ala	Thr	Gly	Lys	Gly	Ile
			35				40					45			
Phe	Val	Pro	Tyr	Ile	Met	Ala	Gly	Asp	His	Glu	Lys	Gly	Leu	Asp	Gly
	50					55				60					
Leu	Ala	Glu	Thr	Ile	His	Phe	Leu	Glu	Asp	Leu	Gly	Val	Ser	Ala	Ile
65				70					75					80	
Glu	Val	Gly	Ile	Pro	Phe	Ser	Asp	Pro	Val	Ala	Asp	Gly	Pro	Val	Ile
				85					90					95	
Glu	Glu	Ala	Gly	Leu	Arg	Ser	Leu	Ala	His	Gly	Thr	Ser	Thr	Gln	Ala
			100					105					110		
Leu	Val	Glu	Thr	Leu	Lys	Thr	Ile	Glu	Thr	Glu	Ile	Pro	Leu	Val	Ile
			115				120					125			
Met	Thr	Tyr	Phe	Asn	Pro	Leu	Phe	Gln	Tyr	Gly	Val	Glu	Asn	Phe	Val
	130					135					140				
Lys	Asp	Leu	Ala	Asp	Thr	Ala	Val	Lys	Gly	Leu	Ile	Ile	Pro	Asp	Leu
145				150						155				160	
Pro	His	Glu	His	Ala	Asn	Phe	Val	Glu	Pro	Phe	Leu	Ala	Asp	Thr	Asp
				165					170					175	
Ile	Ala	Leu	Ile	Pro	Leu	Val	Ser	Leu	Thr	Thr	Gly	Ile	Glu	Arg	Gln
			180					185					190		
Lys	Glu	Leu	Ile	Glu	Gly	Ala	Glu	Gly	Phe	Ile	Tyr	Ala	Val	Ala	Ile
			195				200					205			
Asn	Gly	Val	Thr	Gly	Lys	Ser	Gly	Asn	Tyr	Arg	Ala	Asp	Leu	Asp	Lys
	210					215					220				
His	Leu	Ala	Gln	Leu	His	Gln	Val	Ala	Asp	Ile	Pro	Val	Leu	Thr	Gly
225				230						235				240	
Phe	Gly	Val	Ser	Ser	Gln	Ala	Asp	Leu	Glu	Arg	Phe	Asn	Ala	Val	Ser
				245					250					255	
Asp	Gly	Val	Ile	Val	Gly	Ser	Lys	Ile	Val	Lys	Ala	Leu	His	Gln	Gly
			260					265				270			
Glu	Pro	Ile	Gln	Asp	Phe	Ile	Arg	Gln	Ala	Val	Ala	Tyr	Gln	Lys	
			275				280					285			

(2) INFORMATION FOR SEQ ID NO:3175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...221

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3175:

Ile	Asn	His	Tyr	Phe	Ile	Leu	Phe	Leu	Ala	Arg	Met	Val	Ala	Pro	Ala
1				5					10					15	
Lys	Val	Arg	Arg	Pro	Ala	Ile	Ser	Ser	Ala	Arg	Phe	Glu	Ile	Asp	Pro
				20				25					30		
Val	Asp	Gly	Asn	Asp	Phe	Phe	Gly	Leu	Phe	Val	Ala	Phe	Ser	Phe	Val
		35					40					45			
Glu	Ala	Trp	Leu	Glu	Gly	Cys	Leu	Ser	Leu	Leu	Lys	Leu	Phe	Val	Val
	50					55					60				
Asp	Gly	Phe	Leu	Ser	Ser	Ala	Cys	Gly	Leu	Leu	Leu	Ser	Gly	Phe	Gly
65					70				75					80	
Phe	Ser	Gly	Cys	Gly	Leu	Thr	Ser	Gly	Phe	Gly	Phe	Ser	Gly	Cys	Gly
				85				90					95		
Leu	Thr	Ser	Gly	Phe	Gly	Phe	Ser	Gly	Cys	Gly	Leu	Thr	Ser	Gly	Phe
			100					105					110		
Gly	Phe	Ser	Gly	Cys	Gly	Leu	Thr	Ser	Gly	Phe	Gly	Phe	Ser	Gly	Cys
		115					120					125			
Gly	Leu	Thr	Ser	Gly	Phe	Gly	Phe	Ser	Gly	Cys	Gly	Leu	Thr	Ser	Gly
	130					135					140				
Phe	Gly	Phe	Ser	Gly	Cys	Gly	Leu	Thr	Ser	Gly	Phe	Gly	Phe	Ser	Gly
145					150				155					160	
Cys	Gly	Leu	Thr	Ser	Gly	Phe	Gly	Phe	Ser	Gly	Cys	Gly	Leu	Thr	Ser
				165				170					175		
Gly	Phe	Gly	Phe	Ser	Gly	Cys	Gly	Leu	Thr	Ser	Gly	Phe	Gly	Phe	Ser
			180					185					190		
Gly	Cys	Gly	Leu	Thr	Ser	Gly	Phe	Gly	Phe	Ser	Gly	Cys	Gly	Leu	Thr
	195					200					205				
Ser	Gly	Phe	Gly	Phe	Ser	Ser	Cys	Gly	Leu	Thr	Ser	Gly			
	210					215					220				

(2) INFORMATION FOR SEQ ID NO:3176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...235

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3176:

Lys	Met	Val	Leu	Arg	Gly	Val	Pro	Met	Ser	Gln	Ile	Asp	Leu	Gln	Lys
1				5				10						15	
Leu	Thr	Lys	Lys	Asn	Gln	Glu	Phe	Val	His	Ile	Ala	Thr	Gln	Gln	Phe
			20					25					30		
Ile	Lys	Asp	Gly	Lys	Thr	Asp	Ala	Glu	Ile	Gln	Thr	Ile	Phe	Glu	Glu
		35					40					45			

Val	Ile	Pro	Gln	Ile	Leu	Glu	Gln	Ser	Lys	Gly	Thr	Thr	Ala	Arg
50					55					60				
Ser	Leu	Tyr	Gly	Ala	Pro	Thr	His	Trp	Ala	His	Ser	Phe	Thr	Val
65				70					75					80
Glu	Gln	Tyr	Glu	Lys	Glu	His	Pro	Lys	Glu	Asn	Asp	Asp	Pro	Lys
				85					90					95
Met	Ile	Met	Asp	Ser	Ala	Leu	Phe	Ile	Thr	Ser	Leu	Phe	Ala	Leu
		100						105					110	Val
Ser	Ala	Leu	Thr	Thr	Phe	Phe	Ala	Ala	Asp	Gln	Ala	Phe	Gly	Tyr
		115					120						125	Gly
Leu	Ile	Thr	Leu	Leu	Leu	Val	Gly	Leu	Val	Gly	Gly	Phe	Ala	Phe
	130					135					140			Tyr
Leu	Met	Tyr	Tyr	Phe	Val	Tyr	Gln	Tyr	Tyr	Gly	Pro	Asp	Met	Asp
145					150					155				160
Ser	Gln	Arg	Pro	Pro	Phe	Trp	Lys	Ser	Val	Leu	Val	Ile	Leu	Ala
				165					170					175
Met	Phe	Leu	Trp	Leu	Leu	Val	Phe	Phe	Ala	Thr	Ser	Phe	Leu	Pro
		180						185					190	Ala
Ser	Leu	Asn	Pro	Val	Leu	Asp	Pro	Leu	Pro	Leu	Ala	Ile	Ile	Gly
		195					200						205	Ala
Ala	Leu	Leu	Ala	Leu	Arg	Phe	Tyr	Leu	Lys	Lys	Arg	Leu	Asn	Ile
	210					215					220			Arg
Ser	Ala	Ser	Ala	Gly	Pro	Thr	Arg	Tyr	Gln	Glu				
225					230					235				

(2) INFORMATION FOR SEQ ID NO:3177:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 518 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...518
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3177:

His	Ser	Asn	Tyr	Gln	Gly	Trp	Asp	Met	Lys	Tyr	Arg	Lys	Phe	Gln	Leu
1				5					10					15	
Leu	Met	Ser	Lys	Tyr	Gly	Phe	Ser	Leu	Ser	Ile	Met	Leu	Leu	Glu	Leu
			20					25					30		
Cys	Leu	Val	Phe	Gly	Leu	Phe	Leu	Tyr	Leu	Gly	Arg	Met	Ala	Pro	Ile
		35					40					45			
Leu	Trp	Ile	Thr	Val	Leu	Ile	Leu	Leu	Ile	Ile	Ile	Thr	Ile	Ile	Ser
	50					55					60				
Ile	Phe	Asn	Arg	Asn	Thr	Thr	Pro	Glu	Asn	Lys	Val	Thr	Trp	Leu	Leu
65				70						75				80	
Val	Ala	Phe	Val	Pro	Val	Phe	Gly	Pro	Leu	Leu	Tyr	Leu	Met	Phe	Gly
			85						90					95	

Glu	Arg	Arg	Leu	Ser	Lys	Lys	Glu	Ile	Lys	Gln	Leu	Lys	Lys	Leu	Gly	100	105	110
Ser	Met	His	Phe	Gln	Glu	Ala	Asn	Ser	Gln	Leu	Leu	Lys	Glu	Lys	Leu	115	120	125
Lys	Glu	Ser	Asp	Lys	Ala	Ala	Tyr	Gly	Val	Ile	Lys	Ser	Leu	Leu	Ser	130	135	140
Met	Asp	Thr	Asn	Ala	Asp	Ile	Tyr	Asp	Gln	Thr	Ala	Ser	Thr	Phe	Phe	145	150	155
Pro	Asn	Gly	Glu	Ala	Met	Trp	Lys	Lys	Met	Val	Glu	Asp	Leu	Lys	Lys	165	170	175
Ala	Glu	Lys	Phe	Ile	Phe	Leu	Glu	Tyr	Tyr	Ile	Ile	Glu	Glu	Gly	Leu	180	185	190
Met	Trp	Asn	Arg	Ile	Leu	Asp	Ile	Leu	Glu	Gln	Lys	Val	Ala	Gln	Gly	195	200	205
Val	Glu	Val	Lys	Met	Leu	Tyr	Asp	Asp	Ile	Gly	Cys	Met	Ala	Thr	Leu	210	215	220
Thr	Gly	Asp	Tyr	Ala	His	Arg	Leu	Arg	Gln	Leu	Gly	Ile	Glu	Ala	His	225	230	235
Lys	Phe	Asn	Lys	Val	Ile	Pro	Arg	Leu	Thr	Val	Ala	Tyr	Asn	Asn	Arg	245	250	255
Asp	His	Arg	Lys	Ile	Leu	Ile	Val	Asp	Gly	Gln	Ile	Ala	Tyr	Thr	Gly	260	265	270
Gly	Val	Asn	Leu	Ala	Asp	Glu	Tyr	Ile	Asn	His	Val	Glu	Arg	Phe	Gly	275	280	285
Tyr	Trp	Lys	Asp	Ser	Gly	Ile	Arg	Leu	Asp	Gly	Leu	Ala	Val	Lys	Ala	290	295	300
Leu	Thr	Arg	Leu	Phe	Leu	Thr	Thr	Trp	Tyr	Ile	Asn	Arg	Gly	Glu	Ile	305	310	315
Ser	Asp	Phe	Asp	Gln	Tyr	His	Leu	Glu	Asn	His	Ser	Ile	Pro	Ser	Asp	325	330	335
Gly	Leu	Thr	Ile	Pro	Tyr	Gly	Ser	Gly	Pro	Lys	Pro	Ile	Phe	Arg	Ala	340	345	350
Gln	Val	Gly	Lys	Lys	Val	Tyr	Gln	Ser	Leu	Ile	Asn	Gln	Ala	Thr	Glu	355	360	365
Ser	Val	Tyr	Ile	Thr	Thr	Pro	Tyr	Leu	Ile	Ile	Asp	Tyr	Asp	Leu	Thr	370	375	380
Glu	Thr	Ile	Lys	Asn	Ala	Ala	Met	Arg	Gly	Val	Asp	Val	Arg	Ile	Ile	385	390	395
Thr	Pro	Tyr	Ile	Pro	Asp	Lys	Lys	Phe	Ile	Gln	Leu	Val	Thr	Arg	Gly	405	410	415
Ala	Tyr	Pro	Asp	Phe	Leu	Ser	Ala	Gly	Val	Arg	Ile	Tyr	Glu	Tyr	Ser	420	425	430
Pro	Gly	Phe	Ile	His	Ser	Lys	Gln	Met	Leu	Val	Asp	Glu	Asp	Phe	Ala	435	440	445
Val	Val	Gly	Thr	Ile	Asn	Leu	Asp	Tyr	Arg	Ser	Leu	Val	His	His	Tyr	450	455	460
Glu	Asn	Ala	Val	Leu	Leu	Tyr	Lys	Thr	Pro	Ser	Ile	Arg	Glu	Ile	Ala	465	470	475
Arg	Asp	Phe	Arg	Asn	Ile	Phe	Ala	Asp	Ser	Gln	Glu	Val	Tyr	Pro	His	485	490	495
Ser	Ile	Lys	Thr	Ser	Trp	Tyr	Gln	Lys	Leu	Val	Lys	Glu	Ile	Ala	Gln	500	505	510
Leu	Phe	Ala	Pro	Ile	Leu											515		

(2) INFORMATION FOR SEQ ID NO:3178:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 62 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...62

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3178:

Lys	Leu	Asp	Tyr	Asn	Leu	Leu	Asp	Phe	Leu	Arg	Asn	Lys	Thr	Trp	Tyr
1				5					10					15	
Ser	Ser	Ser	Met	Asn	Tyr	Glu	Ala	Ser	Lys	Gln	Leu	Thr	Asp	Ala	Arg
			20					25					30		
Phe	Lys	Arg	Leu	Val	Gly	Val	Gln	Arg	Thr	Thr	Phe	Glu	Glu	Met	Leu
		35				40						45			
Ala	Val	Leu	Lys	Thr	Ala	Tyr	Gln	Lys	Ser	Arg	Thr	Ser	Trp		
	50					55					60				

(2) INFORMATION FOR SEQ ID NO:3179:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 223 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...223

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3179:

Met	Met	Asp	Tyr	Pro	Tyr	Ala	Thr	Cys	Cys	Ser	Leu	Asn	Asp	Glu	Val
1				5					10					15	
Ala	His	Ala	Phe	Pro	Arg	His	Tyr	Ile	Leu	Lys	Asp	Gly	Asp	Leu	Leu
			20					25					30		
Lys	Val	Asp	Met	Val	Leu	Gly	Arg	Ser	Ile	Ala	Lys	Ser	Asp	Leu	Asn
		35				40						45			
Val	Ser	Lys	Leu	Asn	Phe	Asn	Asn	Val	Glu	Gln	Met	Lys	Lys	Tyr	Thr
	50					55					60				
Gln	Ser	Tyr	Ser	Gly	Gly	Leu	Ala	Asp	Ser	Cys	Trp	Ala	Tyr	Ala	Val
65					70					75					80

Gly	Thr	Pro	Ser	Glu	Glu	Val	Lys	Asn	Leu	Met	Asp	Val	Thr	Lys	Glu
				85					90					95	
Ala	Met	Tyr	Lys	Gly	Ile	Glu	Gln	Ala	Val	Val	Gly	Asn	Arg	Ile	Gly
			100					105					110		
Asp	Ile	Gly	Ala	Ala	Ile	Gln	Glu	Tyr	Ala	Glu	Ser	Arg	Gly	Tyr	Gly
		115					120					125			
Val	Val	Arg	Asp	Leu	Val	Gly	His	Gly	Val	Gly	Pro	Thr	Met	His	Glu
	130					135					140				
Glu	Pro	Met	Val	Pro	Asn	Tyr	Gly	Ile	Ala	Gly	Arg	Gly	Leu	Arg	Leu
145					150					155					160
Arg	Glu	Gly	Met	Val	Leu	Thr	Ile	Glu	Pro	Met	Ile	Asn	Thr	Gly	Asp
			165						170					175	
Trp	Glu	Ile	Asp	Thr	Asp	Met	Lys	Thr	Gly	Trp	Ala	His	Lys	Thr	Ile
			180					185					190		
Asp	Gly	Gly	Leu	Ser	Cys	Gln	Tyr	Glu	His	Gln	Phe	Val	Ile	Thr	Lys
	195						200					205			
Asp	Gly	Pro	Val	Ile	Leu	Thr	Ser	Gln	Gly	Glu	Glu	Gly	Thr	Tyr	
	210					215					220				

(2) INFORMATION FOR SEQ ID NO:3180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 443 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...443

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3180:

Met	Lys	Arg	Tyr	Leu	Gln	Phe	Trp	Leu	Val	Asn	Leu	Ser	Val	Ser	Leu
1				5				10					15		
Ile	Leu	Ile	Ala	Gly	Met	Ala	Leu	Thr	Trp	Ile	Ser	Lys	Gly	Ile	Gly
			20					25					30		
Leu	Phe	Leu	Leu	Ala	Leu	Ser	Leu	Gly	Gln	Gly	Gly	Tyr	Trp	Leu	Phe
	35					40					45				
Cys	Leu	Trp	Lys	Trp	Glu	Val	Ala	Phe	Glu	Thr	Leu	His	Gln	Pro	Leu
	50					55					60				
Leu	Thr	Asn	Ser	Glu	Tyr	Phe	Leu	Glu	Lys	Gly	Gln	Glu	Asp	Leu	Lys
65				70					75					80	
Ser	Leu	Ala	Gln	Tyr	Val	Ser	Ala	Leu	Lys	Thr	Lys	Val	Ser	Gln	Gln
			85					90					95		
Asp	Gln	Gln	Tyr	Lys	Asp	Leu	Pro	Glu	Thr	Met	Glu	Val	Leu	Leu	Ser
		100					105					110			
His	Leu	Thr	Met	Gly	Thr	Phe	Leu	Val	Ser	Ala	Gln	Gly	Gln	Met	Leu
	115						120					125			
Leu	Ser	Ser	Arg	Ser	Leu	Pro	His	Tyr	Phe	Pro	Asp	Val	Asp	Gly	Asp

130		135		140
Ile Ser Ser Leu Asp Asp	Leu Lys Arg Met Asp	Ile Arg Asn Leu Val		
145	150	155	160	
His Gln Ala Phe Asp	Gln Lys Thr Arg Leu Lys	Gln Lys Val Ser Gly		
	165	170	175	
Phe His Glu Gly Asp	Leu Ile Leu Glu Val Thr	Ala Val Pro Val Phe		
	180	185	190	
Ser Pro Thr Gln Ser Val	Glu Ala Val Leu Val Leu	Leu Tyr Asp Leu		
	195	200	205	
Thr Thr Ile Arg Thr Tyr	Glu Lys Leu Asn Leu Ala	Phe Val Ser Asn		
	210	215	220	
Ala Ser His Glu Leu Arg	Thr Pro Val Thr Ser	Ile Lys Gly Phe Ala		
225	230	235	240	
Glu Thr Ile Lys Gly Met	Ser Ala Glu Glu Glu	Ala Leu Lys Asp Asp		
	245	250	255	
Phe Leu Asp Ile Ile Tyr	Lys Glu Ser Leu Arg	Leu Glu His Ile Val		
	260	265	270	
Glu His Leu Leu Thr Leu	Ser Lys Ala Gln Gln	Met Pro Ile Gln Trp		
	275	280	285	
Thr Thr Leu Ser Leu Ala	Glu Phe Val Gln Asp	Leu Thr Gln Ser Leu		
	290	295	300	
Gln Pro Gln Leu Lys Lys	Lys Asp Leu Gln Leu	Lys Val Gln Val Pro		
305	310	315	320	
Asp Asp Val Thr Leu Val	Ser Asp Ser Gln Leu	Leu Ser Gln Ile Leu		
	325	330	335	
Leu Asn Leu Leu Ser Asn	Ala Ile Arg Tyr Thr	Glu Gln Gly Gly Lys		
	340	345	350	
Ile Glu Val Lys Thr Gln	Lys Val Asn Glu Gly	Ile Lys Ile Ser Val		
	355	360	365	
Ser Asp Thr Gly Ile Gly	Ile Ser Gln Leu Glu	Gln Asp Arg Ile Phe		
	370	375	380	
Glu Arg Phe Tyr Arg Val	Asn Lys Gly Arg Ser	Arg Gln Thr Gly Gly		
385	390	395	400	
Thr Gly Leu Gly Leu Ala	Ile Val Lys Glu Leu	Ser Gln Leu Leu Gly		
	405	410	415	
Gly Gln Val Thr Val Thr	Ser Gln Leu Gly Arg	Gly Ser Cys Phe Thr		
	420	425	430	
Ile Phe Leu Pro Asn Gln	Ser Phe Ala Gln Asp			
	435	440		

(2) INFORMATION FOR SEQ ID NO:3181:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 168 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...168

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3181:

Asn	Phe	Gly	Tyr	Asn	Ile	Thr	Thr	Cys	Ser	Ser	Ser	Tyr	Ser	Leu	Gly
1				5					10					15	
Asp	Trp	Val	Val	Ile	Gly	Val	Val	Ala	Arg	Glu	Asn	Ala	Ala	Glu	Gln
		20						25				30			
Ile	Lys	Gln	Tyr	Gln	Lys	Phe	Thr	Val	Asn	Ile	Ser	Asp	Glu	Thr	Ser
	35						40					45			
Met	Leu	Ala	Met	Glu	Gln	Ala	Gly	Phe	Ile	Ser	His	Gln	Glu	Lys	Leu
	50					55					60				
Glu	Arg	Leu	Gly	Val	His	Tyr	Glu	Ile	Ser	Glu	Arg	Thr	Gln	Ile	Ser
65					70				75					80	
Ile	Leu	Asp	Ala	Cys	Pro	Leu	Val	Leu	Asp	Cys	Arg	Val	Asp	Arg	Ile
			85					90					95		
Val	Glu	Glu	Asp	Gly	Ile	Cys	His	Ile	Phe	Ala	Lys	Ile	Leu	Glu	Arg
			100					105					110		
Leu	Val	Ala	Pro	Glu	Phe	Leu	Asp	Glu	Lys	Gly	His	Phe	Lys	Asn	Gln
	115						120					125			
Leu	Phe	Ala	Pro	Thr	Tyr	Phe	Met	Gly	Asp	Gly	Tyr	Gln	Arg	Val	Tyr
	130					135					140				
Arg	Tyr	Leu	Asp	Lys	Arg	Val	Asp	Met	Lys	Gly	Ser	Phe	Ile	Lys	Lys
145				150					155						160
Ala	Arg	Lys	Lys	Asp	Gly	Lys	Asn								
				165											

(2) INFORMATION FOR SEQ ID NO:3182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 599 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...599

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3182:

Ala	Asn	Leu	Tyr	Leu	Lys	Gly	Ile	Leu	Lys	Lys	Gly	Asp	Met	Leu	Met
1				5					10					15	
Lys	Ile	Tyr	Lys	Lys	Leu	Phe	Ala	Tyr	Val	Gln	Asp	Lys	Lys	Tyr	Leu
		20						25				30			
Gly	Val	Leu	Ala	Ile	Ile	Phe	Ser	Ala	Ile	Ser	Ala	Ala	Leu	Thr	Val
	35					40						45			
Tyr	Gly	Tyr	Tyr	Leu	Ile	Tyr	Lys	Phe	Leu	Asp	Lys	Leu	Ile	Ile	Asn
	50					55					60				
Ser	Asn	Leu	Ser	Gly	Ala	Glu	Ser	Ile	Ala	Leu	Lys	Ser	Val	Ile	Thr
65				70					75						80

Leu	Thr	Ser	Gly	Ala	Ile	Phe	Tyr	Phe	Val	Ser	Gly	Met	Phe	Ser	His
				85					90					95	
Ile	Leu	Gly	Phe	Arg	Leu	Glu	Thr	Asn	Leu	Arg	Lys	Arg	Gly	Ile	Asp
			100					105					110		
Gly	Leu	Glu	Lys	Ala	Ser	Phe	Arg	Phe	Phe	Asp	Leu	Asn	Pro	Ser	Gly
		115					120					125			
Gln	Ile	Arg	Lys	Ile	Ile	Asp	Asp	Asn	Ala	Ala	Gln	Thr	His	Gln	Val
	130					135					140				
Val	Ala	His	Met	Ile	Pro	Asp	Ser	Ser	Gln	Ala	Ile	Ile	Thr	Pro	Val
145					150					155					160
Leu	Val	Leu	Ala	Leu	Gly	Phe	Ile	Val	Ser	Ile	Arg	Val	Gly	Ile	Ile
			165						170					175	
Leu	Leu	Ala	Leu	Thr	Ile	Ile	Gly	Gly	Leu	Ile	Leu	Gly	Ala	Met	Met
			180					185					190		
Gly	Glu	Gln	Glu	Phe	Met	Lys	Ile	Tyr	Gln	Glu	Ser	Leu	Ser	Lys	Leu
		195					200					205			
Ser	Ala	Glu	Thr	Val	Glu	Tyr	Val	Arg	Gly	Met	Gln	Val	Val	Lys	Ile
	210					215					220				
Phe	Lys	Ala	Asn	Val	Glu	Ser	Phe	Lys	Ser	Phe	Tyr	Lys	Ala	Ile	Lys
225					230					235					240
Asp	Tyr	Ser	Lys	Tyr	Ala	Tyr	Asp	Tyr	Ser	Leu	Ser	Cys	Lys	Arg	Pro
			245						250					255	
Tyr	Val	Leu	Tyr	Gln	Trp	Leu	Phe	Phe	Gly	Leu	Ile	Ala	Ile	Leu	Ile
		260						265					270		
Ile	Pro	Ile	Val	Tyr	Phe	Met	Thr	Ser	Leu	Ala	Ser	Ala	Lys	Val	Ile
	275					280						285			
Leu	Leu	Glu	Leu	Ile	Met	Ile	Leu	Phe	Leu	Ser	Gly	Val	Leu	Phe	Val
	290				295						300				
Ser	Phe	Met	Arg	Met	Met	Trp	Tyr	Ser	Met	Tyr	Ile	Ser	Gln	Gly	Asn
305					310					315					320
Tyr	Ala	Val	Asp	Thr	Leu	Glu	Ala	Leu	Tyr	Glu	Asp	Met	Gln	Lys	Asp
			325						330					335	
Lys	Leu	Val	His	Gly	Asn	Val	Asn	Asn	Phe	Lys	Asn	Tyr	Asn	Ile	Glu
		340					345						350		
Phe	Glu	Asn	Val	Ser	Phe	Ala	Tyr	Asn	Asp	Lys	Ala	Val	Ile	Glu	Asn
	355					360						365			
Leu	Ser	Phe	Asn	Leu	Glu	Glu	Gly	Lys	Ser	Tyr	Ala	Leu	Val	Gly	Ser
	370				375						380				
Ser	Gly	Ser	Gly	Lys	Ser	Thr	Val	Ala	Lys	Leu	Ile	Ser	Gly	Phe	Tyr
385					390					395					400
Asn	Val	Asn	Lys	Gly	Ser	Ile	Lys	Ile	Gly	Gly	Ile	Ala	Ile	Ser	Glu
			405						410					415	
Tyr	Ser	Asp	Glu	Ala	Leu	Ile	Lys	Ala	Ile	Ser	Phe	Val	Phe	Gln	Asp
		420						425					430		
Ser	Lys	Leu	Phe	Lys	Lys	Ser	Ile	Tyr	Asp	Asn	Val	Ala	Leu	Ala	Asn
	435						440					445			
Lys	Asp	Ala	Thr	Lys	Asp	Asp	Val	Met	Arg	Ala	Leu	Lys	Leu	Ala	Gly
	450				455						460				
Cys	Asp	Leu	Ile	Leu	Asp	Lys	Phe	Pro	Glu	Arg	Glu	Asn	Thr	Ile	Ile
465					470					475					480
Gly	Ser	Lys	Gly	Val	Tyr	Leu	Ser	Gly	Gly	Glu	Lys	Gln	Arg	Ile	Ala
			485						490					495	
Ile	Ala	Arg	Ala	Ile	Leu	Lys	Asp	Ser	Lys	Ile	Ile	Ile	Met	Asp	Glu
	500						505						510		
Ala	Ser	Ala	Ser	Ile	Asp	Pro	Asp	Asn	Glu	Phe	Glu	Leu	Gln	Lys	Ala
	515						520					525			
Phe	Lys	Asn	Leu	Met	Lys	Asp	Lys	Thr	Val	Ile	Met	Ile	Ala	His	Arg

530		535		540
Leu Ser Thr Ile Lys Asp	Leu Asp Glu Ile Ile Val Met Asp Ser Gly			
545	550	555	560	
Lys Ile Ile Glu Arg Gly Ser Asp Lys Glu Leu Met Ser Lys Asp Thr				
	565	570	575	
Arg Tyr Lys Ser Leu Gln Glu Met Phe Asn Ile Ala Asn Glu Trp Arg				
	580	585	590	
Val Ser Asn Glu Arg Val Leu				
595				

(2) INFORMATION FOR SEQ ID NO:3183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...298

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3183:

Arg	Leu	Ser	Leu	Lys	Tyr	Gly	Met	Ile	Lys	Asp	Ile	Gln	Gly	Asp	Lys
1			5						10					15	
Met	Asn	Asn	Asn	Leu	Leu	Val	Leu	Gln	Ser	Asp	Phe	Gly	Leu	Val	Asp
			20					25					30		
Gly	Ala	Val	Ser	Ala	Met	Ile	Gly	Val	Ala	Leu	Glu	Glu	Ser	Pro	Thr
			35				40					45			
Leu	Lys	Ile	His	His	Leu	Thr	His	Asp	Ile	Thr	Pro	Tyr	Asn	Ile	Phe
	50				55				60						
Glu	Gly	Ser	Tyr	Arg	Leu	Phe	Gln	Thr	Val	Asp	Tyr	Trp	Pro	Glu	Gly
65				70					75					80	
Thr	Thr	Phe	Val	Ser	Val	Val	Asp	Pro	Gly	Val	Gly	Ser	Lys	Arg	Lys
			85					90					95		
Ser	Val	Val	Ala	Lys	Thr	Ala	Lys	Asn	Gln	Tyr	Ile	Val	Thr	Pro	Asp
			100					105					110		
Asn	Gly	Thr	Leu	Ser	Phe	Ile	Lys	Lys	His	Val	Gly	Ile	Val	Ala	Ile
			115				120					125			
Arg	Glu	Ile	Ser	Glu	Val	Ala	Asn	Arg	Arg	Gln	Asn	Thr	Glu	His	Ser
	130					135				140					
Tyr	Thr	Phe	His	Gly	Arg	Asp	Val	Tyr	Ala	Tyr	Thr	Gly	Ala	Lys	Leu
145				150					155					160	
Ala	Ser	Gly	His	Ile	Thr	Phe	Glu	Glu	Val	Gly	Pro	Glu	Leu	Ser	Val
			165					170					175		
Glu	Gln	Ile	Val	Glu	Leu	Pro	Val	Val	Ala	Thr	Ile	Ile	Glu	Asp	His
			180				185					190			
Leu	Val	Lys	Gly	Ala	Ile	Asp	Ile	Leu	Asp	Val	Arg	Phe	Gly	Ser	Leu
	195					200				205					
Trp	Thr	Ser	Ile	Thr	Arg	Glu	Glu	Phe	Tyr	Lys	Leu	Glu	Pro	Glu	Phe

210	215	220
Gly Asp Arg Phe Glu Val Thr Ile Tyr His Ala Asp Met Leu Val Tyr		
225	230	235
Gln Asn Gln Val Val Tyr Gly Lys Ser Phe Ala Asp Val Arg Ile Gly		240
	245	250
Gln Pro Ile Leu Tyr Ile Asn Ser Leu Tyr Arg Leu Gly Leu Ala Ile		255
	260	265
Asn Gln Gly Ser Phe Ala Lys Ala Tyr Asn Val Gly Val Gly Ser Ser		270
	275	280
Trp Thr Ile Glu Ile Lys Lys Ile Glu Gly		285
290	295	

(2) INFORMATION FOR SEQ ID NO:3184:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...70

(xi) SEQUENCE DESCRIPTION: .SEQ ID NO:3184:

Arg Leu Leu Tyr Gln Glu Lys Ile Thr Tyr His Val Lys Asp Asn Gln	
1	15
Leu Glu Val Glu Thr Asp Lys Tyr Thr Tyr Thr Ala Ala Arg Asn Gly	
	30
Ser Lys Glu Val Gly Ile Gln Glu Ser Asp Ile Ala Ala Thr Leu Ser	
	45
Ala Asp Glu Tyr Asn Ser Asn Arg Gln Thr Phe Glu Arg Glu Tyr Lys	
50	60
Tyr Lys Ser Lys Cys Pro	
65	70

(2) INFORMATION FOR SEQ ID NO:3185:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...64

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3185:

Tyr	Ser	Leu	Tyr	Tyr	Ile	Asn	Asn	Gln	Leu	Arg	Arg	Asn	Leu	Val	Arg
1				5					10					15	
Ile	His	Ala	Ser	Thr	His	Lys	Glu	Leu	Leu	Lys	Lys	Phe	Thr	Val	Phe
			20					25					30		
Ile	Ile	Ile	Phe	Glu	Glu	Lys	Asn	Ser	Glu	Lys	Lys	Lys	Lys	Ala	Cys
		35				40						45			
Ser	Val	Ser	Tyr	Arg	Phe	Leu	Ala	Asp	Gly	Leu	Phe	Ser	Arg	Leu	Cys
	50					55					60				

(2) INFORMATION FOR SEQ ID NO:3186:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 601 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...601

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3186:

Ser	Ile	Leu	Tyr	Lys	Val	Asn	Tyr	Asp	Asn	Met	Glu	Val	Leu	Cys	Met
1				5					10					15	
Val	Asp	Lys	Gln	Val	Ile	Glu	Glu	Ile	Lys	Asn	Asn	Ala	Asn	Ile	Val
			20					25					30		
Glu	Val	Ile	Gly	Asp	Val	Ile	Ser	Leu	Gln	Lys	Ala	Gly	Arg	Asn	Tyr
		35				40						45			
Leu	Gly	Leu	Cys	Pro	Phe	His	Gly	Glu	Lys	Thr	Pro	Ser	Phe	Asn	Val
	50					55				60					
Val	Glu	Asp	Lys	Gln	Phe	Tyr	His	Cys	Phe	Gly	Cys	Gly	Arg	Ser	Gly
65					70				75						80
Asp	Val	Phe	Lys	Phe	Ile	Glu	Glu	Tyr	Gln	Gly	Val	Thr	Phe	Met	Glu
			85					90						95	
Ala	Val	Gln	Ile	Leu	Gly	Gln	Arg	Val	Gly	Ile	Glu	Val	Glu	Lys	Pro
		100						105					110		
Leu	Tyr	Ser	Glu	Gln	Lys	Pro	Ala	Ser	Pro	His	Gln	Ala	Leu	Tyr	Asp
		115				120						125			
Met	His	Glu	Asp	Ala	Ala	Lys	Phe	Tyr	His	Ala	Ile	Leu	Met	Thr	Thr
	130					135				140					
Thr	Met	Gly	Glu	Glu	Ala	Arg	Asn	Tyr	Leu	Tyr	Gln	Arg	Gly	Leu	Thr
145					150					155					160
Asp	Glu	Val	Leu	Lys	His	Phe	Trp	Ile	Gly	Leu	Ala	Pro	Pro	Glu	Arg

				165					170					175			
Asn	Tyr	Leu	Tyr	Gln	Arg	Leu	Ser	Asp	Gln	Tyr	Arg	Glu	Glu	Asp	Leu		
			180					185						190			
Leu	Asp	Ser	Gly	Leu	Phe	Tyr	Leu	Ser	Asp	Ala	Asn	Gln	Phe	Val	Asp		
		195					200					205					
Thr	Phe	His	Asn	Arg	Ile	Met	Phe	Pro	Leu	Thr	Asn	Asp	Gln	Gly	Lys		
	210					215					220						
Val	Ile	Ala	Phe	Ser	Gly	Arg	Ile	Trp	Gln	Lys	Thr	Asp	Ser	Gln	Thr		
225					230					235					240		
Ser	Lys	Tyr	Lys	Asn	Ser	Arg	Ser	Thr	Ala	Ile	Phe	Asn	Lys	Ser	Tyr		
				245					250					255			
Glu	Leu	Tyr	His	Met	Asp	Arg	Ala	Lys	Lys	Ser	Ser	Gly	Lys	Ala	Ser		
			260					265					270				
Glu	Ile	Tyr	Leu	Met	Glu	Gly	Phe	Met	Asp	Val	Ile	Ala	Ala	Tyr	Arg		
	275						280					285					
Val	Gly	Ile	Glu	Asn	Ala	Val	Ala	Ser	Met	Gly	Thr	Ala	Leu	Ser	Arg		
	290					295					300						
Glu	His	Val	Glu	His	Leu	Lys	Arg	Leu	Thr	Lys	Lys	Leu	Val	Leu	Val		
305					310					315					320		
Tyr	Asp	Gly	Asp	Lys	Ala	Gly	Gln	Ala	Ala	Ile	Leu	Lys	Ala	Leu	Asp		
				325					330					335			
Glu	Ile	Gly	Asp	Met	Pro	Val	Gln	Ile	Val	Ser	Met	Pro	Asp	Asn	Leu		
		340					345						350				
Asp	Pro	Asp	Glu	Tyr	Leu	Gln	Lys	Asn	Gly	Pro	Glu	Asp	Leu	Ala	Tyr		
	355					360					365						
Leu	Leu	Thr	Lys	Thr	Arg	Ile	Ser	Pro	Ile	Glu	Phe	Tyr	Ile	His	Gln		
	370				375						380						
Tyr	Lys	Pro	Glu	Asn	Ser	Glu	Asn	Leu	Gln	Ala	Gln	Ile	Glu	Phe	Ile		
385				390					395						400		
Glu	Lys	Ile	Ala	Pro	Leu	Ile	Val	Lys	Glu	Lys	Ser	Ile	Ala	Ala	Gln		
			405						410				415				
Asn	Ser	Tyr	Ile	His	Ile	Leu	Ala	Asp	Ser	Leu	Ala	Ser	Phe	Asp	Tyr		
			420				425						430				
Ala	Gln	Ile	Glu	Gln	Ile	Val	Asn	Glu	Ser	Arg	Gln	Val	Gln	Arg	Gln		
	435					440						445					
Asn	Arg	Met	Glu	Arg	Ile	Ser	Arg	Pro	Thr	Pro	Ile	Thr	Met	Pro	Val		
	450				455						460						
Thr	Lys	Gln	Leu	Ser	Ala	Ile	Met	Arg	Ala	Glu	Ala	His	Leu	Leu	Tyr		
465				470					475						480		
Arg	Met	Met	Glu	Ser	Pro	Leu	Val	Leu	Asn	Asp	Tyr	Arg	Leu	Arg	Glu		
			485					490					495				
Asp	Phe	Ala	Phe	Ala	Thr	Pro	Glu	Phe	Gln	Val	Leu	Tyr	Asp	Leu	Leu		
		500					505					510					
Gly	Gln	Tyr	Gly	Asn	Leu	Pro	Pro	Glu	Val	Leu	Ala	Glu	Gln	Thr	Glu		
	515					520						525					
Glu	Val	Glu	Arg	Ala	Trp	Tyr	Gln	Val	Leu	Ala	Gln	Asp	Leu	Pro	Ala		
	530				535						540						
Glu	Ile	Ser	Pro	Gln	Glu	Leu	Ser	Glu	Val	Glu	Met	Thr	Arg	Asn	Lys		
545				550					555						560		
Ala	Leu	Leu	Asn	Gln	Asp	Asn	Met	Arg	Ile	Lys	Lys	Lys	Val	Gln	Glu		
			565				570						575				
Ala	Ser	His	Val	Gly	Asp	Thr	Asp	Thr	Ala	Leu	Glu	Glu	Leu	Glu	Arg		
		580				585						590					
Leu	Ile	Ser	Gln	Lys	Arg	Arg	Met	Glu									
	595					600											

(2) INFORMATION FOR SEQ ID NO:3187:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 65 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...65

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3187:

```

Leu Cys Ile Tyr Phe Val Ile Leu Phe Ser Leu Ile Val Ser Asn Ala
1      5      10      15
Leu Val Ala Ser Ser Lys Ile Thr Ile Leu Gly Leu Phe Ile Asn Ala
      20      25      30
Arg Ala Ser Ala Ile Arg Cys Leu Cys Pro Pro Glu Ile Phe Asp Pro
      35      40      45
Ile Ser Glu Met Ile Val Leu Asn Phe Ile Gly Ile Ala Met Ile Ser
50      55      60
Ser
65

```

(2) INFORMATION FOR SEQ ID NO:3188:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 157 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...157

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3188:

```

Arg Ser Ser Leu Asn Ser Gln Phe Ala His Ile Phe Arg Ala Thr Ser
1      5      10      15
Tyr Phe Ser Asp Trp Ile Trp Thr Cys Gly His Asn Phe Thr Lys Lys
      20      25      30
Phe Ser Gln Asp Ser Pro Lys Met Lys Met Gly Thr Tyr Ile Val Val
      35      40      45
Gly Thr Ile Val Leu Leu Val Val Leu Gly Tyr Val Gly Leu Ala Ser

```

50		55		60											
Tyr	Ile	Gln	Glu	Gly	Ala	Phe	Tyr	Ile	Pro	Ala	Pro	Trp	Asp	Ser	Leu
65					70					75					80
Ser	Val	Phe	Thr	Ile	Ser	Leu	Val	Ile	Gly	Ile	Trp	Ser	Trp	Lys	Glu
					85					90					95
Ala	Val	Phe	Arg	Pro	Phe	Val	Ser	Met	Ile	Ile	Ala	His	Leu	Val	Val
					100					105					110
Gly	Ser	Leu	Leu	Arg	Tyr	Tyr	Glu	Trp	Met	Gly	Ile	Ser	Asn	Val	Phe
					115					120					125
Leu	Thr	Lys	Val	Ile	Pro	Leu	Ala	Val	Leu	Phe	Ile	Gly	Ile	Phe	Val
					130					135					140
Leu	Phe	Arg	Gly	Phe	Lys	Lys	Ile	Lys	Trp	Ser	Glu	Val			
145					150					155					

(2) INFORMATION FOR SEQ ID NO:3189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...82

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3189:

Lys	Val	Ile	Tyr	Tyr	Met	Asp	Thr	Lys	Met	Met	Ser	Gln	Phe	Ser	Val
1					5				10					15	
Met	Asp	Asn	Glu	Met	Leu	Val	Arg	Thr	Glu	Asp	Gly	Asp	Val	Ser	Asp
					20				25				30		
Ile	Tyr	Arg	Gly	Tyr	Ala	Asn	Gln	Arg	Ser	Pro	Phe	Ala	Ser	Tyr	Pro
					35			40				45			
Ser	Ile	Leu	Lys	Asn	Ser	Gly	Pro	Phe	Pro	Val	Ser	Gly	Tyr	Cys	Leu
					50		55				60				
Arg	Gly	Tyr	His	Asp	Arg	Gly	Tyr	Ile	Gly	Ala	Gly	Phe	His	Leu	Cys
65					70					75					80
Gly	Ile														

(2) INFORMATION FOR SEQ ID NO:3190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 862 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...862

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3190:

Asp	Thr	Val	Tyr	Ser	Phe	Ser	Phe	Xaa	His	Ile	Ser	Asn	Ser	Phe	Lys
1				5					10					15	
Asn	Gly	Ile	Ile	Val	Thr	Ser	Gln	Asn	Trp	Arg	Glu	Thr	Met	Ser	Phe
			20					25					30		
Tyr	Asn	His	Lys	Glu	Ile	Glu	Pro	Lys	Trp	Gln	Gly	Tyr	Xaa	Ala	Glu
			35				40					45			
His	His	Thr	Xaa	Lys	Thr	Gly	Thr	Asp	Ala	Ser	Lys	Pro	Lys	Phe	Tyr
			50			55					60				
Ala	Leu	Asp	Met	Phe	Pro	Tyr	Pro	Ser	Gly	Ala	Gly	Leu	His	Val	Gly
65				70					75					80	
His	Pro	Glu	Gly	Tyr	Thr	Ala	Thr	Asp	Ile	Leu	Ser	Arg	Tyr	Lys	Arg
				85				90						95	
Ala	Gln	Gly	Tyr	Asn	Val	Leu	His	Pro	Met	Gly	Trp	Asp	Ala	Phe	Gly
			100					105					110		
Leu	Pro	Ala	Glu	Gln	Tyr	Ala	Met	Asp	Thr	Gly	Asn	Asp	Pro	Ala	Glu
			115				120					125			
Phe	Thr	Ala	Glu	Asn	Ile	Ala	Asn	Phe	Lys	Arg	Gln	Ile	Asn	Ala	Leu
			130			135					140				
Gly	Phe	Ser	Tyr	Asp	Trp	Asp	Arg	Glu	Val	Asn	Thr	Thr	Asp	Pro	Asn
145				150					155					160	
Tyr	Tyr	Lys	Trp	Thr	Gln	Trp	Ile	Phe	Thr	Lys	Leu	Tyr	Glu	Lys	Gly
				165				170						175	
Leu	Ala	Tyr	Glu	Ala	Glu	Val	Pro	Val	Asn	Trp	Val	Glu	Glu	Leu	Gly
			180					185					190		
Thr	Ala	Ile	Ala	Asn	Glu	Glu	Val	Leu	Pro	Asp	Gly	Thr	Ser	Glu	Arg
			195				200					205			
Gly	Gly	Tyr	Pro	Val	Val	Arg	Lys	Pro	Met	Arg	Gln	Trp	Met	Leu	Lys
			210			215					220				
Ile	Thr	Ala	Tyr	Ala	Glu	Arg	Leu	Leu	Asn	Asp	Leu	Asp	Glu	Leu	Asp
225				230					235					240	
Trp	Ser	Glu	Ser	Ile	Lys	Asp	Met	Gln	Arg	Asn	Trp	Ile	Gly	Lys	Ser
				245				250						255	
Thr	Gly	Ala	Asn	Val	Thr	Phe	Lys	Val	Lys	Gly	Thr	Asp	Lys	Glu	Phe
			260					265					270		
Thr	Val	Phe	Thr	Thr	Arg	Pro	Asp	Thr	Leu	Phe	Gly	Ala	Thr	Phe	Thr
			275				280					285			
Val	Leu	Ala	Pro	Glu	His	Glu	Leu	Val	Asp	Ala	Ile	Thr	Ser	Ser	Glu
			290			295					300				
Gln	Ala	Glu	Ala	Val	Ala	Asp	Tyr	Lys	His	Gln	Ala	Ser	Leu	Lys	Ser
305				310					315					320	
Asp	Leu	Ala	Arg	Thr	Asp	Leu	Ala	Lys	Glu	Lys	Thr	Gly	Val	Trp	Thr
				325					330					335	
Gly	Ala	Tyr	Ala	Ile	Asn	Pro	Val	Asn	Gly	Lys	Glu	Met	Pro	Ile	Trp
			340				345					350			
Ile	Ala	Asp	Tyr	Val	Leu	Ala	Ser	Tyr	Gly	Thr	Gly	Ala	Val	Met	Ala
		355				360					365				
Val	Pro	Ala	His	Asp	Gln	Arg	Asp	Trp	Glu	Phe	Ala	Lys	Gln	Phe	Asp

370	375	380
Leu Pro Ile Val Glu Val	Leu Glu Gly Gly Asp Val	Lys Glu Ala Ala
385	390	395
Tyr Thr Glu Asp Gly Leu	His Val Asn Ser Asp Phe	Leu Asp Glu Leu
405	410	415
Asn Lys Glu Asp Ala Ile	Ala Lys Ile Val Ala	Trp Leu Glu Glu Lys
420	425	430
Gly Cys Gly Gln Glu Lys	Val Thr Tyr Arg Leu Arg	Asp Trp Leu Phe
435	440	445
Ser Arg Gln Arg Tyr Trp	Gly Glu Pro Ile Pro	Ile Ile His Trp Glu
450	455	460
Asp Gly Thr Ser Thr Ala	Val Pro Glu Thr Glu	Leu Pro Leu Val Leu
465	470	475
Pro Val Thr Lys Asp Ile	Arg Pro Ser Gly Thr	Gly Glu Ser Pro Leu
485	490	495
Ala Asn Leu Thr Asp Trp	Leu Glu Val Thr Arg	Glu Asp Gly Val Lys
500	505	510
Gly Arg Arg Glu Thr Asn	Thr Met Pro Gln Trp	Ala Gly Ser Ser Trp
515	520	525
Tyr Tyr Leu Arg Tyr Ile	Asp Pro His Asn Thr	Glu Lys Leu Ala Asp
530	535	540
Glu Asp Leu Leu Lys Gln	Trp Leu Pro Val Asp	Ile Tyr Val Gly Gly
545	550	555
Ala Glu His Ala Val Leu	His Leu Leu Tyr Ala	Arg Phe Trp His Lys
565	570	575
Phe Leu Tyr Asp Leu Gly	Val Val Pro Thr Lys	Glu Pro Phe Gln Lys
580	585	590
Leu Phe Asn Gln Gly Met	Ile Leu Gly Thr Ser	Tyr Arg Asp His Arg
595	600	605
Gly Ala Leu Val Ala Thr	Asp Lys Val Glu Lys	Arg Asp Gly Ser Phe
610	615	620
Phe His Ile Glu Thr Gly	Glu Glu Leu Glu Gln	Ala Pro Ala Lys Met
625	630	635
Ser Lys Ser Leu Lys Asn	Val Val Asn Pro Asp	Asp Val Val Glu Gln
645	650	655
Tyr Gly Ala Asp Thr Leu	Arg Val Tyr Glu Met	Phe Met Gly Pro Leu
660	665	670
Asp Ala Ser Ile Ala Trp	Ser Glu Glu Gly Leu	Glu Gly Ser Arg Lys
675	680	685
Phe Leu Asp Arg Val Tyr	Arg Leu Ile Thr Ser	Lys Glu Ile Leu Ala
690	695	700
Glu Asn Asn Gly Ala Leu	Asp Lys Ala Tyr Asn	Glu Thr Val Lys Ala
705	710	715
Val Thr Glu Gln Ile Glu	Ser Leu Lys Phe Asn	Thr Ala Ile Ala Gln
725	730	735
Leu Met Val Phe Val Asn	Ala Ala Asn Lys Glu	Asp Lys Leu Tyr Val
740	745	750
Asp Tyr Ala Lys Gly Phe	Ile Gln Leu Ile Ala	Pro Phe Ala Pro His
755	760	765
Leu Ala Glu Glu Leu Trp	Gln Thr Val Ala Glu	Thr Gly Glu Ser Ile
770	775	780
Ser Tyr Val Ala Trp Pro	Thr Trp Asp Glu Ser	Lys Leu Val Glu Asp
785	790	795
Glu Ile Glu Ile Val Val	Gln Ile Lys Gly Lys	Val Arg Ala Lys Leu
805	810	815
Met Val Ala Lys Asp Leu	Ser Arg Glu Glu Leu	Gln Glu Ile Ala Leu
820	825	830

Ala	Asp	Glu	Lys	Val	Lys	Ala	Glu	Ile	Asp	Gly	Lys	Glu	Ile	Val	Lys
		835					840					845			
Val	Ile	Ser	Val	Pro	Asn	Lys	Leu	Val	Asn	Ile	Val	Val	Lys		
	850					855					860				

(2) INFORMATION FOR SEQ ID NO:3191:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 403 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3191:

Pro	Ser	Ser	Leu	Val	Phe	Leu	Trp	Tyr	Asn	Arg	Ala	Met	Lys	His	Phe
1				5					10					15	
Asp	Thr	Ile	Val	Ile	Gly	Gly	Gly	Pro	Ala	Gly	Met	Met	Ala	Thr	Ile
			20					25					30		
Ser	Ser	Asn	Phe	Tyr	Gly	Gln	Lys	Thr	Leu	Leu	Ile	Glu	Lys	Asn	Arg
		35					40					45			
Lys	Leu	Gly	Lys	Lys	Leu	Ala	Gly	Thr	Gly	Gly	Gly	Arg	Cys	Asn	Val
	50					55				60					
Thr	Asn	Asn	Gly	Ser	Leu	Asp	Asn	Leu	Leu	Ala	Gly	Ile	Pro	Gly	Asn
65					70					75					80
Gly	Arg	Phe	Leu	Tyr	Ser	Val	Phe	Ser	Gln	Phe	Asp	Asn	His	Asp	Ile
			85						90					95	
Ile	Asn	Phe	Phe	Thr	Glu	Asn	Gly	Val	Lys	Leu	Lys	Val	Glu	Asp	His
		100						105					110		
Gly	Arg	Val	Phe	Pro	Ala	Ser	Asp	Lys	Ser	Arg	Thr	Ile	Ile	Glu	Ala
		115					120					125			
Leu	Glu	Lys	Lys	Ile	Thr	Glu	Leu	Gly	Gly	Gln	Val	Ala	Thr	Gln	Ile
	130					135					140				
Glu	Ile	Val	Ser	Val	Lys	Lys	Val	Asp	Asp	Gln	Phe	Val	Leu	Lys	Ser
145					150					155					160
Ala	Asp	Gln	Thr	Phe	Thr	Cys	Glu	Lys	Leu	Ile	Val	Thr	Thr	Gly	Gly
			165						170					175	
Lys	Ser	Tyr	Pro	Ser	Thr	Gly	Ser	Thr	Gly	Phe	Gly	His	Glu	Ile	Ala
		180						185					190		
Arg	His	Phe	Lys	His	Thr	Ile	Thr	Asp	Leu	Glu	Ala	Ala	Glu	Ser	Pro
		195					200					205			
Leu	Leu	Thr	Asp	Phe	Pro	His	Lys	Ala	Leu	Gln	Gly	Ile	Ser	Leu	Asp
	210					215					220				
Asp	Val	Thr	Leu	Ser	Tyr	Gly	Lys	His	Val	Ile	Thr	His	Asp	Leu	Leu
225					230					235					240
Phe	Thr	His	Phe	Gly	Leu	Ser	Gly	Pro	Ala	Ala	Leu	Arg	Met	Ser	Ser

				245				250					255				
Phe	Val	Lys	Gly	Gly	Glu	Val	Leu	Ser	Leu	Asp	Val	Leu	Pro	Gln	Leu		
			260					265					270				
Ser	Glu	Lys	Asp	Leu	Val	Thr	Phe	Leu	Glu	Glu	Asn	Arg	Glu	Lys	Ser		
		275					280					285					
Leu	Lys	Asn	Ala	Leu	Lys	Thr	Leu	Leu	Pro	Glu	Arg	Leu	Ala	Glu	Phe		
	290					295					300						
Phe	Val	Gln	Gly	Tyr	Pro	Glu	Lys	Val	Lys	Gln	Leu	Thr	Glu	Lys	Glu		
305					310					315					320		
Arg	Glu	Gln	Leu	Val	Gln	Ser	Ile	Lys	Glu	Leu	Lys	Ile	Pro	Val	Thr		
			325						330				335				
Gly	Lys	Met	Ser	Leu	Ala	Lys	Ser	Phe	Val	Thr	Lys	Gly	Gly	Val	Ser		
		340					345					350					
Leu	Lys	Glu	Ile	Asn	Pro	Lys	Thr	Leu	Glu	Ser	Lys	Leu	Val	Pro	Gly		
	355					360					365						
Leu	His	Phe	Ala	Gly	Glu	Val	Met	Asp	Ile	Asn	Ala	His	Thr	Gly	Gly		
370					375				380								
Phe	Asn	Ile	Thr	Ser	Ala	Leu	Cys	Thr	Gly	Trp	Val	Ala	Gly	Ser	Leu		
385				390					395						400		
His	Tyr	Asp															

(2) INFORMATION FOR SEQ ID NO:3192:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...154

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3192:

Lys	Lys	Ser	Leu	Asn	Lys	Glu	Asp	Thr	Ile	Met	Asp	Ile	Trp	Glu	Lys		
1				5				10					15				
Met	Tyr	Glu	Glu	Ala	Gln	Lys	Leu	Tyr	Asn	Pro	His	Glu	Val	Ser	Asp		
		20					25					30					
Phe	Val	Tyr	Ala	Asn	His	Val	Val	Ala	Ala	Val	Glu	Ala	Glu	Asp	Gly		
	35				40						45						
Gln	Ile	Phe	Thr	Gly	Phe	Cys	Met	Glu	Gly	Thr	Cys	Gly	Val	Phe	His		
	50				55						60						
Leu	Cys	Ala	Glu	Arg	Ala	Ala	Leu	Phe	Asn	Met	Tyr	Gln	Phe	Ser	Gly		
65				70				75						80			
Gln	Thr	Lys	Val	Lys	Lys	Val	Leu	Ala	Phe	Arg	Asp	Lys	Pro	Pro	Tyr		
		85					90					95					
Gly	Gly	Ser	Ser	Ala	Met	Pro	Cys	Gly	Ala	Cys	Arg	Glu	Phe	Leu	Leu		
		100					105					110					

Glu	Leu	Asn	Ala	Glu	Asn	Lys	Asp	Ala	Glu	Phe	Met	Met	Asp	Tyr	Asn
		115					120					125			
Ile	Arg	Lys	Thr	Val	Lys	Val	Ala	Glu	Leu	Ile	Pro	Tyr	Trp	Trp	Gly
	130					135					140				
Glu	Glu	Arg	Ala	Ser	Lys	Phe	Asn	Glu	Arg						
145					150										

(2) INFORMATION FOR SEQ ID NO:3193:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 146 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...146
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3193:

Leu	Ile	Ser	Tyr	His	Cys	Tyr	Ile	Met	Leu	Xaa	Asp	Xaa	Ser	Leu	Val
1				5					10					15	
Leu	Val	Ser	Arg	Leu	Lys	Thr	Leu	Glu	Asn	Leu	Leu	Arg	Ser	Leu	Thr
			20					25					30		
Gly	Val	Ser	Asn	Pro	Thr	Thr	Asp	Ser	Ala	Arg	Leu	Val	Leu	Ala	Glu
			35				40					45			
Ala	Lys	Lys	Ala	Phe	Ala	Asp	Asp	Ser	Leu	Thr	Glu	Gln	Gly	Leu	Arg
			50			55					60				
Asp	Ile	Leu	Gln	Thr	Val	Lys	Asp	Ala	Ile	Ala	Ser	Leu	Glu	Ser	Ile
65					70				75					80	
Lys	Glu	Ser	Gln	Ser	Ala	Thr	Lys	Asp	Gly	Gly	Gln	Thr	Ala	Gly	Lys
				85					90					95	
Glu	Thr	Ala	Asp	Lys	Asp	Val	Leu	Glu	Asn	Ser	Gln	Glu	Glu	Leu	Gln
			100					105					110		
Lys	Ala	Val	Leu	Phe	Leu	Ala	Asp	Glu	Lys	Gly	Ser	Glu	His	Thr	Glu
			115				120					125			
Ala	Glu	Leu	Ile	Asp	Asn	Leu	Lys	Glu	Val	Ile	Ala	Lys	Leu	Lys	Ala
	130					135					140				
Asn	Ala														
145															

(2) INFORMATION FOR SEQ ID NO:3194:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 99 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...99

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3194:

```
Ser Cys Ser Tyr Leu Ile Ser Ile Tyr Tyr Ser Thr Lys Leu Glu Lys
1      5      10      15
Glu Lys Ile Met Thr Lys Thr Ile Leu Val Thr Gly Gly Thr Ser Tyr

      20      25      30
Ile Gly Ser His Thr Val Lys Ala Leu Leu Asn Ala Gly Tyr Gln Val
      35      40      45
His Val Leu Asp Asn Leu Ser Thr Gly Asn Arg Ala Ala Val Asp Ser
      50      55      60
Arg Ala Ser Phe Lys Glu Leu Asp Val Tyr Asp Ala Ser Ala Leu Lys
      65      70      75      80
Ala Tyr Leu Lys Lys Asn Gln Ile Asp Ala Val Phe Pro Phe Pro Val
      85      90      95
Glu Ile Phe
```

(2) INFORMATION FOR SEQ ID NO:3195:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 104 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3195:

```
Asn Ala Ser Tyr Gln Ala Arg Lys Phe His Glu Val Asn Tyr Ser Gln
1      5      10      15
Lys Ala Glu Gln Gln Ala Lys Thr Pro Lys Lys Gly Gly Lys Lys Gln
      20      25      30
Ala Pro Ala Ser Asn Val Pro Lys Trp Ser Asn Pro Asp Tyr Val Asn
      35      40      45
Glu Leu Asp Pro Lys Ile Val Asp Met Leu Val Glu Phe His Lys Ser
      50      55      60
Gln Gly Thr Leu Glu Thr Pro Glu Ala Gln Ala Glu Ile Ala Gln Lys
      65      70      75      80
```

Arg Glu Glu Ile Glu Gln Arg Arg Ala Glu Leu Glu Gly Lys Lys Gln
85 90 95
Glu Leu Leu Asn Arg Leu Asn Lys
100

(2) INFORMATION FOR SEQ ID NO:3196:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 899 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...899

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3196:

Phe Met Ser Leu Gln Lys Leu Glu Asn Tyr Ser Asn Lys Ser Val Val
1 5 10 15
Gln Glu Glu Val Leu Ile Leu Thr Glu Leu Leu Glu Asp Ile Thr Lys
20 25 30
Asn Met Leu Ala Pro Glu Thr Phe Glu Lys Ile Ile Gln Leu Lys Glu
35 40 45
Leu Ser Thr Gln Glu Asp Tyr Gln Gly Leu Asn Arg Leu Val Thr Ser
50 55 60
Leu Ser Asn Asp Glu Met Val Tyr Ile Ser Arg Tyr Phe Ser Ile Leu
65 70 75 80
Pro Leu Leu Ile Asn Ile Ser Glu Asp Val Asp Leu Ala Tyr Glu Ile
85 90 95
Asn His Gln Asn Asn Ile Asp Gln Asp Tyr Leu Gly Lys Leu Ser Thr
100 105 110
Thr Ile Lys Leu Val Ala Glu Lys Glu Asn Ala Val Glu Ile Leu Glu
115 120 125
His Leu Asn Val Val Pro Val Leu Thr Ala His Pro Thr Gln Val Gln
130 135 140
Arg Lys Ser Met Leu Asp Leu Thr Asn His Ile His Ser Leu Leu Arg
145 150 155 160
Lys Tyr Arg Asp Val Lys Leu Gly Leu Ile Asn Lys Asp Lys Trp Tyr
165 170 175
Asn Asp Leu Arg Arg Tyr Ile Glu Ile Ile Met Gln Thr Asp Met Ile
180 185 190
Arg Glu Lys Lys Leu Lys Val Thr Asn Glu Ile Thr Asn Ala Met Glu
195 200 205
Tyr Tyr Asn Ser Ser Phe Leu Lys Ala Val Pro His Leu Thr Thr Glu
210 215 220
Tyr Lys Arg Leu Ala Gln Ala His Gly Leu Asn Leu Lys Gln Ala Lys
225 230 235 240
Pro Ile Thr Met Gly Met Trp Ile Gly Gly Asp Arg Asp Gly Asn Pro
245 250 255

Phe	Val	Thr	Ala	Lys	Thr	Leu	Lys	Gln	Ser	Ala	Leu	Thr	Gln	Cys	Glu	260	265	270
Val	Ile	Met	Asn	Tyr	Tyr	Asp	Lys	Lys	Ile	Tyr	Gln	Leu	Tyr	Arg	Glu	275	280	285
Phe	Ser	Leu	Ser	Thr	Ser	Ile	Val	Asn	Val	Ser	Lys	Gln	Val	Arg	Glu	290	295	300
Met	Ala	Arg	Gln	Ser	Lys	Asp	Asn	Ser	Ile	Tyr	Arg	Glu	Lys	Glu	Leu	305	310	315
Tyr	Arg	Arg	Ala	Leu	Phe	Asp	Ile	Gln	Ser	Lys	Ile	Gln	Ala	Thr	Lys	325	330	335
Thr	Tyr	Leu	Ile	Glu	Asp	Glu	Glu	Val	Gly	Thr	Arg	Tyr	Glu	Thr	Ala	340	345	350
Asn	Asp	Phe	Tyr	Lys	Asp	Leu	Ile	Ala	Ile	Arg	Asp	Ser	Leu	Leu	Glu	355	360	365
Asn	Lys	Gly	Glu	Ser	Leu	Ile	Ser	Gly	Asp	Phe	Val	Glu	Leu	Leu	Gln	370	375	380
Ala	Val	Glu	Ile	Phe	Gly	Phe	Tyr	Leu	Ala	Ser	Ile	Asp	Met	Arg	Gln	385	390	395
Asp	Ser	Ser	Val	Tyr	Glu	Ala	Cys	Val	Ala	Glu	Leu	Leu	Lys	Ser	Ala	405	410	415
Gly	Ile	His	Ser	Arg	Tyr	Ser	Glu	Leu	Ser	Glu	Glu	Glu	Lys	Cys	Asp	420	425	430
Leu	Leu	Leu	Lys	Glu	Leu	Glu	Glu	Asp	Pro	Arg	Ile	Leu	Ser	Ala	Thr	435	440	445
His	Ala	Glu	Lys	Ser	Glu	Leu	Leu	Ala	Lys	Glu	Leu	Ala	Ile	Phe	Lys	450	455	460
Thr	Ala	Arg	Val	Leu	Lys	Asp	Lys	Leu	Gly	Asp	Asp	Val	Ile	Arg	Gln	465	470	475
Thr	Ile	Ile	Ser	His	Ala	Thr	Ser	Leu	Ser	Asp	Met	Leu	Glu	Leu	Ala	485	490	495
Ile	Leu	Leu	Lys	Glu	Val	Gly	Leu	Val	Asp	Thr	Glu	Arg	Ala	Arg	Val	500	505	510
Gln	Ile	Val	Pro	Leu	Phe	Glu	Thr	Ile	Glu	Asp	Leu	Asp	His	Ser	Glu	515	520	525
Glu	Thr	Met	Arg	Lys	Tyr	Leu	Ser	Leu	Ser	Leu	Ala	Lys	Lys	Trp	Ile	530	535	540
Asp	Ser	Arg	Asn	Asn	Tyr	Gln	Glu	Ile	Met	Leu	Gly	Tyr	Ser	Asp	Ser	545	550	555
Asn	Lys	Asp	Gly	Gly	Tyr	Leu	Ser	Ser	Cys	Trp	Thr	Leu	Tyr	Lys	Ala	565	570	575
Gln	Gln	Gln	Leu	Thr	Ala	Ile	Gly	Asp	Glu	Phe	Gly	Val	Lys	Val	Thr	580	585	590
Phe	Phe	His	Gly	Arg	Gly	Gly	Thr	Val	Gly	Arg	Gly	Gly	Gly	Pro	Thr	595	600	605
Tyr	Glu	Ala	Ile	Thr	Ser	Gln	Pro	Leu	Lys	Ser	Ile	Lys	Asp	Arg	Ile	610	615	620
Arg	Leu	Thr	Glu	Gln	Gly	Glu	Val	Ile	Gly	Asn	Lys	Tyr	Gly	Asn	Lys	625	630	635
Asp	Ala	Ala	Tyr	Tyr	Asn	Leu	Glu	Met	Leu	Val	Ser	Ala	Ala	Ile	Asn	645	650	655
Arg	Met	Ile	Thr	Gln	Lys	Lys	Ser	Asp	Thr	Asn	Thr	Pro	Asn	Arg	Tyr	660	665	670
Glu	Ala	Ile	Met	Asp	Gln	Val	Val	Asp	Arg	Ser	Tyr	Asp	Val	Tyr	Arg	675	680	685
Asp	Leu	Val	Phe	Gly	Asn	Glu	His	Phe	Tyr	Asp	Tyr	Val	Phe	Glu	Ser	690	695	700

Ser	Pro	Ile	Lys	Ala	Ile	Ser	Ser	Phe	Asn	Ile	Gly	Ser	Arg	Pro	Ala
705					710				715						720
Ala	Arg	Lys	Thr	Ile	Thr	Glu	Ile	Gly	Gly	Leu	Arg	Ala	Ile	Pro	Trp
				725					730						735
Val	Phe	Ser	Trp	Ser	Gln	Ser	Arg	Val	Met	Phe	Pro	Gly	Trp	Tyr	Gly
			740					745					750		
Val	Gly	Ser	Ser	Phe	Lys	Glu	Phe	Ile	Asn	Lys	Asn	Pro	Glu	Asn	Ile
		755					760					765			
Ala	Ile	Leu	Arg	Asp	Met	Tyr	Gln	Asn	Trp	Pro	Phe	Phe	Gln	Ser	Leu
	770					775					780				
Leu	Ser	Asn	Val	Asp	Met	Val	Leu	Ser	Lys	Ser	Asn	Met	Asn	Ile	Ala
785					790					795					800
Phe	Glu	Tyr	Ala	Lys	Leu	Cys	Glu	Asp	Glu	Gln	Val	Lys	Ala	Ile	Tyr
				805					810					815	
Glu	Thr	Ile	Leu	Asn	Glu	Trp	Gln	Val	Thr	Lys	Asn	Val	Ile	Leu	Ala
			820					825					830		
Ile	Glu	Gly	His	Asp	Glu	Leu	Leu	Ala	Asp	Asn	Pro	Tyr	Leu	Lys	Ala
		835					840					845			
Ser	Leu	Asp	Tyr	Arg	Met	Pro	Tyr	Phe	Asn	Ile	Leu	Asn	Tyr	Ile	Gln
	850					855					860				
Leu	Glu	Leu	Ile	Lys	Arg	Gln	Arg	Arg	Gly	Glu	Leu	Ser	Ser	Asp	Gln
865					870					875					880
Glu	Arg	Leu	Ile	His	Ile	Thr	Ile	Asn	Gly	Ile	Ala	Thr	Gly	Leu	Arg
				885					890					895	
Asn	Ser	Gly													

(2) INFORMATION FOR SEQ ID NO:3197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...481

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3197:

Lys	Met	Thr	Tyr	Glu	Val	Lys	Ser	Leu	Asn	Glu	Glu	Cys	Gly	Val	Phe
1				5					10					15	
Gly	Ile	Trp	Gly	His	Pro	Asp	Ala	Ala	Lys	Leu	Thr	Tyr	Phe	Gly	Leu
			20					25					30		
His	Ser	Leu	Gln	His	Arg	Gly	Gln	Glu	Gly	Ala	Gly	Ile	Leu	Ser	Asn
		35					40					45			
Asp	Gln	Gly	Gln	Leu	Lys	Arg	His	Arg	Asp	Met	Gly	Leu	Leu	Ser	Glu
	50					55				60					
Val	Phe	Arg	Asn	Pro	Ala	Asn	Leu	Asp	Lys	Leu	Thr	Gly	Ala	Gly	Ala

65					70					75				80
Ile	Gly	His	Val	Arg	Tyr	Ala	Thr	Ala	Gly	Glu	Ala	Ser	Val	Asp
				85					90					95
Ile	Gln	Pro	Phe	Leu	Phe	Arg	Phe	His	Asp	Met	Gln	Phe	Gly	Leu
			100					105					110	
His	Asn	Gly	Asn	Leu	Thr	Asn	Ala	Ala	Ser	Leu	Lys	Lys	Glu	Leu
		115					120					125		
Gln	Arg	Gly	Ala	Ile	Phe	Ser	Ala	Thr	Ser	Asp	Ser	Glu	Ile	Leu
	130					135					140			
His	Leu	Ile	Arg	Arg	Ser	His	Asn	Pro	Ser	Leu	Met	Gly	Lys	Ile
145					150					155				160
Glu	Ala	Leu	Ser	Leu	Val	Lys	Gly	Gly	Phe	Ala	Tyr	Ile	Leu	Leu
			165						170					175
Glu	Asn	Lys	Leu	Ile	Ala	Ala	Leu	Asp	Pro	Asn	Gly	Phe	Arg	Pro
		180						185					190	
Ser	Ile	Gly	Lys	Met	Ala	Asn	Gly	Ala	Val	Val	Val	Ser	Ser	Glu
		195					200						205	
Cys	Ala	Phe	Glu	Val	Ile	Gly	Ala	Glu	Trp	Ile	Arg	Asp	Leu	Lys
210						215					220			
Gly	Glu	Ile	Val	Ile	Ile	Asp	Asp	Glu	Gly	Ile	Gln	Tyr	Asp	Ser
225					230					235				240
Thr	Asp	Asp	Thr	Gln	Leu	Ala	Ile	Cys	Ser	Met	Glu	Tyr	Ile	Tyr
			245						250					255
Ala	Arg	Pro	Asp	Ser	Asn	Ile	His	Gly	Val	Asn	Val	His	Thr	Ala
		260						265					270	
Lys	Arg	Met	Gly	Ala	Gln	Leu	Ala	Arg	Glu	Phe	Lys	His	Glu	Ala
		275					280					285		
Ile	Val	Val	Gly	Val	Pro	Asn	Ser	Ser	Leu	Ser	Ala	Ala	Met	Gly
	290					295					300			
Ala	Glu	Glu	Ser	Gly	Leu	Pro	Asn	Glu	Met	Gly	Leu	Ile	Lys	Asn
305					310					315				320
Tyr	Thr	Gln	Arg	Thr	Phe	Ile	Gln	Pro	Thr	Gln	Glu	Leu	Arg	Glu
			325						330					335
Gly	Val	Arg	Met	Lys	Leu	Ser	Ala	Val	Ser	Gly	Val	Val	Lys	Gly
		340						345					350	
Arg	Val	Val	Met	Val	Asp	Asp	Ser	Ile	Val	Arg	Gly	Thr	Thr	Ser
		355					360					365		
Arg	Ile	Val	Gln	Leu	Leu	Lys	Glu	Ala	Gly	Ala	Thr	Glu	Val	His
	370					375					380			
Ala	Ile	Gly	Ser	Pro	Ala	Leu	Ala	Tyr	Pro	Cys	Phe	Tyr	Gly	Ile
385					390					395				400
Ile	Gln	Thr	Arg	Gln	Glu	Leu	Ile	Ala	Ala	Asn	His	Thr	Val	Glu
			405						410					415
Thr	Arg	Gln	Ile	Ile	Gly	Ala	Asp	Ser	Leu	Thr	Tyr	Leu	Ser	Ile
		420					425						430	
Ser	Leu	Ile	Glu	Ser	Ile	Gly	Ile	Glu	Thr	Asp	Ala	Pro	Asn	Gly
		435				440					445			
Leu	Cys	Val	Ala	Tyr	Phe	Asp	Gly	Asp	Tyr	Pro	Thr	Pro	Leu	Tyr
	450					455					460			
Tyr	Glu	Glu	Asp	Tyr	Arg	Arg	Ser	Leu	Glu	Glu	Lys	Thr	Ser	Phe
465					470					475				480
Lys														

(2) INFORMATION FOR SEQ ID NO:3198:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 63 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...63

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3198:

Ala	Trp	Thr	Tyr	Pro	Lys	Gly	Asn	Asn	Phe	Thr	Thr	Val	Phe	Leu	Arg
1				5					10					15	
Ala	Leu	Phe	Gly	Asp	Gln	Gln	Leu	Ile	Arg	Ile	Met	Leu	Trp	Phe	Leu
			20					25					30		
Val	Leu	Leu	Leu	Leu	Val	Leu	Asn	Val	Glu	Asp	Phe	Glu	Leu	Phe	Glu
		35					40					45			
Arg	Val	Asp	Leu	Thr	Gly	Asp	Leu	Ser	Arg	Ala	Gln	Gly	Asp	Asp	
	50					55					60				

(2) INFORMATION FOR SEQ ID NO:3199:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 408 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...408

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3199:

Ser	Met	Ala	Tyr	Gln	Glu	Pro	Asn	Lys	Asp	Gly	Phe	Tyr	Gly	Lys	Phe
1				5					10					15	
Gly	Gly	Arg	Phe	Val	Pro	Glu	Thr	Leu	Met	Thr	Ala	Val	Leu	Glu	Leu
			20					25					30		
Glu	Lys	Ala	Tyr	Arg	Glu	Ser	Gln	Ala	Asp	Pro	Ser	Phe	Gln	Glu	Glu
		35					40					45			
Leu	Asn	Gln	Leu	Leu	Arg	Gln	Tyr	Val	Gly	Arg	Glu	Thr	Pro	Leu	Tyr
	50					55					60				
Tyr	Ala	Lys	Asn	Leu	Thr	Gln	His	Ile	Gly	Gly	Ala	Lys	Ile	Tyr	Leu
65					70				75					80	
Lys	Arg	Glu	Asp	Leu	Asn	His	Thr	Gly	Ala	His	Lys	Ile	Asn	Asn	Ala

				85					90					95					
Leu	Gly	Gln	Val	Trp	Leu	Ala	Lys	Arg	Met	Gly	Lys	Lys	Lys	Ile	Ile				
			100					105						110					
Ala	Glu	Thr	Gly	Ala	Gly	Gln	His	Gly	Val	Ala	Thr	Ala	Thr	Ala	Ala				
		115					120						125						
Ala	Leu	Phe	Asn	Met	Glu	Cys	Thr	Ile	Tyr	Met	Gly	Glu	Glu	Asp	Val				
	130					135					140								
Lys	Arg	Gln	Ala	Leu	Asn	Val	Phe	Arg	Met	Glu	Leu	Leu	Gly	Ala	Lys				
145					150					155					160				
Val	Glu	Ala	Val	Thr	Asp	Gly	Ser	Arg	Val	Leu	Lys	Asp	Ala	Val	Asn				
			165						170					175					
Ala	Ala	Leu	Arg	Ser	Trp	Val	Ala	Asn	Ile	Asp	Asp	Thr	His	Tyr	Ile				
		180						185					190						
Leu	Gly	Ser	Ala	Leu	Gly	Pro	His	Pro	Phe	Pro	Glu	Ile	Val	Arg	Asp				
		195				200							205						
Phe	Gln	Ser	Val	Ile	Gly	Arg	Glu	Ala	Lys	Gln	Gln	Tyr	Arg	Asp	Leu				
	210					215					220								
Thr	Gly	Gln	Asn	Leu	Pro	Asp	Ala	Leu	Val	Ala	Cys	Val	Gly	Gly	Gly				
225					230					235					240				
Ser	Asn	Ala	Ile	Gly	Leu	Phe	His	Pro	Phe	Val	Glu	Asp	Glu	Ser	Val				
			245						250					255					
Ala	Met	Tyr	Gly	Ala	Glu	Ala	Ala	Gly	Leu	Gly	Val	Asp	Thr	Glu	His				
		260						265					270						
His	Ala	Ala	Thr	Leu	Thr	Lys	Gly	Arg	Pro	Gly	Val	Leu	His	Gly	Ser				
		275					280					285							
Leu	Met	Asp	Val	Leu	Gln	Asp	Ala	His	Gly	Gln	Ile	Leu	Glu	Ala	Phe				
	290					295					300								
Ser	Ile	Ser	Ala	Gly	Leu	Asp	Tyr	Pro	Gly	Ile	Gly	Pro	Glu	His	Ser				
305					310					315					320				
His	Tyr	His	Asp	Ile	Lys	Arg	Ala	Ser	Tyr	Val	Pro	Val	Thr	Asp	Glu				
			325						330					335					
Glu	Ala	Leu	Glu	Gly	Phe	Gln	Leu	Leu	Ser	Arg	Val	Glu	Gly	Ile	Ile				
		340						345					350						
Pro	Ala	Leu	Glu	Ser	Ser	His	Ala	Ile	Ala	Phe	Ala	Val	Lys	Leu	Ala				
		355					360					365							
Lys	Glu	Leu	Gly	Pro	Glu	Lys	Ser	Met	Ile	Val	Cys	Leu	Ser	Gly	Arg				
	370					375					380								
Gly	Asp	Lys	Asp	Val	Val	Gln	Val	Lys	Asp	Arg	Leu	Glu	Ala	Asp	Ala				
385					390					395					400				
Ala	Lys	Lys	Gly	Glu	Ala	His	Ala												
				405															

(2) INFORMATION FOR SEQ ID NO:3200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...96

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3200:

Ile	Ala	Lys	Tyr	Glu	Ile	Leu	Tyr	Ile	Ile	Arg	Pro	Asn	Ile	Glu	Glu
1				5					10					15	
Glu	Ala	Lys	Asn	Ala	Leu	Val	Ala	Arg	Phe	Asp	Ser	Ile	Leu	Thr	Asp
			20					25					30		
Asn	Gly	Ala	Thr	Val	Val	Glu	Ser	Lys	Thr	Trp	Glu	Lys	Arg	Arg	Leu
		35					40					45			
Ala	Tyr	Glu	Ile	Gln	Asp	Phe	Arg	Glu	Gly	Leu	Tyr	His	Ile	Val	Asn
	50					55					60				
Val	Glu	Ala	Asn	Asp	Asp	Ala	Ala	Leu	Lys	Glu	Phe	Asp	Arg	Leu	Ser
65				70						75				80	
Lys	Ile	Asn	Ala	Asp	Ile	Leu	Arg	His	Met	Ile	Val	Lys	Ile	Asp	Ala
				85					90					95	

(2) INFORMATION FOR SEQ ID NO:3201:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 367 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...367

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3201:

Gln	Ile	Lys	Tyr	Ala	Glu	Gly	Tyr	Pro	Gly	Arg	Arg	Tyr	Tyr	Gly	Gly
1				5					10					15	
Thr	Asp	Val	Val	Asp	Val	Val	Glu	Thr	Leu	Ala	Ile	Glu	Arg	Ala	Lys
			20					25					30		
Glu	Ile	Phe	Gly	Ala	Lys	Phe	Ala	Asn	Val	Gln	Pro	His	Ser	Gly	Ser
		35					40					45			
Gln	Ala	Asn	Cys	Ala	Ala	Tyr	Met	Ser	Leu	Ile	Glu	Pro	Gly	Asp	Thr
	50					55					60				
Val	Met	Gly	Met	Asp	Leu	Ala	Ala	Gly	Gly	His	Leu	Thr	His	Gly	Ala
65					70				75					80	
Pro	Val	Ser	Phe	Ser	Gly	Gln	Thr	Tyr	Asn	Phe	Leu	Ser	Tyr	Ser	Val
				85					90					95	
Asp	Pro	Glu	Thr	Glu	Leu	Leu	Asp	Phe	Asp	Ala	Ile	Leu	Lys	Gln	Ala
			100					105					110		
Gln	Glu	Val	Lys	Pro	Lys	Leu	Ile	Val	Ala	Gly	Ala	Ser	Ala	Tyr	Ser
		115					120					125			
Gln	Ile	Ile	Asp	Phe	Ser	Lys	Phe	Arg	Glu	Ile	Ala	Asp	Ala	Val	Gly
	130					135					140				

Ala	Lys	Leu	Met	Val	Asp	Met	Ala	His	Ile	Ala	Gly	Leu	Val	Ala	Ala	145	150	155	160
Gly	Leu	His	Pro	Ser	Pro	Val	Pro	Tyr	Ala	His	Ile	Thr	Thr	Thr	Thr	165	170		175
Thr	His	Lys	Thr	Leu	Arg	Gly	Pro	Arg	Gly	Gly	Leu	Ile	Leu	Thr	Asn	180	185		190
Asp	Glu	Asp	Leu	Ala	Lys	Lys	Ile	Asn	Ser	Ala	Ile	Phe	Pro	Gly	Ile	195	200		205
Gln	Gly	Gly	Pro	Leu	Glu	His	Val	Val	Ala	Ala	Lys	Ala	Val	Ser	Phe	210	215		220
Lys	Glu	Val	Leu	Asp	Pro	Ala	Phe	Lys	Glu	Tyr	Ala	Ala	Asn	Val	Ile	225	230		235
Lys	Asn	Ser	Lys	Ala	Met	Ala	Asp	Val	Phe	Leu	Gln	Asp	Pro	Asp	Phe	245	250		255
Arg	Ile	Ile	Ser	Gly	Gly	Thr	Glu	Asn	His	Leu	Phe	Leu	Val	Asp	Val	260	265		270
Thr	Lys	Val	Val	Glu	Asn	Gly	Lys	Val	Ala	Gln	Asn	Leu	Leu	Asp	Glu	275	280		285
Val	Asn	Ile	Thr	Leu	Asn	Lys	Asn	Ser	Ile	Pro	Tyr	Glu	Thr	Leu	Ser	290	295		300
Pro	Phe	Lys	Thr	Ser	Gly	Ile	Arg	Ile	Gly	Ala	Ala	Ala	Ile	Thr	Ala	305	310		315
Arg	Gly	Phe	Gly	Glu	Glu	Glu	Ser	Arg	Lys	Val	Ala	Glu	Leu	Ile	Ile	325	330		335
Lys	Thr	Leu	Lys	Asn	Ser	Glu	Asn	Glu	Ala	Val	Leu	Glu	Glu	Val	Arg	340	345		350
Ser	Ala	Val	Lys	Glu	Leu	Thr	Asp	Ala	Phe	Pro	Leu	Tyr	Glu	Glu		355	360		365

(2) INFORMATION FOR SEQ ID NO:3202:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 74 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...74
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3202:

Ser	Lys	Lys	Tyr	Ala	Ile	Met	Leu	Lys	Lys	Tyr	Phe	Ser	Lys	Tyr	Lys	1	5	10	15
Trp	Thr	Asp	Leu	Phe	Trp	Ile	Leu	Phe	Val	Ile	Leu	Thr	Cys	Leu	Tyr	20	25		30
Ile	Gly	Asn	His	Asp	Leu	Phe	Thr	Leu	Asn	His	Gln	Glu	Phe	Ser	Phe	35	40		45
Arg	Gly	Ser	Val	Trp	Gly	Leu	Val	Leu	Ala	Leu	Tyr	His	Leu	Leu	Phe	50	55		60

Ile Asp Lys Phe Val Ile Ser Asn Arg Lys
65 70

(2) INFORMATION FOR SEQ ID NO:3203:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 487 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...487

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3203:

Val	Glu	Lys	Tyr	Leu	Val	Gln	Ser	Pro	His	Arg	Asn	Gln	Asp	Leu	Asp	1	5	10	15
Leu	Ala	Tyr	Leu	Arg	Ser	Gly	Ile	Ala	Asp	Leu	Gly	His	Leu	Ser	Tyr	20	25	30	
Pro	Glu	Gln	Leu	Lys	Phe	Lys	Thr	Lys	Gln	Val	Lys	Asp	Ser	Leu	Tyr	35	40	45	
Lys	Ile	Ala	Gly	Ile	Ala	Asp	Val	Glu	Val	Ala	Glu	Thr	Leu	Gly	Met	50	55	60	
Glu	His	Pro	Val	Lys	Tyr	Arg	Asn	Lys	Ala	Gln	Val	Pro	Val	Arg	Arg	65	70	75	80
Val	Asn	Gly	Val	Leu	Glu	Thr	Gly	Phe	Phe	Arg	Lys	Asn	Ser	His	Asp	85	90	95	
Leu	Met	Pro	Leu	Glu	Asp	Phe	Phe	Ile	Gln	Asp	Pro	Val	Ile	Asp	Gln	100	105	110	
Val	Val	Val	Ala	Leu	Arg	Asp	Leu	Leu	Arg	Arg	Phe	Asp	Leu	Lys	Pro	115	120	125	
Tyr	Asp	Glu	Lys	Glu	Gln	Ser	Gly	Leu	Ile	Arg	Asn	Leu	Val	Val	Arg	130	135	140	
Arg	Gly	His	Tyr	Ser	Gly	Gln	Ile	Met	Val	Val	Leu	Val	Thr	Thr	Arg	145	150	155	160
Pro	Lys	Val	Phe	Arg	Val	Asp	Gln	Leu	Ile	Glu	Gln	Val	Ile	Lys	Gln	165	170	175	
Phe	Pro	Glu	Ile	Val	Ser	Val	Met	Gln	Asn	Ile	Asn	Asp	Gln	Asn	Thr	180	185	190	
Asn	Ala	Ile	Phe	Gly	Lys	Glu	Trp	Arg	Thr	Leu	Tyr	Gly	Gln	Asp	Tyr	195	200	205	
Ile	Thr	Asp	Gln	Met	Leu	Gly	Asn	Asp	Phe	Gln	Ile	Ala	Gly	Pro	Ala	210	215	220	
Phe	Tyr	Gln	Val	Asn	Thr	Glu	Met	Ala	Glu	Lys	Leu	Tyr	Gln	Thr	Ala	225	230	235	240
Ile	Asp	Phe	Ala	Glu	Leu	Lys	Lys	Asp	Asp	Val	Ile	Ile	Asp	Ala	Tyr	245	250	255	

Ser Gly Ile Gly Thr Ile Gly Leu Ser Val Ala Lys His Val Lys Glu

260 265 270

Val Tyr Gly Val Glu Leu Ile Pro Glu Ala Val Glu Asn Ser Lys Lys

275 280 285

Asn Ala Gln Leu Asn Asn Ile Ser Asn Ala His Tyr Val Cys Asp Thr

290 295 300

Ala Glu Asn Ala Met Lys Asn Trp Leu Lys Asp Gly Ile Gln Pro Thr

305 310 315 320

Val Ile Leu Val Asp Pro Pro Arg Lys Gly Leu Thr Glu Ser Phe Ile

325 330 335

Lys Ala Ser Ala Gln Thr Gly Ala Asp Arg Ile Ala Tyr Ile Ser Cys

340 345 350

Asn Val Ala Thr Met Ala Arg Asp Ile Lys Leu Tyr Gln Glu Leu Gly

355 360 365

Tyr Glu Leu Lys Lys Val Gln Pro Val Asp Leu Phe Pro Gln Thr His

370 375 380

His Val Glu Thr Val Ala Leu Leu Ser Lys Leu Asp Val Asp Lys His

385 390 395 400

Ile Ser Val Glu Ile Glu Leu Asp Glu Met Asn Leu Thr Ser Ala Glu

405 410 415

Ser Lys Ala Thr Tyr Ala Gln Ile Lys Glu Tyr Val Trp Asn Lys Phe

420 425 430

Glu Leu Lys Val Ser Thr Leu Tyr Ile Ala Gln Ile Lys Lys Lys Cys

435 440 445

Gly Ile Glu Leu Arg Glu His Tyr Asn Lys Ser Lys Lys Asp Lys Gln

450 455 460

Ile Ile Pro Gln Cys Thr Pro Glu Lys Glu Glu Ala Ile Met Asp Ala

465 470 475 480

Leu Arg His Phe Lys Met Ile

485

(2) INFORMATION FOR SEQ ID NO:3204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 413 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...413

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3204:

Gly Gly Lys Tyr Met Ser Ser His Pro Ile Gln Val Phe Ser Glu Ile

1 5 10 15

Gly Lys Leu Lys Lys Val Met Leu His Arg Pro Gly Lys Glu Leu Glu

20 25 30

Asn Leu Leu Pro Asp Tyr Leu Glu Arg Leu Leu Phe Asp Asp Ile Pro

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...78

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3205:

Trp	Arg	Lys	Tyr	Ile	Met	Ile	Leu	Met	Thr	Lys	Asn	Ile	Asn	Leu	Thr
1				5					10					15	
Asn	Glu	Glu	Leu	Glu	Leu	Ile	Gln	Gly	Gly	Ala	Asp	Pro	Tyr	Gly	Lys
			20					25					30		
Asn	Pro	Asn	Gly	Arg	Tyr	Asp	Trp	Glu	Ile	Glu	Pro	Val	Leu	Thr	Leu
		35					40					45			
Pro	Val	His	Gly	Phe	Cys	Pro	Arg	Gly	Thr	Tyr	Asp	Leu	Gly	Tyr	Ile
	50					55					60				
Gly	Gly	Gly	Asn	His	Leu	Cys	Lys	Gly	Ser	Ala	Ala	Arg	Phe		
65					70				75						

(2) INFORMATION FOR SEQ ID NO:3206:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 63 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...63

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3206:

Gln	Ser	Glu	Tyr	Tyr	Val	Arg	Phe	Arg	Val	Leu	His	Ala	Pro	Thr	Lys
1				5					10					15	
Ile	Trp	Val	Ala	Ser	Leu	Arg	Gly	Leu	Pro	Arg	Ser	Thr	Leu	Ser	Val
		20					25					30			
Ser	Arg	Lys	Thr	Pro	Ser	Leu	Trp	His	Phe	Gln	Ala	Tyr	Ser	Gly	Leu
		35				40					45				
Ser	Lys	Asp	Leu	Ala	Ile	Ser	Thr	Ala	Val	Thr	Ile	Pro	Arg	Pro	
	50					55				60					

(2) INFORMATION FOR SEQ ID NO:3207:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...123
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3207:

```

Ile Met Glu Tyr Lys Leu Phe Glu Glu Phe Ile Thr Leu Gln Ala Leu
1      5      10      15
Leu Lys Glu Leu Gly Ile Thr His Ser Gly Gly Ala Ile Lys Ser Phe
20     25     30
Leu Ser Glu His Ser Val Tyr Phe Asn Arg Glu Leu Glu Ser Arg Arg
35     40     45
Gly Lys Lys Leu Arg Ile Gly Asp Lys Val Asp Ile Pro Asp Met Asn
50     55     60
Ile Asp Ile Leu Leu Thr Gln Pro Thr Ser Glu Glu Gln Asp Glu Tyr
65     70     75     80
Gln Ala Asp Lys Val Glu Lys Glu Arg Ile Ala Lys Leu Val Lys Lys
85     90     95
Met Asn Lys Gly Val Lys Lys Asp Lys Ser Lys Pro Ala Ser Ser Pro
100    105    110
Lys Ser Gln Gln Ala Pro Arg Phe Pro Gly Arg
115    120

```

(2) INFORMATION FOR SEQ ID NO:3208:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 664 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...664
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3208:

```

Leu Cys Arg Tyr Leu Arg Arg Ile His Gly Arg Thr Ser Tyr Pro Asp
1      5      10      15
Leu His Leu Ser Arg Arg Cys Gln Ser Leu Arg Cys Pro Cys Gln Leu
20     25     30
Ala Thr Gly Gly Lys Ala Met Val Arg Phe Thr Gly Leu Ser Pro Lys
35     40     45

```

Gln	Thr	Gln	Ala	Ile	Glu	Val	Leu	Lys	Gly	His	Ile	Ser	Leu	Pro	Asp
50					55					60					
Val	Glu	Val	Ala	Val	Thr	Gln	Ser	Asp	Gln	Ala	Ser	Ile	Ser	Ile	Glu
65					70				75						80
Gly	Glu	Glu	Gly	His	Tyr	Gln	Leu	Thr	Tyr	Arg	Lys	Pro	His	Gln	Leu
				85					90					95	
Tyr	Arg	Ala	Leu	Ser	Leu	Leu	Val	Thr	Val	Leu	Ala	Glu	Ala	Asp	Lys
			100					105					110		
Val	Glu	Ile	Glu	Glu	Gln	Ala	Ala	Tyr	Glu	Asp	Leu	Ala	Tyr	Met	Val
		115					120					125			
Asp	Cys	Ser	Arg	Asn	Ala	Val	Leu	Asn	Val	Ala	Ser	Ala	Lys	Gln	Met
		130					135				140				
Ile	Glu	Ile	Leu	Ala	Leu	Met	Gly	Tyr	Ser	Thr	Phe	Glu	Leu	Tyr	Met
145					150					155					160
Glu	Asp	Thr	Tyr	Gln	Ile	Glu	Gly	Gln	Pro	Tyr	Phe	Gly	Tyr	Phe	Arg
				165					170					175	
Gly	Ala	Tyr	Ser	Ala	Glu	Glu	Leu	Gln	Glu	Ile	Glu	Ala	Tyr	Val	Gln
			180					185					190		
Gln	Phe	Asp	Met	Thr	Phe	Val	Pro	Cys	Ile	Gln	Thr	Leu	Ala	His	Leu
		195					200					205			
Ser	Ala	Phe	Val	Lys	Trp	Gly	Val	Lys	Glu	Val	Gln	Glu	Leu	Arg	Asp
		210				215					220				
Val	Glu	Asp	Ile	Leu	Leu	Ile	Gly	Glu	Glu	Lys	Val	Tyr	Asp	Leu	Ile
225					230					235					240
Asp	Gly	Met	Phe	Ala	Thr	Leu	Ser	Lys	Leu	Lys	Thr	Arg	Lys	Val	Asn
				245					250					255	
Ile	Gly	Met	Asp	Glu	Ala	His	Leu	Val	Gly	Leu	Gly	Arg	Tyr	Leu	Ile
			260					265					270		
Leu	Asn	Gly	Val	Val	Asp	Arg	Ser	Leu	Leu	Met	Cys	Gln	His	Leu	Glu
		275					280					285			
Arg	Val	Leu	Asp	Ile	Ala	Asp	Lys	Tyr	Gly	Phe	His	Cys	Gln	Met	Trp
		290				295					300				
Ser	Asp	Met	Phe	Phe	Lys	Leu	Met	Ser	Ala	Asp	Gly	Gln	Tyr	Asp	Arg
305					310					315					320
Asp	Val	Glu	Ile	Pro	Glu	Glu	Thr	Arg	Val	Tyr	Leu	Asp	Arg	Leu	Lys
				325					330					335	
Asp	Arg	Val	Thr	Leu	Val	Tyr	Trp	Asp	Tyr	Tyr	Arg	Asp	Ser	Glu	Glu
			340					345					350		
Lys	Tyr	Asn	Arg	Asn	Phe	Arg	Asn	His	His	Lys	Ile	Ser	His	Asp	Leu
		355					360					365			
Ala	Phe	Ala	Gly	Gly	Ala	Trp	Lys	Trp	Ile	Gly	Phe	Thr	Pro	His	Asn
		370				375					380				
His	Phe	Ser	Arg	Leu	Val	Ala	Ile	Glu	Ala	Asn	Lys	Ala	Cys	Arg	Ala
385					390					395					400
Asn	Gln	Ile	Lys	Glu	Val	Ile	Val	Thr	Gly	Trp	Gly	Asp	Asn	Gly	Gly
				405					410					415	
Glu	Thr	Ala	Gln	Phe	Ser	Ile	Leu	Ser	Ser	Leu	Gln	Ile	Trp	Ala	Glu
			420					425					430		
Leu	Ser	Tyr	Arg	Asn	Asp	Leu	Asp	Ser	Leu	Ser	Ala	His	Phe	Lys	Thr
		435					440					445			
Asn	Thr	Gly	Leu	Thr	Val	Glu	Asp	Phe	Met	Gln	Ile	Asp	Leu	Ala	Asn
		450				455					460				
Leu	Leu	Pro	Asp	Leu	Pro	Gly	Asn	Leu	Ser	Gly	Ile	Asn	Pro	Asn	Arg
465					470					475					480
Tyr	Val	Phe	Tyr	Gln	Asp	Val	Leu	Cys	Pro	Ile	Leu	Asp	Arg	His	Met
				485					490					495	
Thr	Pro	Glu	Gln	Asp	Lys	Pro	His	Phe	Ala	Gln	Ala	Ala	Glu	Thr	Leu

(2) INFORMATION FOR SEQ ID NO:3210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 565 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...565

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3210:

Arg	Arg	Arg	Tyr	Ile	Thr	Met	Lys	Lys	Ile	Lys	Pro	His	Gly	Pro	Leu
1				5					10					15	
Pro	Ser	Gln	Thr	Gln	Leu	Ala	Tyr	Leu	Gly	Asp	Glu	Leu	Ala	Ala	Phe
			20					25					30		
Ile	His	Phe	Gly	Pro	Asn	Thr	Phe	Tyr	Asp	Gln	Glu	Trp	Gly	Thr	Gly
		35					40					45			
Gln	Glu	Asp	Pro	Glu	Arg	Phe	Asn	Pro	Ser	Gln	Leu	Asp	Ala	Arg	Glu
	50					55				60					
Trp	Val	Arg	Val	Leu	Lys	Glu	Thr	Gly	Phe	Lys	Lys	Leu	Ile	Leu	Val
65					70					75					80
Val	Lys	His	His	Asp	Gly	Phe	Val	Leu	Tyr	Pro	Thr	Ala	His	Thr	Asp
				85					90					95	
Tyr	Ser	Val	Lys	Val	Ser	Pro	Trp	Arg	Arg	Gly	Lys	Gly	Asp	Leu	Leu
			100					105					110		
Leu	Glu	Val	Ser	Gln	Ala	Ala	Thr	Glu	Phe	Asp	Met	Asp	Met	Gly	Val
	115						120					125			
Tyr	Leu	Ser	Pro	Trp	Asp	Ala	His	Ser	Pro	Leu	Tyr	His	Val	Asp	Arg
	130					135					140				
Glu	Ala	Asp	Tyr	Asn	Ala	Tyr	Tyr	Leu	Ala	Gln	Leu	Lys	Glu	Ile	Leu
145					150					155					160
Ser	Asn	Pro	Asn	Tyr	Gly	Asn	Ala	Gly	Lys	Phe	Ala	Glu	Val	Trp	Met
				165					170					175	
Asp	Gly	Ala	Arg	Gly	Glu	Gly	Ala	Gln	Lys	Val	Asn	Tyr	Glu	Phe	Glu
			180					185					190		
Lys	Trp	Phe	Glu	Thr	Ile	Arg	Asp	Leu	Gln	Gly	Ala	Cys	Leu	Ile	Phe
	195						200					205			
Ser	Thr	Glu	Gly	Thr	Ser	Ile	Arg	Trp	Ile	Gly	Asn	Glu	Arg	Gly	Tyr
	210					215					220				
Ala	Gly	Asp	Pro	Leu	Trp	Gln	Lys	Val	Asn	Pro	Asp	Lys	Leu	Gly	Thr
225					230					235					240
Glu	Ala	Glu	Leu	Asn	Tyr	Leu	Gln	His	Gly	Asp	Pro	Ser	Gly	Thr	Ile
				245					250					255	
Phe	Ser	Ile	Gly	Glu	Ala	Asp	Val	Ser	Ile	Arg	Pro	Gly	Trp	Phe	Tyr
			260					265					270		
His	Glu	Asp	Gln	Asp	Pro	Lys	Ser	Leu	Glu	Glu	Leu	Val	Glu	Ile	Tyr
	275						280					285			
Phe	His	Ser	Val	Gly	Arg	Gly	Thr	Pro	Leu	Leu	Leu	Asn	Ile	Pro	Pro

290		295		300											
Asn	Gln	Ala	Gly	Leu	Phe	Asp	Ala	Lys	Asp	Ile	Glu	Arg	Leu	Tyr	Glu
305					310					315					320
Phe	Ala	Thr	Tyr	Arg	Asn	Glu	Leu	Tyr	Lys	Glu	Asp	Leu	Ala	Leu	Gly
				325					330						335
Ala	Glu	Val	Ser	Gly	Pro	Ala	Leu	Ser	Ala	Asp	Phe	Ala	Cys	Arg	His
			340					345					350		
Leu	Thr	Asp	Gly	Leu	Glu	Thr	Ser	Ser	Trp	Ala	Asn	Asp	Ala	Ala	Leu
		355					360					365			
Pro	Ile	Gln	Leu	Glu	Leu	Asp	Leu	Gly	Ser	Pro	Lys	Thr	Phe	Asp	Val
		370				375					380				
Ile	Glu	Leu	Arg	Glu	Asp	Leu	Lys	Leu	Gly	Gln	Arg	Ile	Ala	Ala	Phe
385					390					395					400
His	Val	Gln	Val	Glu	Val	Asp	Gly	Val	Trp	Gln	Glu	Phe	Gly	Ser	Gly
			405					410						415	
His	Thr	Val	Gly	Tyr	Lys	Arg	Leu	Leu	Arg	Gly	Ala	Val	Val	Glu	Ala
		420					425					430			
Gln	Lys	Ile	Arg	Val	Val	Ile	Thr	Glu	Ser	Gln	Val	Leu	Pro	Leu	Leu
	435					440					445				
Thr	Lys	Ile	Ser	Leu	Tyr	Lys	Thr	Pro	Arg	Leu	Ser	Gln	Thr	Val	Ala
	450					455				460					
Val	Gln	Gly	Leu	Ala	Phe	Ala	Glu	Lys	Ser	Leu	Ala	Val	Ala	Lys	Gly
465				470					475						480
Glu	Thr	Leu	His	Phe	Arg	Ile	Glu	Arg	Ser	Glu	Ser	Ser	Ser	Ser	Leu
			485				490							495	
Glu	Ala	Lys	Ile	Ser	Ile	Gln	Pro	Gly	Thr	Gly	Val	His	Gly	Val	Ala
		500				505					510				
Tyr	Gln	Asp	Glu	Ile	Gln	Val	Leu	Gln	Phe	Gln	Ala	Gly	Glu	Ser	Lys
	515					520					525				
Lys	Asp	Leu	His	Leu	Pro	Thr	Leu	Tyr	Phe	Ala	Gly	Asp	Lys	Thr	Leu
	530				535					540					
Asp	Phe	Tyr	Leu	Asn	Leu	Thr	Val	Asp	Gly	Gln	Leu	Val	Asp	Gln	Leu
545				550				555							560
Gln	Val	Gln	Val	Ser											
			565												

(2) INFORMATION FOR SEQ ID NO:3211:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 156 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...156
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3211:

Gly Val Thr Leu Met Asp Asp Ile Leu Gln Ala Leu Ala Lys Met Leu

1		5		10		15									
Asn	Met	Thr	Val	Asp	Glu	Val	Ser	Ser	Leu	Leu	Thr	Thr	Phe	Lys	Gly
		20		25		30									
Asn	Ala	Pro	Gln	Ile	Tyr	Glu	Met	Phe	Val	Lys	Glu	Lys	Met	Phe	Tyr
		35		40		45									
Asp	Leu	Phe	Ser	Leu	Phe	Gln	Ile	Met	Ser	Ile	Val	Ile	Phe	Ser	Ile
		50		55		60									
Ser	Ala	Val	Val	Leu	Ala	Val	Leu	Thr	Leu	Ile	Tyr	Phe	Thr	Tyr	Asp
		65		70		75									
Gly	Gly	Phe	Val	Tyr	Ser	Tyr	Asp	Ile	Arg	Thr	Gly	Lys	Thr	Glu	Glu
				85		90									
Glu	Ile	Lys	Leu	Glu	Arg	Ile	Glu	Arg	Lys	Arg	Lys	Asp	Leu	Lys	Ile
		100		105		110									
Pro	Leu	Lys	Ile	Ser	Cys	Ile	Ser	Ser	Ser	Ala	Ser	Leu	Ile	Thr	Leu
		115		120		125									
Val	Ile	Ala	Ile	Val	Leu	Lys	Ala	Thr	Leu	Ala	Pro	Asn	Tyr	Ile	Phe
		130		135		140									
Ile	Val	Asn	Glu	Ile	Leu	Pro	Lys	Leu	Thr	Lys	Arg				
		145		150		155									

(2) INFORMATION FOR SEQ ID NO:3212:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 97 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...97
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3212:

Ile	Thr	Thr	Leu	Leu	Leu	Asn	Ser	Leu	Glu	Leu	Thr	Val	Val	Ser	Ile
1			5			10			15						
Val	Val	Leu	Leu	Ala	Leu	Arg	Ser	Val	Ile	Ala	Glu	Leu	Ile	Leu	Ser
		20		25		30									
Lys	Lys	Leu	Asp	Val	Ser	Val	Lys	Lys	Asp	Ile	Val	Leu	Glu	Phe	Leu
		35		40		45									
Leu	Thr	Ile	Val	Phe	Ile	Ser	Ser	Ser	Trp	Tyr	Leu	Pro	Ile	Trp	Pro
		50		55		60									
Ala	Val	Ile	Val	Tyr	Leu	Leu	Ala	Tyr	Thr	Leu	Tyr	Leu	Tyr	Leu	Lys
		65		70		75									
Arg	Lys	Asp	Ile	Lys	Met	Tyr	Ile	Glu	Tyr	Phe	Arg	Lys	Lys	Ile	Phe
				85		90									
Glu															

(2) INFORMATION FOR SEQ ID NO:3213:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...60
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3213:

```

Ile Asn Thr Leu Arg Lys Ser Leu Gln Thr Val Ser Val Leu Ser Ala
1      5      10      15
Thr Ser Lys Arg Cys Phe Glu Gln Pro Val Ala Ser Phe Leu Val Cys
      20      25      30
Ser Leu Ile Phe Ile Glu Tyr Lys Leu Ser Lys Glu Thr Ser Phe Ser
      35      40      45
Glu Lys Gln Gly Ser Phe Cys Cys Leu Phe His Pro
      50      55      60

```

(2) INFORMATION FOR SEQ ID NO:3214:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 71 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...71
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3214:

```

Thr Asn Thr Leu Arg Lys Ser Leu Gln Thr Thr Ser Ala Ser Pro Cys
1      5      10      15
Arg Ile Ser Ala Thr Ser Lys Gln Cys Phe Glu Leu Thr Ser Ser Val
      20      25      30
Leu Ser Thr Thr Ser Lys Arg Cys Phe Glu Gln Pro Val Ala Ser Phe
      35      40      45
Leu Val Cys Ser Leu Ile Phe Ile Glu Tyr Lys Glu Leu Gly Asn Arg
      50      55      60
Leu Phe Leu Tyr Cys Val Tyr
65      70

```

(2) INFORMATION FOR SEQ ID NO:3215:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 427 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...427

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3215:

Trp	Ile	Thr	Leu	Gln	Asn	Gln	Lys	Tyr	Leu	Arg	Asn	Tyr	Tyr	Ile	Lys
1				5					10					15	
Met	Asp	Phe	Ser	Arg	Lys	Asp	Asn	Gln	Ser	Met	Glu	Tyr	Arg	Lys	Ile
			20					25					30		
Gln	Glu	Ala	Leu	Glu	Ala	Leu	Gln	Lys	Gly	Arg	Leu	Val	Leu	Val	Ile
			35					40				45			
Asp	Asp	Lys	Asp	Arg	Glu	Asn	Glu	Gly	Asp	Leu	Ile	Cys	Ser	Ala	Gln
			50				55				60				
Ala	Ala	Thr	Thr	Glu	Asn	Val	Asn	Phe	Met	Ala	Thr	Tyr	Ala	Lys	Gly
65					70				75						80
Leu	Ile	Cys	Met	Pro	Met	Ser	Glu	Ser	Leu	Ala	Asn	Gln	Leu	Met	Leu
				85					90					95	
Ser	Pro	Met	Val	Glu	Asn	Asn	Thr	Asp	Asn	His	Lys	Thr	Ala	Phe	Thr
			100					105					110		
Val	Ser	Ile	Asp	Tyr	Lys	Glu	Thr	Thr	Thr	Gly	Ile	Ser	Ala	Glu	Glu
			115				120					125			
Arg	Gly	Leu	Thr	Ala	Arg	Met	Cys	Val	Ala	Glu	Asp	Ile	Thr	Pro	Ser
						135					140				
Asp	Phe	Arg	Arg	Pro	Gly	His	Met	Phe	Pro	Leu	Ile	Ala	Lys	Lys	Gly
145					150					155					160
Gly	Val	Leu	Glu	Arg	Asn	Gly	His	Thr	Glu	Ala	Thr	Val	Asp	Leu	Leu
				165					170					175	
Lys	Leu	Ala	Gly	Leu	Lys	Glu	Cys	Gly	Leu	Cys	Cys	Glu	Ile	Met	Asn
			180					185					190		
His	Asp	Gly	Lys	Met	Met	Arg	Thr	Asp	Asp	Leu	Ile	Gln	Phe	Ser	Lys
			195				200					205			
Lys	His	Asn	Ile	Pro	Leu	Ile	Thr	Ile	Lys	Glu	Leu	Gln	Glu	Tyr	Arg
			210				215					220			
Lys	Val	Tyr	Asp	Gln	Leu	Ile	Glu	Arg	Val	Ser	Thr	Val	Asn	Met	Pro
225					230					235					240
Thr	Arg	Tyr	Gly	Asn	Phe	Lys	Ala	Ile	Ser	Tyr	Ile	Asp	Lys	Leu	Asn
				245					250					255	
Gly	Glu	His	His	Leu	Ala	Leu	Ile	Met	Gly	Asn	Ile	Glu	Asp	Glu	Ala
			260					265					270		
Asn	Val	Leu	Cys	Arg	Val	His	Ser	Glu	Cys	Leu	Thr	Gly	Asp	Val	Leu
			275				280						285		

Gly	Ser	Leu	Arg	Cys	Asp	Cys	Gly	Gln	Gln	Phe	Asp	Lys	Ala	Met	Lys
290						295					300				
Met	Ile	Val	Glu	Asn	Gly	Ser	Gly	Val	Leu	Leu	Tyr	Leu	Arg	Gln	Glu
305				310						315					320
Gly	Arg	Gly	Ile	Gly	Leu	Ile	Asn	Lys	Leu	Lys	Ala	Tyr	His	Leu	Gln
			325						330					335	
Asp	Gln	Gly	Met	Asp	Thr	Leu	Asp	Ala	Asn	Leu	Ala	Leu	Gly	Phe	Glu
		340					345						350		
Gly	Asp	Leu	Arg	Glu	Tyr	His	Ile	Gly	Ala	Gln	Met	Leu	Lys	Asp	Leu
	355						360					365			
Gly	Leu	Gln	Ser	Leu	His	Leu	Leu	Thr	Asn	Asn	Pro	Asp	Lys	Val	Glu
370						375					380				
Gln	Leu	Glu	Lys	Tyr	Gly	Ile	Thr	Ile	Ser	Ser	Arg	Ile	Ser	Ile	Glu
385					390					395					400
Ile	Glu	Ala	Asn	Pro	Tyr	Asp	Ser	Phe	Tyr	Leu	Glu	Thr	Lys	Lys	Asn
			405						410					415	
Arg	Met	Gly	His	Ile	Leu	Asn	Met	Glu	Glu	Lys					
		420						425							

(2) INFORMATION FOR SEQ ID NO:3216:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1217 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1217

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3216:

Met	Ala	Thr	Leu	Asp	Glu	Leu	Lys	Val	Met	Ile	Asp	Ala	Glu	Ile	Ala
1			5					10					15		
Pro	Phe	Arg	Lys	Lys	Met	Lys	Glu	Val	Glu	Asn	Gln	Val	Lys	Gly	Thr
		20					25					30			
Ser	Asp	Gln	Val	Lys	Asn	Ala	Thr	Ala	Lys	Val	Arg	Glu	Gln	Ser	Ser
	35					40					45				
Ser	Ile	Gly	Ser	Ala	Phe	Gly	Lys	Leu	Ala	Lys	Phe	Ala	Gly	Phe	Ala
	50				55					60					
Ile	Leu	Gly	Lys	Lys	Leu	Leu	Asp	Val	Gly	Met	Tyr	Ser	Thr	Gln	Thr
65				70				75						80	
Ala	Leu	Glu	Val	Ser	Ala	Ser	Met	Asn	Gln	Ile	Lys	Arg	Gln	Met	Gly
			85					90					95		
Glu	Ser	Ser	Gln	Ser	Phe	Leu	Lys	Trp	Val	Asn	Asp	Asn	Ala	Asn	Ala
		100					105						110		
Met	Asn	Met	Gly	Val	Gly	Glu	Ala	Thr	Asn	Tyr	Gly	Ala	Val	Tyr	Ser
	115					120						125			
Asn	Leu	Phe	Ser	Gly	Phe	Ile	Lys	Asp	Thr	Asn	Lys	Leu	Ser	Ala	Tyr
	130					135					140				

Thr	Ala	Lys	Met	Leu	Gln	Thr	Ser	Ala	Val	Val	Ala	Glu	Gly	Ser	Gly
145					150					155					160
Arg	Thr	Ile	Thr	Asp	Val	Met	Glu	Arg	Ile	Arg	Ser	Gly	Leu	Leu	Gly
				165					170						175
Asn	Thr	Glu	Ala	Ile	Glu	Asp	Leu	Gly	Ile	Asn	Val	Asn	Val	Ala	Met
			180					185					190		
Ile	Glu	Ser	Thr	Glu	Ala	Phe	Lys	Lys	Phe	Ala	Asn	Gly	Gln	Ser	Trp
		195					200					205			
Gln	Gln	Leu	Asp	Tyr	Gln	Thr	Gln	Gln	Gln	Ile	Arg	Leu	Met	Ala	Ile
	210					215					220				
Leu	Glu	Gln	Ala	Thr	Ala	Lys	Tyr	Gly	Asp	Thr	Leu	Ser	Asn	Ser	Val
225					230					235					240
Asn	Gly	Arg	Ile	Ser	Leu	Phe	Lys	Ser	Leu	Met	Lys	Asp	Ala	Ala	Leu
				245					250						255
Asn	Leu	Gly	Asn	Ser	Met	Leu	Pro	Ile	Ile	Asn	Ala	Ile	Met	Pro	Val
			260					265					270		
Leu	Asn	Ser	Phe	Ala	Met	Val	Leu	Lys	Asn	Val	Thr	Ala	Lys	Leu	Ala
		275					280					285			
Glu	Phe	Ile	Ala	Leu	Met	Phe	Asn	Lys	Lys	Ala	Thr	Val	Lys	Asp	Gly
	290					295					300				
Val	Gly	Gly	Ala	Val	Gly	Asp	Met	Gly	Asn	Ala	Met	Lys	Asp	Ala	Ala
305					310					315					320
Gly	Gly	Ala	Gly	Asp	Leu	Ala	Asp	Ala	Val	Asp	Asp	Ala	Gly	Asp	Ser
				325					330					335	
Ala	Gly	Gly	Leu	Ala	Asp	Asn	Leu	Gly	Asp	Ser	Ala	Lys	Asn	Ala	Lys
			340					345					350		
Lys	Ala	Ala	Lys	Glu	Leu	Leu	Gly	Leu	Leu	Gly	Phe	Asp	Glu	Ile	Asn
		355					360					365			
Ile	Leu	Gln	Lys	Pro	Lys	Asp	Asp	Asp	Ala	Gly	Gly	Ser	Gly	Gly	Gly
	370					375						380			
Gly	Lys	Gly	Gly	Lys	Gly	Lys	Gly	Gly	Gly	Gly	Gly	Pro	Phe	Lys	Asp
385					390					395					400
Ile	Leu	Pro	Glu	Val	Glu	Leu	Thr	Asp	Met	Asp	Asn	Lys	Phe	Lys	Ser
				405					410					415	
Ile	Phe	Asp	Gly	Leu	Gly	Asp	Lys	Leu	Lys	Gly	Leu	Phe	Asp	Leu	Phe
			420					425				430			
Lys	Lys	Gly	Phe	Asp	Ala	Ala	Phe	Arg	Pro	Glu	Gly	Ile	Glu	Arg	Ile
		435					440					445			
Lys	Thr	Ala	Leu	Asp	Gln	Ile	Ala	Lys	Thr	Met	Gly	Glu	Ile	Ala	Thr
	450					455					460				
Asp	Pro	Arg	Val	Val	Asn	Ala	Phe	Asn	Arg	Met	Ala	Glu	Lys	Ile	Ala
465					470					475					480
Tyr	Ala	Leu	Gly	Gln	Val	Thr	Gly	Ser	Ile	Thr	Thr	Ile	Gly	Leu	Gly
				485					490					495	
Ile	Gly	Val	Phe	Leu	Ala	Glu	Ser	Ile	Ala	Asn	Gly	Leu	Gly	Arg	Gln
			500					505					510		
Lys	Glu	Arg	Ile	Thr	Arg	Ala	Leu	Val	Ala	Leu	Phe	Asp	Asn	Ile	Gly
		515					520					525			
Asn	Ile	Ser	Glu	Ala	Val	Gly	Asn	Ile	Ala	Gln	Asp	Phe	Ser	Ser	Thr
	530					535					540				
Phe	Tyr	Asp	Val	Ile	Thr	Ser	Thr	Gly	Ala	Val	Arg	Ile	Gly	Ser	Ala
545					550					555					560
Ile	Val	Ser	Thr	Leu	Leu	Ser	Leu	Thr	Ser	Thr	Ile	Val	Glu	Val	Gly
				565					570					575	
Ser	Lys	Leu	Ala	Gly	Ser	Leu	Phe	Lys	Gly	Phe	Glu	Lys	Val	Val	Val
			580					585					590		
Thr	Ser	Ala	Pro	Lys	Ile	Ser	Ser	Val	Phe	Gln	Ser	Leu	Leu	Asp	Thr

	595					600				605					
Val	Ala	Pro	Val	Phe	Glu	Ser	Ile	Glu	Arg	Ser	Val	Asn	Lys	Phe	Gly
	610					615					620				
Asp	Gly	Leu	Ser	Arg	Val	Tyr	Asp	Glu	His	Val	Ala	Pro	Ala	Ile	Asn
	625				630					635					640
Ser	Ile	Ala	Asn	Ala	Phe	Asn	Gly	Leu	Ile	Asp	Ile	Ile	Gln	Ile	Leu
			645					650						655	
Trp	Glu	Asn	Ser	Trp	Gln	Pro	Phe	Ala	Glu	Phe	Leu	Ser	Gly	Val	Phe
		660						665					670		
Gly	Val	Ser	Ile	Glu	Gly	Ile	Ser	Asp	Leu	Leu	Gly	Gly	Gly	Leu	Leu
	675					680						685			
Ala	Thr	Leu	Gly	Leu	Leu	Ala	Asp	Ala	Ile	Lys	Leu	Val	Ala	Asp	Gly
	690					695					700				
Phe	Thr	Val	Phe	Ser	Asp	Trp	Cys	Lys	Glu	Asn	Lys	Glu	Pro	Ile	Leu
	705				710					715					720
Ala	Leu	Ile	Thr	Thr	Trp	Gln	Thr	Ile	Asn	Phe	Leu	Ser	Trp	Ala	Glu
				725				730						735	
Gln	Ala	Gly	Gly	Leu	Ala	Gly	Ala	Phe	Ser	Leu	Leu	Gly	Ser	Lys	Val
		740				745						750			
Ser	Leu	Ile	Val	Gly	Gly	Ile	Lys	Asn	Leu	Gly	Leu	Ala	Ile	Lys	Ala
	755					760					765				
Leu	Thr	Phe	Asp	Lys	Leu	Val	Ser	Phe	Gly	Glu	Thr	Ile	Tyr	Leu	Asn
	770				775						780				
Thr	Leu	Tyr	Ala	Lys	Asp	Phe	Val	Val	Asn	Ser	Gly	Lys	Thr	Ile	Ala
	785				790				795						800
Gln	Leu	Gly	Lys	Thr	Ala	Leu	Glu	Leu	Gly	Lys	Ser	Ala	Leu	Ala	Trp
				805				810						815	
Thr	Ala	His	Ala	Ala	Lys	Met	Gly	Leu	Ala	Thr	Ala	Ala	Glu	Phe	Ala
		820					825						830		
His	Ser	Val	Ala	Ala	Gly	Val	Ala	Thr	Ala	Ala	Thr	Trp	Ala	Phe	Asn
	835					840					845				
Ala	Ala	Leu	Ala	Val	Leu	Thr	Ser	Pro	Ile	Thr	Trp	Ile	Ile	Ala	Ala
	850				855						860				
Ile	Ala	Ala	Leu	Ile	Ala	Ile	Gly	Val	Leu	Leu	Tyr	Gln	Asn	Trp	Asp
	865				870				875						880
Thr	Val	Val	Glu	Phe	Ala	Lys	Thr	Ala	Trp	Gln	Gly	Leu	Cys	Asp	Phe
				885				890						895	
Ile	Ser	Gly	Ile	Cys	Arg	Ala	Ile	Gly	Glu	Phe	Phe	Ser	Gly	Leu	Trp
		900					905						910		
Thr	Lys	Leu	Gln	Glu	Ile	Phe	Glu	Pro	Ile	Gly	Gln	Trp	Phe	Gly	Glu
	915					920						925			
Lys	Phe	Gln	Gln	Ala	Trp	Asp	Ala	Ile	Val	Asn	Ile	Phe	Ser	Gly	Ile
	930				935						940				
Gly	Glu	Trp	Phe	Ser	Gly	Val	Phe	Gln	Gly	Ala	Trp	Asp	Ala	Ile	Val
	945				950					955					960
Asn	Ile	Phe	Thr	Pro	Ile	Gly	Ser	Trp	Phe	Gly	Gln	Arg	Trp	Ala	Asp
			965						970					975	
Val	Thr	Ser	Ala	Leu	Ala	Asn	Ile	Gly	Ala	Trp	Phe	Thr	Asp	Ile	Phe
		980						985					990		
Gln	Lys	Ala	Trp	Thr	Gly	Leu	Thr	Asn	Ile	Phe	Ser	Lys	Leu	Gly	Leu
	995					1000						1005			
Trp	Phe	Gly	Glu	Arg	Trp	Ala	Asp	Val	Thr	Ser	Val	Leu	Ala	Asn	Val
	1010				1015						1020				
Ser	Ser	Trp	Phe	Gly	Asn	Met	Phe	Thr	Ser	Ala	Tyr	Asn	Ala	Val	Lys
	1025				1030					1035					1040
Asn	Ala	Phe	Ser	Ser	Ile	Gly	Gly	Phe	Phe	Ser	Gly	Val	Trp	Ser	Thr

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...418

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3218:

Ile	Val	Leu	Tyr	Glu	Ser	Ile	Arg	Leu	Val	Tyr	Met	Lys	Arg	Ser	Leu
1				5					10					15	
Asp	Ser	Arg	Val	Asp	Tyr	Ser	Leu	Leu	Leu	Pro	Val	Phe	Phe	Leu	Leu
			20					25					30		
Val	Ile	Gly	Val	Val	Ala	Ile	Tyr	Ile	Ala	Val	Ser	His	Asp	Tyr	Pro
		35					40					45			
Asn	Asn	Ile	Leu	Pro	Ile	Leu	Gly	Gln	Gln	Val	Ala	Trp	Ile	Ala	Leu
	50					55					60				
Gly	Leu	Val	Ile	Gly	Phe	Val	Val	Met	Leu	Phe	Asn	Thr	Glu	Phe	Leu
65					70					75					80
Trp	Lys	Val	Thr	Pro	Phe	Leu	Tyr	Ile	Leu	Gly	Leu	Gly	Leu	Met	Ile
				85					90					95	
Leu	Pro	Ile	Val	Phe	Tyr	Asn	Pro	Ser	Leu	Val	Ala	Ser	Thr	Gly	Ala
			100					105						110	
Lys	Asn	Trp	Val	Ser	Ile	Asn	Gly	Ile	Thr	Leu	Phe	Gln	Pro	Ser	Glu
		115					120					125			
Phe	Met	Lys	Ile	Ser	Tyr	Ile	Leu	Met	Leu	Ala	Arg	Val	Ile	Val	Gln
	130						135				140				
Phe	Thr	Lys	Lys	His	Lys	Glu	Trp	Arg	Arg	Thr	Val	Pro	Leu	Asp	Phe
145					150					155					160
Leu	Leu	Ile	Phe	Trp	Met	Ile	Leu	Phe	Thr	Ile	Pro	Val	Leu	Val	Leu
				165					170					175	
Leu	Ala	Leu	Gln	Ser	Asp	Leu	Gly	Thr	Ala	Leu	Val	Phe	Val	Ala	Ile
		180					185						190		
Phe	Ser	Gly	Ile	Val	Leu	Leu	Ser	Gly	Val	Ser	Trp	Lys	Ile	Ile	Ile
		195					200					205			
Pro	Val	Phe	Val	Thr	Ala	Val	Thr	Gly	Val	Ala	Gly	Phe	Leu	Ala	Ile
	210					215					220				
Phe	Ile	Ser	Lys	Asp	Gly	Arg	Ala	Phe	Leu	His	Gln	Ile	Gly	Met	Pro
225					230					235					240
Thr	Tyr	Gln	Ile	Asn	Arg	Ile	Leu	Ala	Trp	Leu	Asn	Pro	Phe	Glu	Phe
				245					250					255	
Ala	Gln	Thr	Thr	Thr	Tyr	Gln	Gln	Ala	Gln	Gly	Gln	Ile	Ala	Ile	Gly
		260						265					270		
Ser	Gly	Gly	Leu	Phe	Gly	Gln	Gly	Phe	Asn	Ala	Ser	Asn	Leu	Leu	Ile
		275					280					285			
Pro	Val	Arg	Glu	Ser	Asp	Met	Ile	Phe	Thr	Val	Ile	Ala	Glu	Asp	Phe
	290					295					300				
Gly	Phe	Ile	Gly	Ser	Val	Leu	Val	Ile	Ala	Leu	Tyr	Leu	Met	Leu	Ile
305					310					315					320
Tyr	Arg	Met	Leu	Lys	Ile	Thr	Leu	Lys	Ser	Asn	Asn	Gln	Phe	Tyr	Thr
				325					330					335	
Tyr	Ile	Ser	Thr	Gly	Leu	Ile	Met	Met	Leu	Leu	Phe	His	Ile	Phe	Glu
			340					345					350		

Asn	Ile	Gly	Ala	Val	Thr	Gly	Leu	Leu	Pro	Leu	Thr	Gly	Ile	Pro	Leu
		355					360					365			
Pro	Phe	Ile	Ser	Gln	Gly	Gly	Ser	Ala	Ile	Ile	Ser	Asn	Leu	Ile	Gly
	370				375						380				
Val	Gly	Leu	Leu	Leu	Ser	Met	Ser	Tyr	Gln	Thr	Asn	Leu	Ala	Glu	Glu
385				390					395						400
Lys	Ser	Gly	Lys	Val	Pro	Phe	Lys	Arg	Lys	Lys	Val	Val	Leu	Lys	Gln
			405					410						415	
Ile	Lys														

(2) INFORMATION FOR SEQ ID NO:3219:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 191 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...191
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3219:

Asn	Ala	Leu	Tyr	Gln	Val	Leu	Gly	Ala	Asp	Ile	Met	Arg	Phe	Ser	Ala
1				5					10					15	
Phe	Lys	Ile	Phe	Ser	Asn	Ser	Val	Cys	Lys	Arg	Ile	Ile	Thr	Lys	Gly
		20					25					30			
Leu	Gly	Phe	Arg	Ala	Leu	Leu	Leu	Tyr	Thr	Ile	Ser	Lys	Val	Lys	Leu
	35				40						45				
Arg	Glu	Asp	Ile	Leu	Val	Ser	Gln	Ser	Ile	Val	Pro	Val	Glu	Ile	Pro
	50				55					60					
Gln	Tyr	Cys	Arg	Phe	Asp	Ser	Lys	Lys	Arg	Asn	Gly	Ile	Leu	Phe	Asn
65			70						75					80	
Val	Arg	Ile	Ala	Asn	Leu	Lys	Phe	Thr	Phe	Phe	Arg	Leu	Asp	Phe	Leu
			85					90					95		
Arg	Asn	Lys	Ile	Trp	Tyr	Ser	Ser	Ser	Met	Asn	Asp	Glu	Ala	Ser	Lys
	100						105						110		
Gln	Leu	Thr	Asp	Ala	Arg	Phe	Lys	Arg	Leu	Val	Gly	Val	Gln	Arg	Thr
	115					120					125				
Thr	Phe	Glu	Glu	Met	Leu	Ala	Val	Leu	Lys	Thr	Ala	Tyr	Gln	Leu	Lys
	130				135					140					
His	Ala	Lys	Gly	Gly	Arg	Lys	Pro	Lys	Leu	Ser	Leu	Glu	Asp	Leu	Leu
145				150					155					160	
Met	Ala	Thr	Leu	Gln	Tyr	Val	Arg	Glu	Tyr	Arg	Thr	Tyr	Glu	Glu	Ile
			165					170					175		
Ala	Ala	Val	Phe	Gly	Ile	His	Glu	Ser	Asn	Leu	Ile	Arg	Arg	Ser	
		180					185						190		

(2) INFORMATION FOR SEQ ID NO:3220:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 123 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...123
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3220:

Met	Asn	Met	Tyr	Arg	Val	Ile	Glu	Met	Tyr	Gly	Asp	Phe	Glu	Pro	Trp
1				5					10					15	
Trp	Phe	Leu	Glu	Gly	Trp	Glu	Glu	Asp	Ile	Val	Ala	Ser	Arg	Lys	Phe
			20					25					30		
Asp	Gln	Tyr	Tyr	Asp	Ala	Leu	Lys	Tyr	Tyr	Lys	Thr	Cys	Trp	Phe	Arg
		35					40					45			
Leu	Glu	Gln	Glu	Ser	Pro	Leu	Tyr	Lys	Ser	Arg	Ser	Asp	Leu	Met	Thr
		50					55				60				
Ile	Phe	Trp	Asp	Pro	Glu	Asp	Gln	Arg	Trp	Cys	Asp	Glu	Cys	Asp	Glu
65					70				75						80
Tyr	Leu	Gln	Gln	Tyr	His	Ser	Leu	Ala	Leu	Leu	Gln	Asp	Glu	Gln	Val
				85					90					95	
Ile	Pro	Asp	Glu	Lys	Leu	Arg	Ser	Gly	Tyr	Glu	Lys	Gln	Thr	Ser	Gln
			100					105					110		
Glu	Arg	Asn	Arg	Ser	Cys	Arg	Met	Lys	Leu	Lys					
		115					120								

(2) INFORMATION FOR SEQ ID NO:3221:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 119 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...119
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3221:

Glu Met Val Tyr Gln Val Phe Ser Val Leu Phe Ser Ser Glu Arg Ala

1		5		10		15									
Tyr	Ser	Phe	Ser	Pro	Val	Ala	Leu	Gln	Lys	Leu	Arg	Lys	Ile	Lys	
		20					25					30			
Met	Arg	Ile	Arg	Arg	Lys	Leu	Met	Lys	Lys	Glu	Lys	Lys	Gln	Leu	Arg
		35				40						45			
Tyr	Pro	Gly	Leu	Lys	Ala	Gly	Ser	Ile	Tyr	Gly	Thr	Val	Ile	Phe	Phe
	50					55					60				
Ile	Ile	Pro	Leu	Ile	Asp	Thr	Leu	Thr	Ser	Glu	Asn	Pro	Asn	Phe	Ile
65					70					75					80
Ser	Ser	Leu	Leu	Asn	Thr	Lys	His	Ile	Phe	Lys	Thr	Met	Leu	Gly	Ala
				85					90					95	
Phe	Phe	Phe	Gly	Val	Met	Ile	His	Ile	Val	Asp	Ser	Leu	Arg	Ile	Ala
			100					105					110		
Arg	Ala	Lys	Lys	Asp	Gln	Asp									
			115												

(2) INFORMATION FOR SEQ ID NO:3222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...254

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3222:

Gln	Asn	Asp	Leu	Phe	Trp	Ser	Arg	Ile	Met	Gly	Leu	Thr	Tyr	Gln	Met
1			5					10					15		
Lys	Met	Lys	Ile	Pro	Phe	Asp	Met	Ala	Asp	Met	Asn	Gly	His	Ile	Lys
		20						25				30			
Leu	Pro	Asp	Val	Ile	Leu	Leu	Ser	Leu	Gln	Val	Ser	Gly	Met	Gln	Ser
		35				40						45			
Ile	Glu	Leu	Gly	Val	Ser	Asp	Lys	Ala	Ile	Leu	Glu	Glu	Tyr	Asn	Leu
	50				55					60					
Val	Trp	Ile	Ile	Val	Glu	Tyr	Asp	Ile	Glu	Val	Phe	Arg	Leu	Pro	Arg
65				70					75						80
Phe	Ala	Glu	Glu	Ile	Thr	Ile	Glu	Thr	Glu	Ala	Leu	Ser	Tyr	Asn	Arg
			85					90					95		
Leu	Phe	Cys	Tyr	Arg	Arg	Phe	Thr	Ile	Tyr	Asn	Glu	Ala	Glu	Gln	Glu
			100					105					110		
Leu	Ile	His	Met	Met	Ala	Thr	Phe	Val	Leu	Met	Asp	Arg	Asp	Ser	Arg
		115				120						125			
Lys	Val	His	Val	Val	Glu	Pro	Glu	Ile	Val	Ala	Pro	Tyr	Gln	Ser	Asp
	130					135				140					
Phe	Asp	Lys	Lys	Leu	Ile	Arg	Gly	Pro	Lys	Tyr	Glu	Ser	Leu	Glu	Glu
145				150					155						160
Pro	Ile	Ser	Lys	Asp	Tyr	His	Val	Arg	Phe	Tyr	Asp	Leu	Asp	Met	Asn

				165					170					175					
Gly	His	Val	Asn	Asn	Ser	Lys	Tyr	Leu	Asp	Trp	Ile	Phe	Glu	Val	Met				
			180					185					190						
Gly	Ala	Asp	Phe	Leu	Thr	His	Tyr	Ile	Pro	Lys	Lys	Ile	Asn	Leu	Lys				
		195					200					205							
Tyr	Val	Lys	Glu	Val	Arg	Pro	Gly	Gly	Val	Ile	Thr	Ser	Ala	Val	Glu				
	210					215					220								
Arg	Thr	Gly	Leu	Glu	Ser	Lys	His	Glu	Ile	Thr	Ser	Asp	Gly	Val	Ile				
225					230					235					240				
Asn	Ala	Gln	Ala	Ile	Ile	Thr	Trp	Gln	Glu	Ile	Lys	Lys	Ala						
				245					250										

(2) INFORMATION FOR SEQ ID NO:3223:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 178 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...178

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3223:

Glu	Asn	Asp	Leu	Val	Thr	Lys	Val	Glu	Thr	Ala	Arg	Ser	Leu	Ala	Leu				
1				5				10					15						
Ala	Val	Leu	Glu	Asp	Val	Phe	Val	Asn	Gln	Ala	Tyr	Ser	Asn	Ile	Ala				
		20						25				30							
Leu	Asn	Lys	His	Leu	Lys	Gly	Ser	Gln	Leu	Ser	Ala	Ala	Asp	Lys	Gly				
	35					40					45								
Leu	Val	Thr	Glu	Leu	Val	Tyr	Gly	Thr	Val	Ala	Arg	Lys	Leu	Thr	Leu				
	50					55				60									
Glu	Trp	Tyr	Leu	Ser	His	Phe	Ile	Glu	Asp	Arg	Asp	Gln	Leu	Asp	Ser				
65				70					75				80						
Trp	Leu	Tyr	Val	Leu	Leu	Leu	Met	Ser	Ala	Tyr	Gln	Leu	Arg	Tyr	Leu				
			85					90					95						
Asp	Lys	Ile	Pro	Asp	His	Ala	Val	Val	Asn	Glu	Ala	Val	Glu	Leu	Ala				
		100						105				110							
Lys	Leu	Arg	Lys	Lys	Gly	Ser	Glu	Lys	Leu	Val	Asn	Ala	Val	Leu	Arg				
	115					120					125								
Arg	Ile	Leu	Arg	Glu	Gly	Trp	Pro	Asp	Ile	Ala	Ser	Ile	Lys	Arg	Lys				
	130				135				140										
Asn	Lys	Arg	Asp	Ser	Ile	Ala	Tyr	Ser	Leu	Pro	Val	Trp	Leu	Val	Thr				
145				150				155					160						
Lys	Leu	Lys	Glu	Glu	Tyr	Gly	Glu	Glu	Arg	Ala	Lys	Ala	Ile	Phe	Glu				
			165					170					175						
Ser	Leu																		

(2) INFORMATION FOR SEQ ID NO:3224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...142

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3224:

Asp	Leu	Ser	Tyr	Lys	Ser	Arg	Leu	Pro	Ala	Tyr	Gly	Tyr	Asp	Trp	Phe
1				5					10					15	
Leu	Thr	Arg	Arg	Gln	Tyr	Thr	Gln	Phe	Ile	Gly	Leu	Glu	Tyr	Gln	Asp
			20					25					30		
Gln	Ile	Gly	Cys	Leu	Gly	Val	Phe	Ser	Ser	Ala	Asn	Trp	Leu	His	Gln
		35				40						45			
Glu	Ala	Phe	Asn	Arg	Tyr	Ile	Glu	Cys	Gln	Lys	Leu	Ser	Pro	Asp	Gln
	50					55					60				
Arg	Ile	Phe	Ile	Tyr	Val	Gly	Thr	Glu	Glu	Ala	Asp	Asp	Thr	Asp	Lys
65					70					75					80
Thr	Leu	Met	Asp	Gly	Asn	Ile	Lys	Gln	Ala	Tyr	Ile	Asp	Ser	Ser	Leu
				85					90					95	
Cys	Tyr	Tyr	His	Asp	Leu	Ile	Ala	Gly	Gly	Val	His	Leu	Asp	Asn	Leu
			100					105					110		
Val	Leu	Lys	Val	Gln	Ser	Gly	Ala	Ile	His	Ser	Glu	Ile	Pro	Trp	Ser
		115					120					125			
Glu	Asn	Leu	Pro	Asp	Cys	Leu	Arg	Phe	Phe	Ala	Glu	Lys	Trp		
	130						135					140			

(2) INFORMATION FOR SEQ ID NO:3225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3225:

Phe	Ser	Asp	Phe	Thr	Met	Cys	His	Leu	Ile	Ala	Ser	Ile	Gly	Leu	Asn
1				5					10					15	
Met	Asp	Ser	Thr	Pro	Val	Ile	Ile	Gly	Ala	Met	Leu	Ile	Ser	Pro	Leu
			20					25					30		
Met	Thr	Pro	Ile	Leu	Gly	Val	Gly	Leu	Ser	Leu	Ala	Ile	Phe	Asp	Phe
			35				40					45			
Lys	Leu	Leu	Arg	Lys	Ser	Phe	Lys	Ile	Leu	Ala	Ile	Gln	Ile	Leu	Ala
			50			55					60				
Ser	Leu	Ile	Ala	Ser	Thr	Leu	Tyr	Phe	Tyr	Leu	Ser	Pro	Ile	Ser	Tyr
65					70				75					80	
Ala	Ser	Ser	Glu	Ile	Val	Ala	Arg	Thr	Ser	Pro	Thr	Ile	Trp	Asp	Val
			85					90						95	
Leu	Ile	Ala	Phe	Val	Gly	Gly	Ile	Ala	Gly	Ile	Ile	Gly	Ala	Arg	Lys
			100					105					110		
Lys	Glu	Thr	Asn	Asn	Ile	Val	Pro	Gly	Val	Ala	Ile	Ala	Thr	Ala	Leu
			115				120					125			
Met	Pro	Pro	Leu	Cys	Thr	Val	Gly	Tyr	Ala	Ile	Ala	Ser	Ala	Asn	Leu
			130			135					140				
Lys	Phe	Ile	Ile	Gly	Ser	Ser	Tyr	Leu	Phe	Leu	Ile	Asn	Cys	Ser	Phe
145					150					155				160	
Ile	Val	Ile	Ala	Thr	Tyr	Ile	Gly	Val	Arg	Leu	Met	Met	Val	Lys	Lys
			165					170						175	
His	Tyr	Phe	Lys	Asp	Asn	Glu	Glu	Asp	Ser	Lys	Met	Arg	Arg	Ile	Leu
			180					185					190		
Leu	Leu	Val	Ala	Val	Leu	Leu	Met	Ile	Pro	Ser	Phe	Ile	Ser	Ala	Thr
			195				200					205			
Thr	Leu	Val	Arg	Glu	Thr	Leu	Lys	Lys	Glu	Ser	Leu	Lys	Lys	Phe	Ile
			210			215					220				
Ser	Glu	Gln	Val	Ser	Gly	Ala									
225					230										

(2) INFORMATION FOR SEQ ID NO:3226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...110

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3226:

Ala	Phe	Gln	Tyr	Leu	Thr	Ile	Leu	Tyr	Phe	Leu	Arg	Asn	Lys	Ile	Trp
1				5				10						15	
Tyr	Ser	Ser	Ser	Met	Asn	Asp	Glu	Ala	Ser	Lys	Gln	Leu	Thr	Asp	Ala
			20					25					30		

Arg	Phe	Lys	Arg	Leu	Val	Gly	Val	Gln	Arg	Thr	Thr	Phe	Glu	Glu	Met
		35					40					45			
Leu	Ala	Val	Leu	Lys	Thr	Ala	Tyr	Gln	Leu	Lys	His	Ala	Lys	Gly	Gly
		50					55				60				
Arg	Lys	Pro	Lys	Leu	Ser	Leu	Glu	Asp	Leu	Leu	Met	Ala	Thr	Leu	His
65					70					75					80
Met	Cys	Glu	Asn	Ile	Glu	Leu	Met	Asn	Lys	Leu	Arg	Leu	Ile	Leu	Val
				85					90					95	
Phe	Thr	Lys	Ala	Thr	Leu	Ser	Val	Gly	Ala	Asn	Gly	Leu	Lys		
			100					105					110		

(2) INFORMATION FOR SEQ ID NO:3227:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 545 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...545

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3227:

Lys	Glu	Lys	Tyr	Lys	Leu	Ser	Pro	Ile	Gly	Trp	Leu	Arg	Thr	Thr	Phe
1				5					10					15	
Arg	Lys	Lys	Asn	Asn	Val	Lys	Phe	Asn	Glu	Leu	Asn	Leu	Ser	Ala	Asp
			20					25					30		
Leu	Leu	Ala	Glu	Ile	Glu	Lys	Ala	Gly	Phe	Val	Glu	Ala	Ser	Pro	Ile
		35					40					45			
Gln	Glu	Gln	Thr	Ile	Pro	Leu	Ala	Leu	Glu	Gly	Lys	Asp	Val	Ile	Gly
	50					55					60				
Gln	Ala	Gln	Thr	Gly	Thr	Gly	Lys	Thr	Ala	Ala	Phe	Gly	Leu	Pro	Thr
65					70					75					80
Leu	Glu	Lys	Ile	Arg	Thr	Glu	Glu	Ala	Thr	Ile	Gln	Ala	Leu	Val	Ile
				85					90					95	
Ala	Pro	Thr	Arg	Glu	Leu	Ala	Val	Gln	Ser	Gln	Glu	Glu	Leu	Phe	Arg
			100					105					110		
Phe	Gly	Arg	Ser	Lys	Gly	Val	Lys	Val	Arg	Ser	Val	Tyr	Gly	Gly	Ser
		115					120					125			
Ser	Ile	Glu	Lys	Gln	Ile	Lys	Ala	Leu	Lys	Ser	Gly	Ala	His	Ile	Val
	130					135					140				
Val	Gly	Thr	Pro	Gly	Arg	Leu	Leu	Asp	Leu	Ile	Lys	Arg	Lys	Ala	Leu
145					150					155					160
Lys	Leu	Gln	Asp	Ile	Glu	Thr	Leu	Ile	Leu	Asp	Glu	Ala	Asp	Glu	Met
				165					170					175	
Leu	Asn	Met	Gly	Phe	Leu	Glu	Asp	Ile	Glu	Ala	Ile	Ile	Ser	Arg	Val
		180					185						190		
Pro	Glu	Asn	Arg	Gln	Thr	Leu	Leu	Phe	Ser	Ala	Thr	Met	Pro	Asp	Ala
		195					200					205			

Ile	Lys	Arg	Ile	Gly	Val	Gln	Phe	Met	Lys	Ala	Pro	Glu	His	Val	Lys
210						215					220				
Ile	Ala	Ala	Lys	Glu	Leu	Thr	Thr	Glu	Leu	Val	Asp	Gln	Tyr	Tyr	Ile
225					230					235					240
Arg	Val	Lys	Glu	Gln	Glu	Lys	Phe	Asp	Thr	Met	Thr	Arg	Leu	Met	Asp
				245					250					255	
Val	Ala	Gln	Pro	Glu	Leu	Ala	Ile	Val	Phe	Gly	Arg	Thr	Lys	Arg	Arg
			260					265					270		
Val	Asp	Glu	Leu	Thr	Arg	Gly	Leu	Lys	Ile	Arg	Gly	Phe	Arg	Ala	Glu
		275					280					285			
Gly	Ile	His	Gly	Asp	Leu	Asp	Gln	Asn	Lys	Arg	Leu	Arg	Val	Leu	Arg
	290					295					300				
Asp	Phe	Lys	Asn	Gly	Asn	Leu	Asp	Val	Leu	Val	Ala	Thr	Asp	Val	Ala
305					310					315					320
Ala	Arg	Gly	Leu	Asp	Ile	Ser	Gly	Val	Thr	His	Val	Tyr	Asn	Tyr	Asp
				325					330					335	
Ile	Pro	Gln	Asp	Pro	Glu	Ser	Tyr	Val	His	Arg	Ile	Gly	Arg	Thr	Gly
			340					345					350		
Arg	Ala	Gly	Lys	Ser	Gly	Gln	Ser	Ile	Thr	Phe	Val	Ala	Pro	Asn	Glu
		355					360					365			
Met	Gly	Tyr	Leu	Gln	Ile	Ile	Glu	Asn	Leu	Thr	Lys	Lys	Arg	Met	Lys
	370					375					380				
Gly	Leu	Lys	Pro	Ala	Ser	Val	Glu	Glu	Ser	Phe	Gln	Ser	Lys	Lys	Gln
385					390					395					400
Val	Ala	Leu	Lys	Lys	Ile	Glu	Arg	Asp	Phe	Ala	Asp	Glu	Thr	Ile	Arg
				405					410					415	
Ala	Asn	Phe	Glu	Lys	Phe	Gly	Lys	Asp	Ala	Arg	Lys	Leu	Ala	Ala	Glu
			420					425					430		
Phe	Thr	Pro	Glu	Glu	Leu	Ala	Met	Tyr	Ile	Leu	Ser	Leu	Thr	Val	Gln
		435					440					445			
Asp	Pro	Asp	Ser	Leu	Pro	Glu	Val	Glu	Ile	Ala	Arg	Glu	Lys	Pro	Leu
	450					455					460				
Pro	Phe	Lys	Pro	Ser	Gly	Asn	Gly	Phe	Gly	Gly	Lys	Ala	Lys	Gly	Gly
465					470					475					480
Arg	Gly	Gly	Arg	Arg	Gly	Asp	Asp	Arg	Arg	Glu	Arg	Asp	Arg	Arg	Gly
				485					490					495	
Asn	Gly	Arg	Arg	Asp	Glu	Phe	Lys	Lys	Gly	Ser	Arg	Gly	Asn	Asp	Arg
		500						505					510		
Phe	Asp	Lys	Glu	Lys	Arg	Tyr	Arg	Lys	Asp	Asn	Lys	Lys	Pro	Arg	Asn
		515					520					525			
Thr	Leu	Ser	Glu	Lys	Gln	Thr	Gly	Phe	Val	Ile	Arg	Asn	Lys	Gly	Asp
	530					535					540				
Lys															
545															

(2) INFORMATION FOR SEQ ID NO:3228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...280

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3228:

Tyr	Arg	Lys	Tyr	Asp	Ser	Arg	Arg	Ile	Ile	Asn	Thr	Ser	Phe	Arg	Lys
1				5					10					15	
Lys	Val	Tyr	Glu	Glu	Lys	Gln	Tyr	Phe	Ile	Phe	Ile	Leu	Leu	Leu	Cys
			20					25					30		
Ile	Gly	Leu	Gln	Tyr	Glu	Thr	Ile	Tyr	Tyr	Thr	Asp	Gly	Ser	Arg	Ser
		35					40					45			
Gly	Ala	Glu	Tyr	Gly	Leu	Met	Gly	Val	Ser	Ile	Phe	Leu	Ala	Leu	Phe
	50					55					60				
Tyr	Met	Ile	Pro	Ala	Leu	Tyr	Phe	Leu	Phe	Arg	Ile	Gly	Lys	Lys	Trp
65					70					75					80
Glu	Leu	Pro	Lys	Lys	Val	Leu	Ile	Leu	Ser	Leu	Leu	Gly	Gly	Met	Phe
			85						90					95	
Leu	Ala	Gly	Trp	Leu	Ser	Ser	Phe	Ala	Asn	Thr	Tyr	Ile	His	Asp	Leu
		100						105					110		
Leu	Gly	Val	Leu	Phe	Pro	Asp	Ser	Pro	Phe	Leu	Asn	Ala	Phe	Glu	Ser
	115					120					125				
Ala	Ile	Val	Ala	Pro	Leu	Val	Glu	Glu	Pro	Leu	Lys	Leu	Leu	Pro	Leu
	130					135					140				
Val	Phe	Val	Leu	Ala	Leu	Ile	Pro	Val	Arg	Lys	Leu	Lys	Phe	Leu	Phe
145					150					155					160
Leu	Leu	Gly	Ile	Ala	Ser	Gly	Leu	Gly	Phe	Gln	Met	Ile	Glu	Asp	Ile
			165					170					175		
Gly	Tyr	Ile	Arg	Thr	Asp	Leu	Pro	Glu	Gly	Phe	Asp	Phe	Thr	Ile	Ser
		180						185					190		
Arg	Ile	Leu	Glu	Arg	Ile	Ile	Ser	Gly	Ile	Ala	Ser	His	Trp	Thr	Phe
	195						200					205			
Ser	Gly	Leu	Ala	Val	Val	Gly	Val	Tyr	Leu	Leu	Tyr	Arg	Ala	Tyr	Lys
	210					215					220				
Gly	Gln	Lys	Val	Gly	Lys	Lys	Gln	Gly	Leu	Ile	Phe	Leu	Gly	Leu	Ala
225					230					235					240
Leu	Gly	Thr	His	Phe	Leu	Phe	Asn	Ser	Pro	Phe	Cys	Gly	Val	Gly	Asn
			245						250					255	
Arg	Val	Ala	Phe	Ser	Asp	Ser	Ser	Gly	Tyr	Gly	Tyr	Cys	Ser	Leu	Trp
		260						265					270		
Phe	Leu	Ser	Cys	Leu	Leu	Leu	Cys								
	275						280								

(2) INFORMATION FOR SEQ ID NO:3229:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 291 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...291

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3229:

```
Met Lys Glu Tyr Asp Met Lys Lys Trp Trp Lys Glu Leu Ile Asp Lys
1      5      10      15
Pro Leu Leu Lys Ala Phe Leu His Tyr Tyr Gln Ala Ser Asp Ser Glu
      20      25      30
Leu Thr Ser Val Ala Val Ala Tyr Tyr Trp Leu Ile Ser Ile Phe Pro
      35      40      45
Leu Leu Leu Val Val Val Asn Ile Leu Pro Tyr Phe Gln Ile Pro Val
      50      55      60
Gly Glu Phe Leu Gly Phe Met Lys Asp Val Leu Pro Pro Ser Leu Tyr
65      70      75      80
Glu Gly Val Glu Lys Ile Ala Arg Glu Val Leu Thr Gln Pro Ser Thr
      85      90      95
Gly Leu Leu Ser Phe Ser Val Leu Ser Ala Leu Trp Ser Phe Ser Lys
      100     105     110
Ser Met Asn Phe Leu Gln Lys Ala Phe Asn Lys Ala Tyr Gly Val Glu
      115     120     125
Lys Ser Arg Gly Leu Ile Ser His Gln Met Leu Ser Leu Leu Val Ser
      130     135     140
Phe Gly Leu Gln Ile Leu Phe Ala Phe Ala Leu Phe Leu Ile Leu Phe
145     150     155     160
Gly Gln Met Ile Leu Ala Leu Leu Ala His Tyr Trp Thr Lys Asp Gly
      165     170     175
Ile Ile Tyr Gln Ala Leu Gln Gly Leu Ala Gly Pro Leu Ile Tyr Ala
      180     185     190
Leu Leu Phe Ala Ile Leu Val Met Leu Tyr Tyr Phe Leu Pro Asn Leu
      195     200     205
Ser Asn Arg Lys Ile Ser Tyr Thr Leu Pro Gly Ser Ala Phe Val Leu
      210     215     220
Leu Val Ile Leu Gly Leu Leu Thr Leu Phe Ser Ser Tyr Leu Asn Tyr
225     230     235     240
Tyr Val His His Leu Val Asp Val Arg Ile Leu Gly Ser Val Leu Leu
      245     250     255
Val Val Met Met Phe Trp Phe Ile Leu Ile Ala Lys Ile Val Ile Leu
      260     265     270
Gly Ala Val Ile Asn Ala Ser Met Gln Ser Leu Lys Asp Pro Val Phe
      275     280     285
Lys Lys Asp
290
```

(2) INFORMATION FOR SEQ ID NO:3230:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 399 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...399

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3230:

Lys	Lys	Glu	Tyr	Leu	Arg	Asn	Met	Lys	Lys	Lys	Ile	Leu	Ala	Ser	Leu
1				5				10						15	
Leu	Leu	Ser	Thr	Val	Met	Val	Ser	Gln	Val	Ala	Val	Leu	Thr	Thr	Ala
			20					25					30		
His	Ala	Glu	Thr	Thr	Asp	Asp	Lys	Ile	Ala	Ala	Gln	Asp	Asn	Lys	Ile
		35					40					45			
Ser	Asn	Leu	Thr	Ala	Gln	Gln	Gln	Glu	Ala	Gln	Lys	Gln	Val	Asp	Gln
	50					55					60				
Ile	Gln	Glu	Gln	Val	Ser	Ala	Ile	Gln	Ala	Glu	Gln	Ser	Asn	Leu	Gln
65					70					75				80	
Ala	Glu	Asn	Asp	Arg	Leu	Gln	Ala	Glu	Ser	Lys	Lys	Leu	Glu	Gly	Glu
			85					90						95	
Ile	Thr	Glu	Leu	Ser	Lys	Asn	Ile	Val	Ser	Arg	Asn	Gln	Ser	Leu	Glu
		100						105					110		
Lys	Gln	Ala	Arg	Ser	Ala	Gln	Thr	Asn	Gly	Ala	Val	Thr	Ser	Tyr	Ile
		115					120						125		
Asn	Thr	Ile	Val	Asn	Ser	Lys	Ser	Ile	Thr	Glu	Ala	Ile	Ser	Arg	Val
	130					135					140				
Ala	Ala	Met	Ser	Glu	Ile	Val	Ser	Ala	Asn	Asn	Lys	Met	Leu	Glu	Gln
145					150					155				160	
Gln	Lys	Ala	Asp	Lys	Lys	Ala	Ile	Ser	Glu	Lys	Gln	Val	Ala	Asn	Asn
			165					170						175	
Asp	Ala	Ile	Asn	Thr	Val	Ile	Ala	Asn	Gln	Gln	Lys	Leu	Ala	Asp	Asp
		180						185					190		
Ala	Gln	Ala	Leu	Thr	Thr	Lys	Gln	Ala	Glu	Leu	Lys	Ala	Ala	Glu	Leu
	195					200						205			
Ser	Leu	Ala	Ala	Glu	Lys	Ala	Thr	Ala	Glu	Gly	Glu	Lys	Ala	Ser	Leu
	210				215						220				
Leu	Glu	Gln	Lys	Ala	Ala	Ala	Glu	Ala	Glu	Ala	Arg	Ala	Ala	Ala	Val
225					230					235					240
Ala	Glu	Ala	Ala	Tyr	Lys	Glu	Lys	Arg	Ala	Ser	Gln	Gln	Gln	Ser	Val
			245					250						255	
Leu	Ala	Ser	Ala	Asn	Thr	Asn	Leu	Thr	Ala	Gln	Val	Gln	Ala	Val	Ser
		260					265						270		
Glu	Ser	Ala	Ala	Ala	Pro	Val	Arg	Ala	Lys	Val	Arg	Pro	Thr	Tyr	Ser
	275					280						285			
Thr	Asn	Ala	Ser	Ser	Tyr	Pro	Ile	Gly	Glu	Cys	Thr	Trp	Gly	Val	Lys
	290				295						300				
Thr	Leu	Ala	Pro	Trp	Ala	Gly	Asp	Tyr	Trp	Gly	Asn	Gly	Ala	Gln	Trp
305					310					315				320	
Ala	Thr	Ser	Ala	Ala	Ala	Ala	Gly	Phe	Arg	Thr	Gly	Ser	Thr	Pro	Gln
			325					330						335	
Val	Gly	Ala	Ile	Ala	Cys	Trp	Asn	Asp	Gly	Gly	Tyr	Gly	His	Val	Ala
		340					345						350		
Val	Val	Thr	Ala	Val	Glu	Ser	Thr	Thr	Arg	Ile	Gln	Val	Ser	Glu	Ser
		355				360						365			
Asn	Tyr	Ala	Gly	Asn	Arg	Thr	Ile	Gly	Asn	His	Arg	Gly	Trp	Phe	Asn

370	375	380
Pro Thr Thr Thr Ser Glu Gly Phe Val Thr Tyr Ile Tyr Ala Asp		
385	390	395

(2) INFORMATION FOR SEQ ID NO:3231:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 156 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3231:

Ile	Asn	Trp	Tyr	Lys	Met	Thr	Arg	Tyr	Ala	Leu	Leu	Val	Arg	Gly	Ile
1				5					10					15	
Asn	Val	Gly	Gly	Lys	Asn	Lys	Val	Val	Met	Ala	Glu	Leu	Arg	Gln	Glu
				20				25					30		
Leu	Thr	Asn	Leu	Gly	Leu	Glu	Lys	Val	Glu	Ser	Tyr	Ile	Asn	Ser	Gly
				35			40					45			
Asn	Ile	Phe	Phe	Thr	Ser	Ile	Asp	Ser	Lys	Ala	Gln	Leu	Val	Glu	Lys
						55					60				
Leu	Glu	Thr	Phe	Phe	Ala	Val	His	Tyr	Pro	Phe	Ile	Gln	Ser	Phe	Ser
65					70				75					80	
Leu	Leu	Ser	Leu	Glu	Asp	Phe	Glu	Ala	Glu	Leu	Glu	Asn	Leu	Pro	Ala
				85				90						95	
Trp	Trp	Ser	Arg	Asp	Leu	Ala	Arg	Lys	Asp	Phe	Leu	Phe	Tyr	Thr	Glu
			100					105					110		
Gly	Leu	Asp	Val	Asp	Gln	Val	Ile	Ala	Thr	Val	Glu	Ser	Leu	Glu	Leu
		115				120					125				
Lys	Asp	Glu	Val	Leu	Tyr	Phe	Gly	Lys	Leu	Gly	Ile	Phe	Trp	Gly	Lys
	130					135					140				
Phe	Ser	Glu	Glu	Ser	Tyr	Ser	Lys	Thr	Ala	Tyr	Gln				
145					150					155					

(2) INFORMATION FOR SEQ ID NO:3232:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 292 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...292

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3232:

Glu	Leu	Trp	Tyr	Asn	Lys	Arg	Met	Asn	Tyr	Pro	Lys	Ile	Asp	Leu	Lys
1				5				10						15	
Thr	Ile	Arg	Gln	Glu	Ser	Lys	His	Phe	Gln	Ala	Asp	Thr	Pro	Arg	Leu
			20					25					30		
Phe	Leu	Leu	Tyr	Ile	Leu	Pro	Ser	Met	Leu	Val	Ile	Leu	Ser	Gly	Phe
		35					40					45			
Leu	Asn	Pro	Leu	Ser	Arg	Ile	His	Gly	Thr	Val	Leu	Glu	Gln	Pro	Phe
	50					55				60					
Phe	Ser	Ile	Leu	Gly	Gln	Ile	Leu	Gln	Thr	Tyr	Leu	Phe	Pro	Leu	Leu
65				70					75					80	
Val	Ser	Phe	Ile	Gly	Thr	Ile	Leu	Leu	Thr	Ser	Ser	Val	Tyr	Ala	Thr
			85					90					95		
Leu	Thr	Leu	Met	Lys	Asp	Ser	Lys	Thr	Glu	Pro	Ser	Val	Lys	Asn	Ser
		100						105					110		
Leu	Ala	Leu	Phe	Asp	Glu	Glu	Arg	Phe	Ser	Gln	Thr	Phe	Leu	Thr	Leu
	115					120						125			
Leu	Leu	Lys	Arg	Phe	Tyr	Leu	Phe	Leu	Trp	Ser	Ile	Pro	Asn	Leu	Leu
	130					135					140				
Gly	Ile	Tyr	Leu	Leu	Phe	Tyr	Ser	Ser	Phe	Leu	Ala	Lys	Lys	Phe	Val
145				150					155					160	
Thr	Leu	His	Pro	Glu	Phe	Pro	Asn	Leu	Asp	Leu	Ser	Ser	Val	Glu	Thr
			165					170						175	
Glu	Arg	Phe	Leu	Met	Val	Phe	Gly	Leu	Tyr	Phe	Leu	Ala	Ser	Leu	Ile
		180					185						190		
Leu	Ile	Ile	Val	Gly	Asn	Ile	Leu	Tyr	Ile	Pro	Gln	Tyr	Tyr	Ala	Tyr
	195					200						205			
Ser	Gln	Val	Glu	Phe	Leu	Leu	Cys	Tyr	Ser	Leu	Asp	Leu	Gly	Gln	Val
	210					215					220				
Pro	Pro	Arg	Arg	Ile	Leu	Lys	Thr	Ser	Arg	Ser	Phe	Met	Lys	Gly	Tyr
225				230					235					240	
Lys	Phe	Gln	His	Phe	Val	Leu	Asp	Leu	Gln	Leu	Leu	Pro	Trp	Tyr	Phe
			245					250						255	
Leu	Asn	Trp	Ile	Thr	Phe	Gly	Ile	Ala	Ser	Phe	Ser	Leu	Leu	Pro	Tyr
	260					265						270			
Ile	Gln	Cys	Thr	Lys	Ile	Met	Phe	Tyr	Arg	Ala	Val	Leu	Ala	Arg	Lys
	275					280						285			
Arg	Pro	Lys	Ala												
	290														

(2) INFORMATION FOR SEQ ID NO:3233:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 376 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...376

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3233:

```
Met Leu Asp Leu Ile Gln Thr Arg Arg Asp Leu His Gln Ile Pro Glu
1      5      10      15
Ile Gly Leu Glu Glu Phe Lys Thr Gln Ala Tyr Leu Leu Asp Val Ile
      20      25      30
Glu Lys Leu Thr Thr Gly Lys Asp Phe Val Gln Ile Arg Thr Trp Arg
      35      40      45
Thr Gly Ile Leu Val Tyr Leu Gln Gly Ser Gln Pro Glu Arg Thr Ile
      50      55      60
Gly Trp Arg Thr Asp Ile Asp Gly Leu Pro Ile Val Glu Gln Thr Gly
      65      70      75      80
Leu Pro Phe Ala Ser Gln His Gln Gly Arg Met His Ala Cys Gly His
      85      90      95
Asp Phe His Met Thr Ile Ala Leu Gly Cys Leu Glu Arg Ala Leu Glu
      100      105      110
Glu Gln Pro Lys Asn Asn Leu Leu Phe Leu Phe Gln Pro Ala Glu Glu
      115      120      125
Asn Glu Ala Gly Gly Met Leu Met Tyr Glu Asp Gly Ala Phe Gly Asp
      130      135      140
Trp Leu Pro Asn Gln Phe Tyr Gly Leu His Val Arg Pro Asp Leu Lys
      145      150      155      160
Val Gly Gln Ile Ala Thr Asn Thr His Thr Leu Phe Ala Gly Thr Cys
      165      170      175
Glu Val Lys Ile Arg Phe Lys Gly Lys Gly Gly His Ala Ala Phe Pro
      180      185      190
His Glu Ala Asn Asp Ala Leu Val Ala Ala Ser Tyr Phe Val Thr Gln
      195      200      205
Val Gln Ser Val Val Ser Arg Asn Val Asn Pro Ile Glu Gly Ala Val
      210      215      220
Val Thr Phe Gly Val Phe Gln Ala Gly Thr Thr Asn Asn Val Ile Thr
      225      230      235      240
Asp Thr Ala Phe Leu His Gly Thr Ile Arg Ala Leu Thr Gln Asp Met
      245      250      255
Ser Leu Leu Val Gln Lys Arg Val Lys Thr Val Ala Glu Gly Val Ala
      260      265      270
Ala Ala Phe Asp Met Glu Val Glu Val Glu Leu Lys Gln Gly Gly Tyr
      275      280      285
Leu Pro Val Glu Asn Asn Pro Ala Leu Ala Arg Glu Leu Met Asp Phe
      290      295      300
Phe Asp Glu Lys Asp Gly Ile Glu Leu Ile Asp Ile Glu Pro Ala Met
      305      310      315      320
Thr Gly Glu Asp Phe Gly Tyr Leu Leu Ser Lys Val Asp Gly Val Met
      325      330      335
Phe Trp Leu Gly Ile Asp Ser Pro Tyr Ala Leu His His Pro Gln Met
      340      345      350
Ser Pro Lys Glu Glu Val Leu Ala Ile Gly Val Ala Ala Val Ser Ser
      355      360      365
Phe Leu Lys Lys Lys Ala Ala Glu
```

(2) INFORMATION FOR SEQ ID NO:3234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3234:

```

Leu Ala Trp Tyr Asp Asp Arg Arg Ala Gly Gly Ser Asn Asp Cys Lys
1           5           10           15
Cys Arg Thr Asn Phe Trp Ile Gly Gln Gln Val Met Lys Glu Lys Ile
          20           25           30
Ser Gln Val Ile Val Val Glu Gly Arg Asp Asp Thr Val Asn Leu Lys
          35           40           45
Arg Tyr Phe Asp Val Glu Thr Tyr Glu Thr Arg Gly Ser Ala Ile Asn
          50           55           60
Asp Gln Asp Ile Glu Arg Ile Gln Arg Leu His Gln Arg His Gly Val
65           70           75           80
Ile Val Phe Thr Asp Pro Asp Phe Asn Gly Glu Arg Ile Arg Arg Met
          85           90           95
Ile Met Thr Ala Ile Pro Thr Val Gln His Ala Phe Leu Lys Arg Asp
          100          105          110
Glu Ala Val Pro Lys Ser Lys Thr Lys Gly Arg Ser Leu Gly Ile Glu
          115          120          125
His Ala Ser Tyr Glu Asp Leu Lys Thr Ala Leu Ala Gln Val Thr Glu
          130          135          140
Gln Phe Glu His Glu Ser Gln Phe Asp Ile Ser Arg Ser Asp Leu Ile
145          150          155          160
Arg Leu Gly Phe Leu Ala Gly Ala Asp Ser Arg Lys Arg Arg Glu Tyr
          165          170          175
Leu Gly Glu Thr Leu Arg Ile Gly Tyr Ser Asn Gly Lys Gln Leu Leu
          180          185          190
Lys Arg Leu Glu Leu Phe Gly Val Thr Leu Ala Glu Val Glu Glu Ala
          195          200          205
Met Lys Ser Tyr Glu
210

```

(2) INFORMATION FOR SEQ ID NO:3235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...187
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3235:

```

Glu Lys Arg Tyr Leu Met Thr Thr Phe Thr Ile His Thr Val Glu Ser
1      5      10      15
Ala Pro Ala Glu Val Lys Glu Ile Leu Glu Thr Val Glu Lys Asp Asn
20      25      30
Asn Gly Tyr Ile Pro Asn Leu Ile Gly Leu Leu Ala Asn Ala Pro Thr
35      40      45
Val Leu Glu Ala Tyr Gln Ile Val Ser Ser Ile His Arg Arg Asn Ser
50      55      60
Leu Thr Pro Val Glu Arg Glu Val Val Gln Ile Thr Ala Ala Val Thr
65      70      75      80
Asn Gly Cys Ala Phe Cys Val Ala Gly His Thr Ala Phe Ser Ile Lys
85      90      95
Gln Ile Gln Met Asn Asp Asp Leu Ile Gln Ala Leu Arg Asn Arg Thr
100     105     110
Pro Ile Glu Thr Asp Pro Lys Leu Asp Thr Leu Ala Lys Phe Thr Leu
115     120     125
Ala Val Ile Asn Thr Lys Gly Arg Val Gly Asp Glu Ala Leu Ser Glu
130     135     140
Phe Leu Glu Ala Gly Tyr Thr Gln Gln Asn Ala Leu Asp Val Val Phe
145     150     155     160
Gly Val Ser Leu Ala Ile Leu Cys Asn Tyr Ala Asn Asn Leu Ala Asn
165     170     175
Thr Pro Ile Asn Pro Glu Leu Gln Pro Tyr Ala
180     185

```

(2) INFORMATION FOR SEQ ID NO:3236:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 369 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...369

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3236:

Ile	Trp	Arg	Tyr	Cys	Met	Ser	Lys	Glu	Leu	His	Ile	Asn	Thr	Ile	Leu
1				5				10						15	
Ala	Gln	Ala	Gly	Ile	Lys	Ser	Asp	Glu	Ala	Thr	Gly	Ala	Leu	Val	Thr
			20					25					30		
Pro	Leu	His	Phe	Ser	Thr	Thr	Tyr	Gln	His	Pro	Glu	Phe	Gly	Arg	Ser
		35					40					45			
Thr	Gly	Phe	Asp	Tyr	Thr	Arg	Thr	Lys	Asn	Pro	Thr	Arg	Ser	Lys	Ala
	50					55					60				
Glu	Glu	Val	Leu	Ala	Thr	Ile	Glu	Ser	Ala	Asp	Tyr	Ala	Leu	Ala	Thr
65					70					75					80
Ser	Ser	Gly	Met	Ser	Ala	Ile	Val	Leu	Ala	Phe	Ser	Gly	Phe	Pro	Val
			85						90					95	
Gly	Ser	Lys	Val	Leu	Ala	Val	Arg	Asp	Leu	Tyr	Gly	Gly	Ser	Phe	Arg
		100						105					110		
Trp	Phe	Asn	Gln	Val	Glu	Gln	Glu	Gly	Arg	Phe	His	Phe	Thr	Tyr	Ala
	115						120					125			
Asn	Thr	Glu	Glu	Glu	Leu	Ile	Ala	Glu	Leu	Glu	Lys	Asp	Val	Asp	Val
130					135						140				
Leu	Tyr	Ile	Glu	Thr	Pro	Thr	Asn	Pro	Leu	Met	Leu	Glu	Phe	Asp	Ile
145					150					155					160
Glu	Lys	Leu	Ala	Lys	Leu	Ala	His	Ala	Lys	Gly	Ala	Lys	Val	Val	Val
			165						170					175	
Asp	Asn	Thr	Phe	Tyr	Ser	Pro	Ile	Tyr	Gln	Arg	Pro	Ile	Glu	Asp	Gly
		180						185					190		
Ala	Asp	Ile	Val	Leu	His	Ser	Ala	Thr	Lys	Tyr	Leu	Ala	Gly	His	Asn
	195						200					205			
Asp	Val	Leu	Ala	Gly	Val	Val	Val	Thr	Asn	Ser	Leu	Glu	Leu	Tyr	Glu
	210					215					220				
Lys	Leu	Phe	Tyr	Asn	Leu	Asn	Thr	Thr	Gly	Ala	Val	Leu	Ser	Pro	Phe
225					230					235					240
Asp	Ser	Tyr	Gln	Leu	Leu	Arg	Gly	Leu	Lys	Thr	Leu	Ser	Leu	Arg	Met
			245						250					255	
Glu	Arg	Ser	Thr	Ala	Asn	Ala	Gln	Glu	Val	Val	Ala	Phe	Leu	Lys	Asp
		260						265					270		
Ser	Pro	Ala	Val	Lys	Glu	Val	Leu	Tyr	Thr	Gly	Arg	Gly	Gly	Met	Ile
	275						280					285			
Ser	Phe	Lys	Val	Ala	Asp	Glu	Thr	Arg	Ile	Pro	His	Ile	Leu	Asn	Ser
	290				295					300					
Leu	Lys	Val	Phe	Ser	Phe	Ala	Glu	Ser	Leu	Gly	Gly	Val	Glu	Ser	Leu
305					310					315					320
Ile	Thr	Tyr	Pro	Thr	Thr	Gln	Thr	His	Ala	Asp	Ile	Pro	Ala	Glu	Val
			325						330					335	
Arg	His	Ser	Tyr	Gly	Leu	Thr	Asp	Asp	Leu	Leu	Arg	Leu	Ser	Ile	Gly
		340					345						350		
Ile	Glu	Asp	Ala	Arg	Asp	Leu	Ile	Ala	Asp	Leu	Arg	Gln	Ala	Leu	Glu
		355					360						365		

Gly

(2) INFORMATION FOR SEQ ID NO:3237:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 201 amino acids

(B) TYPE: amino acid

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...201
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3237:

```

Ala Ala Asp Leu Ala Ile Gly Asp Phe Glu Gly Thr Ile Asn Lys Asp
1      5      10      15
His Tyr Leu Ala Gly Tyr Leu Leu Phe Asn Ala Pro Val Glu Val Met
      20      25      30
Asp Ala Ile Lys Glu Ala Gly Tyr His Val Leu Asp Leu Ala His Asn
      35      40      45
His Ile Leu Asp Ser Gln Ile Glu Gly Val Ile Ser Thr Ala Asp Ile
      50      55      60
Ile Glu Lys Ala Gly Ile Thr Pro Ile Gly Val Tyr Thr His Glu Pro
65      70      75      80
Arg Asp Gln Ala Pro Leu Val Ile Lys Glu Val Asn Ala Ile Lys Val
      85      90      95
Ala Leu Leu Ala Tyr Ser Tyr Gly Phe Asn Gly Ile Glu Gln Tyr Ile
      100     105     110
Phe Gln Glu Asp Tyr Asn Arg Tyr Leu Ser Asp Leu Asn Glu Asp Lys
      115     120     125
Ile Lys Ala Glu Val Glu Arg Ala Glu Lys Glu Ala Asp Ile Thr Ile
      130     135     140
Ile Met Pro Gln Met Gly Val Glu Tyr Arg Leu Glu Pro Thr Glu Glu
145     150     155     160
Gln Lys Ala Leu Tyr His Lys Met Ile Asp Trp Gly Ala Asp Ile Ile
      165     170     175
Phe Gly Gly His Pro His Val Val Glu Pro Ser Glu Thr Val Glu Lys
      180     185     190
Asp Gly Asp Lys Lys Leu Ile Ile Tyr
      195     200

```

(2) INFORMATION FOR SEQ ID NO:3238:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 276 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3238:

Ala	Ile	Xaa	Tyr	Asp	Met	Asn	Leu	Asn	Met	Ser	Ile	Xaa	Ser	Met	Val
1				5					10					15	
Leu	Val	Val	Val	Val	Ala	Val	Phe	Ala	Gly	Leu	Glu	Gly	Ile	Leu	Asp
			20					25					30		
Gln	Phe	Gln	Phe	His	Gln	Pro	Leu	Val	Ala	Cys	Thr	Leu	Ile	Gly	Leu
		35					40					45			
Val	Thr	Gly	His	Leu	Glu	Ala	Gly	Ile	Ile	Leu	Gly	Gly	Ser	Leu	Gln
	50					55					60				
Met	Ile	Ala	Leu	Gly	Trp	Ser	Asn	Ile	Gly	Ala	Ala	Ile	Ala	Pro	Asp
65					70					75				80	
Ala	Ala	Leu	Ala	Ser	Val	Ala	Ala	Ala	Ile	Ile	Met	Val	Leu	Gly	Gly
			85						90					95	
Asp	Phe	Thr	Lys	Thr	Gly	Ile	Gly	Val	Ala	Gln	Ala	Val	Ala	Ile	Pro
		100						105					110		
Leu	Ala	Val	Ala	Gly	Leu	Phe	Leu	Thr	Met	Ile	Val	Arg	Thr	Ile	Ser
	115						120					125			
Val	Gly	Leu	Val	His	Thr	Ala	Asp	Ala	Ala	Ala	Lys	Lys	Gly	Asp	Phe
	130					135					140				
Gly	Ala	Val	Glu	Arg	Ala	His	Phe	Ile	Ala	Leu	Leu	Phe	Gln	Gly	Leu
145					150					155					160
Arg	Ile	Ala	Leu	Pro	Ala	Ala	Leu	Leu	Leu	Met	Val	Pro	Thr	Glu	Thr
			165						170					175	
Val	Gln	Ser	Ile	Leu	Ser	Ala	Met	Pro	Asp	Trp	Leu	Lys	Asp	Gly	Met
		180						185					190		
Ala	Ile	Gly	Gly	Gly	Met	Val	Val	Ala	Val	Gly	Tyr	Ala	Met	Val	Ile
		195					200					205			
Asn	Met	Met	Ala	Thr	Arg	Glu	Val	Trp	Pro	Phe	Phe	Ala	Leu	Gly	Phe
	210					215					220				
Val	Leu	Ala	Ala	Val	Ser	Asp	Ile	Thr	Leu	Ile	Gly	Phe	Gly	Ala	Ile
225					230					235					240
Gly	Val	Ala	Ile	Ala	Leu	Ile	Tyr	Leu	His	Leu	Ser	Lys	Thr	Gly	Gly
			245						250					255	
Asn	Gly	Gly	Gly	Gly	Ala	Ala	Thr	Ser	Asn	Asp	Pro	Ile	Gly	Asp	Ile
		260						265					270		
Leu	Glu	Asp	Tyr												
		275													

(2) INFORMATION FOR SEQ ID NO:3239:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 260 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3239:

Asn	Gln	Tyr	Leu	Leu	Met	Glu	Lys	Val	Met	Ser	Lys	His	Pro	His	Tyr
1				5					10					15	
Glu	Leu	Leu	Asn	Leu	Ile	Gly	Tyr	Gly	Leu	Ala	Lys	Phe	Asp	Lys	Leu
			20					25					30		
Phe	Ile	Lys	Glu	Phe	Gln	Cys	Ser	Ser	Lys	Ser	Glu	Phe	Tyr	Arg	Tyr
		35				40						45			
Val	Val	Ser	Leu	Gly	Ile	Ala	Glu	Thr	Thr	Gly	Val	Val	Lys	Asn	Arg
	50					55					60				
Met	Asp	Leu	Phe	Asp	Pro	Tyr	Phe	Asp	Asn	Asn	Arg	Lys	Gly	Trp	Trp
65					70				75					80	
Gln	Lys	Ala	Glu	Val	Tyr	Arg	Phe	Arg	Lys	Asp	Leu	Ile	Asp	Met	Met
			85						90					95	
Phe	Gly	Asn	Glu	Asp	Val	His	Ser	Tyr	Ala	Glu	Ile	Val	Lys	Met	Leu
		100						105					110		
Leu	Ala	Ser	Glu	Gly	Lys	Lys	Thr	Gly	Ile	Thr	Ile	Val	Glu	Lys	Pro
		115					120					125			
Ile	Val	Arg	Thr	Lys	Phe	Lys	Arg	Leu	Gln	Glu	Thr	Gly	Met	Glu	Ala
	130					135					140				
Glu	Asn	Tyr	Phe	Ile	Leu	His	Phe	Asp	Lys	Glu	Glu	Lys	Phe	Gln	Gly
145					150				155					160	
Gly	Gln	Leu	Thr	Asp	Ala	Arg	Leu	Tyr	Gly	Asp	Gly	Tyr	Asp	Phe	Gln
			165						170					175	
Val	Asp	Val	Gln	Glu	Tyr	Ser	Tyr	Leu	Ala	Glu	Val	Lys	Gly	Ile	Arg
		180					185						190		
Lys	Ser	Lys	Gly	Arg	Val	Arg	Leu	Thr	Ala	Lys	Glu	Phe	Glu	Lys	Val
		195				200						205			
Lys	Glu	Phe	Gln	Ser	Asp	Phe	Ile	Leu	Ser	Leu	Val	Thr	Asn	Leu	Asp
	210					215					220				
Asp	Ile	Pro	Lys	Leu	Val	Leu	Ile	Asp	Asn	Pro	Leu	Lys	His	Phe	Glu
225					230				235					240	
Phe	Lys	Lys	Asn	Ile	Ile	Lys	Asn	Glu	Ile	Ile	Glu	Tyr	Arg	Ser	Val
			245					250						255	
Glu	Asp	Leu	Tyr												
		260													

(2) INFORMATION FOR SEQ ID NO:3240:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 101 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3240:

Glu	Met	Tyr	Leu	Val	Ile	Gly	Ile	Val	Leu	Ala	Phe	Ile	Val	Ser	Phe
1				5					10					15	
Trp	Lys	Asp	Asn	Arg	Ser	Leu	Trp	Asn	Pro	Val	Leu	Phe	Leu	Leu	Ser
			20					25					30		
Leu	Ile	Ser	Ser	Tyr	Phe	Tyr	Leu	Ser	Tyr	Leu	Phe	Tyr	Lys	Asn	Gly
		35					40					45			
Tyr	Glu	Asn	Val	Gln	Leu	Ala	Phe	Tyr	Val	Phe	Ala	Phe	Val	Leu	Leu
	50					55				60					
Pro	Phe	Leu	Leu	Phe	Leu	Ser	Gly	Ile	Phe	Leu	Ile	Tyr	Asn	Gly	Val
65					70					75				80	
Ile	Leu	Leu	Lys	Arg	Glu	Gly	Arg	Ser	Lys	Pro	His	Tyr	Leu	Ser	Met
				85					90					95	
Leu	Phe	Asp	Phe	Tyr											
				100											

(2) INFORMATION FOR SEQ ID NO:3241:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 290 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...290

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3241:

Gln	Met	Asp	Phe	Thr	Trp	Ala	Leu	Lys	Tyr	Ala	Thr	Glu	Phe	Leu	Gly
1				5					10					15	
Thr	Ala	Ile	Leu	Ile	Ile	Leu	Gly	Asn	Gly	Ala	Val	Ala	Asn	Val	Glu
			20					25					30		
Leu	Lys	Gly	Thr	Lys	Gly	His	Gln	Ser	Gly	Trp	Ile	Val	Ile	Ala	Val
		35				40						45			
Gly	Tyr	Gly	Met	Gly	Val	Met	Ile	Pro	Ala	Leu	Met	Phe	Gly	Asn	Val
	50					55				60					
Ser	Gly	Asn	His	Ile	Asn	Pro	Ala	Phe	Thr	Leu	Gly	Leu	Ala	Val	Ser
65					70					75				80	
Gly	Leu	Phe	Pro	Trp	Ala	Gln	Val	Val	Pro	Tyr	Ile	Ile	Ala	Gln	Val
				85					90					95	
Leu	Gly	Ala	Ile	Phe	Gly	Gln	Ala	Leu	Val	Val	Ala	Thr	Tyr	Arg	Pro
		100					105						110		
Phe	Tyr	Leu	Lys	Thr	Glu	Asn	Pro	Asn	Asn	Ile	Leu	Gly	Thr	Phe	Ser
	115						120					125			
Thr	Ile	Ser	Ser	Ile	Asp	His	Gly	Thr	Lys	Glu	Ser	Arg	Tyr	Ala	Ala
	130					135				140					
Thr	Val	Asn	Gly	Leu	Ile	Asn	Glu	Phe	Val	Gly	Ser	Phe	Val	Leu	Phe

145		150		155		160									
Phe	Ala	Ala	Leu	Gly	Leu	Thr	Lys	Asn	Phe	Phe	Gly	Ala	Glu	Val	Leu
		165		170		175									
Gln	Phe	Met	Lys	Gln	Lys	Ala	Ile	Glu	Ala	Gly	Gln	Thr	Val	Asp	Phe
		180		185		190									
Ser	Asp	Leu	Ala	Ile	Lys	Ala	Gln	Val	Ala	Pro	His	Thr	Ala	Ser	Gly
		195		200		205									
Leu	Ser	Val	Ala	His	Leu	Ala	Leu	Gly	Phe	Leu	Val	Met	Ala	Leu	Val
		210		215		220									
Thr	Ser	Leu	Gly	Gly	Pro	Thr	Gly	Pro	Ala	Leu	Asn	Pro	Ala	Arg	Asp
225				230		235									
Leu	Gly	Pro	Arg	Leu	Leu	His	Ala	Phe	Leu	Pro	Lys	Ser	Val	Leu	Gly
		245		250		255									
Glu	His	Lys	Gly	Asp	Ser	Lys	Trp	Trp	Tyr	Ser	Trp	Val	Pro	Val	Val
		260		265		270									
Ala	Pro	Ile	Ala	Ala	Ala	Ile	Ala	Ala	Val	Ala	Val	Phe	Lys	Phe	Leu
		275		280		285									
Tyr	Leu														
290															

(2) INFORMATION FOR SEQ ID NO:3242:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 84 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...84
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3242:

Lys	His	His	Leu	Leu	Gly	Gln	Val	Ile	Asn	Leu	Asp	Trp	Phe	Ala	His
1			5					10					15		
Ile	Lys	Asp	Lys	Asp	Phe	Pro	Ile	Phe	Gly	Ile	Ser	Thr	Ser	Met	Asp
		20				25					30				
Asn	Gln	Thr	Thr	Ser	Phe	Trp	Asn	Gly	His	Lys	Val	Thr	Gly	His	Ala
		35				40					45				
Glu	Val	Cys	His	Arg	Tyr	Arg	Pro	Thr	Phe	Ser	Asn	Leu	Thr	Phe	Lys
		50				55					60				
Asp	Trp	Asn	Asp	Thr	Thr	Thr	Ala	Thr	Lys	Asn	Ile	Pro	Lys	Thr	Asn
65				70				75					80		
Cys	Thr	Val	Gly												

(2) INFORMATION FOR SEQ ID NO:3243:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 169 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...169

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3243:

Phe	Lys	Asp	Phe	Leu	Lys	Gly	Val	Glu	Asp	Phe	Ser	Thr	Val	Thr	Lys
1				5					10					15	
Gly	Phe	Phe	Lys	Cys	Trp	Arg	Thr	Asn	Trp	Gln	Asp	His	Glu	Leu	Leu
			20					25					30		
Glu	Ser	Asp	Trp	Ser	Val	Arg	Val	Arg	Thr	Thr	Val	Asp	Asp	Val	His
		35					40					45			
His	Trp	Ser	Trp	Lys	Asn	Phe	Ser	Val	Glu	Ser	Thr	Lys	Val	Ala	Val
	50					55					60				
Lys	Trp	Asp	Phe	Lys	Val	Val	Ser	Ser	Ser	Thr	Ser	Tyr	Ser	Asp	Arg
65					70					75					80
His	Thr	Glu	Asp	Cys	Ile	Arg	Thr	Pro	Phe	Thr	Phe	Val	Arg	Ser	Thr
				85					90					95	
Val	Lys	Cys	Asp	His	Ser	Thr	Val	Asn	Ser	Leu	Leu	Ile	Thr	Tyr	Ile
			100					105					110		
Val	Ala	Asn	Asp	Ser	Phe	Ser	Asn	Asp	Val	Val	Tyr	Val	Val	Asn	Ser
		115					120					125			
Phe	Leu	Cys	Thr	Lys	Thr	Thr	Val	Thr	Arg	Phe	Val	Thr	Val	Ala	Lys
	130					135					140				
Phe	Asn	Cys	Phe	Val	Phe	Thr	Ser	Arg	Lys	Leu	Leu	Asp	Gly	Thr	Ile
145					150					155					160
Pro	Arg	Pro	Lys	Ala	Pro	Asp	Ser	Val							
				165											

(2) INFORMATION FOR SEQ ID NO:3244:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 263 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3244:

Ala	Asn	Asn	Leu	Glu	Arg	Ser	Gln	Val	Lys	Gln	Met	Thr	Ala	Ile	Val
1			5						10					15	
Glu	Leu	Lys	Asn	Ala	Thr	Lys	Ile	Val	Lys	Asn	Gly	Phe	Asp	Glu	Glu
			20					25					30		
Lys	Ile	Ile	Leu	Asn	Asp	Val	Ser	Leu	Glu	Ile	Phe	Glu	Arg	Asp	Phe
		35					40					45			
Ile	Thr	Ile	Leu	Gly	Gly	Asn	Gly	Ala	Gly	Lys	Ser	Thr	Leu	Phe	Asn
	50					55					60				
Thr	Ile	Ala	Gly	Thr	Leu	Ser	Leu	Thr	Ser	Gly	Thr	Ile	Arg	Ile	Leu
65					70					75					80
Gly	Glu	Glu	Leu	Thr	Lys	Phe	Ser	Pro	Glu	Lys	Arg	Ala	Lys	Tyr	Leu
				85					90					95	
Ser	Arg	Val	Phe	Gln	Asp	Pro	Lys	Met	Gly	Thr	Ala	Pro	Arg	Met	Thr
			100					105					110		
Val	Ala	Glu	Asn	Leu	Leu	Ile	Ala	Lys	Phe	Arg	Gly	Glu	Lys	Arg	Gly
		115					120					125			
Leu	Leu	Pro	Arg	Arg	Leu	Thr	Ser	Tyr	Lys	Asp	Glu	Phe	Gln	Ala	Thr
	130					135					140				
Ile	Glu	Lys	Val	Gly	Asn	Gly	Leu	Glu	Lys	His	Leu	Asn	Thr	Pro	Ile
145					150					155					160
Glu	Phe	Leu	Ser	Gly	Gly	Gln	Arg	Gln	Ala	Leu	Ser	Leu	Leu	Met	Ala
				165					170					175	
Thr	Leu	Lys	Arg	Pro	Glu	Leu	Leu	Leu	Leu	Asp	Glu	His	Thr	Ala	Ala
			180					185					190		
Leu	Asp	Pro	Lys	Thr	Ser	Val	Ala	Leu	Met	Gly	Leu	Thr	Asp	Glu	Phe
	195						200					205			
Val	Lys	Lys	Asp	Gln	Leu	Thr	Ala	Leu	Met	Ile	Thr	His	His	Met	Glu
	210					215					220				
Asp	Ala	Leu	Lys	Tyr	Gly	Asn	Arg	Leu	Ile	Val	Met	Lys	Glu	Gly	Arg
225					230					235					240
Val	Ile	Gln	Asp	Leu	Lys	Gln	Glu	Glu	Lys	Ala	Lys	Met	Lys	Ile	Ser
				245					250					255	
Asp	Tyr	Tyr	Gln	Leu	Phe	Glu									
			260												

(2) INFORMATION FOR SEQ ID NO:3245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...93

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3245:

Glu	Val	Asn	Leu	Met	Ala	Lys	Lys	Ser	Met	Val	Ala	Arg	Glu	Ala	Lys
1				5					10					15	
Arg	Gln	Lys	Ile	Val	Asp	Arg	Tyr	Ala	Glu	Lys	Arg	Ala	Ala	Leu	Lys
			20					25					30		
Ala	Ala	Gly	Asp	Tyr	Glu	Gly	Leu	Ser	Lys	Leu	Pro	Arg	Asn	Ala	Ser
		35					40					45			
Pro	Thr	Arg	Leu	His	Asn	Arg	Cys	Arg	Val	Thr	Gly	Arg	Pro	His	Ser
	50					55					60				
Val	Tyr	Arg	Lys	Phe	Gly	Leu	Ser	Arg	Ile	Ala	Phe	Arg	Glu	Leu	Ala
65					70					75					80
His	Lys	Gly	Gln	Ile	Pro	Gly	Val	Thr	Lys	Ala	Ser	Trp			
			85					90							

(2) INFORMATION FOR SEQ ID NO:3246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...113

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3246:

Phe	Phe	Phe	His	Phe	Pro	Pro	His	Pro	Pro	Pro	Phe	Pro	Phe	Leu	Pro
1				5					10					15	
Phe	Phe	Pro	Pro	Pro	Asn	Leu	Pro	Pro	Xaa	Pro	Pro	Phe	Pro	Ser	Pro
			20					25					30		
Phe	Phe	Pro	Xaa	Pro	Pro	Xaa	Thr	Pro	Phe	Phe	Ser	Phe	Phe	Ser	Pro
		35					40					45			
Pro	Xaa	Pro	Ser	Pro	Xaa	Leu	Pro	Pro	Phe	Pro	Pro	Ser	Pro	Pro	Phe
	50					55				60					
Ser	Pro	Pro	Pro	Ser	Xaa	Phe	Pro	Leu	Phe	Phe	Xaa	Phe	Pro	Phe	Xaa
65					70					75					80
Xaa	Xaa	Xaa	Phe	Phe	Phe	Phe	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Ile	Xaa	Xaa
			85					90					95		
Pro	Pro	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Ile
			100					105					110		

Gln

(2) INFORMATION FOR SEQ ID NO:3247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 434 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...434

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3247:

Val	Ser	Phe	His	Gln	Glu	Glu	Arg	Leu	Phe	Lys	Lys	Asn	Lys	Asp	Ile
1				5					10					15	
Leu	Asn	Ile	Ala	Leu	Pro	Ala	Met	Gly	Glu	Asn	Phe	Leu	Gln	Met	Leu
			20					25					30		
Met	Gly	Met	Val	Asp	Ser	Tyr	Leu	Val	Ala	His	Leu	Gly	Leu	Ile	Ala
		35				40						45			
Ile	Ser	Gly	Val	Ser	Val	Ala	Gly	Asn	Ile	Ile	Thr	Ile	Tyr	Gln	Ala
	50					55					60				
Ile	Phe	Ile	Ala	Leu	Gly	Ala	Ala	Ile	Ser	Ser	Val	Ile	Ser	Lys	Ser
65				70						75				80	
Ile	Gly	Gln	Lys	Asp	Gln	Ser	Lys	Leu	Ala	Tyr	His	Val	Thr	Glu	Ala
			85					90						95	
Leu	Lys	Ile	Thr	Leu	Leu	Leu	Ser	Phe	Leu	Leu	Gly	Phe	Leu	Ser	Ile
			100					105					110		
Phe	Ala	Gly	Lys	Glu	Met	Ile	Gly	Leu	Leu	Gly	Thr	Glu	Arg	Asp	Val
		115				120						125			
Ala	Glu	Ser	Gly	Gly	Leu	Tyr	Leu	Ser	Leu	Val	Gly	Gly	Ser	Ile	Val
	130					135					140				
Leu	Leu	Gly	Leu	Met	Thr	Ser	Leu	Gly	Ala	Leu	Ile	Arg	Ala	Thr	His
145				150						155				160	
Asn	Pro	Arg	Leu	Pro	Leu	Tyr	Val	Ser	Phe	Leu	Ser	Asn	Ala	Leu	Asn
			165					170						175	
Ile	Leu	Phe	Ser	Ser	Leu	Ala	Ile	Phe	Val	Leu	Asp	Met	Gly	Ile	Ala
		180				185						190			
Gly	Val	Ala	Trp	Gly	Thr	Ile	Val	Ser	Arg	Leu	Val	Gly	Leu	Val	Ile
	195					200						205			
Leu	Trp	Ser	Gln	Leu	Lys	Leu	Pro	Tyr	Gly	Lys	Pro	Thr	Phe	Gly	Leu
	210				215						220				
Asp	Lys	Glu	Leu	Leu	Thr	Leu	Ala	Leu	Pro	Ala	Ala	Gly	Glu	Arg	Leu
225				230					235					240	
Met	Met	Arg	Ala	Gly	Asp	Val	Val	Ile	Ile	Ala	Leu	Val	Val	Ser	Phe
			245					250						255	
Gly	Thr	Glu	Ala	Val	Ala	Gly	Asn	Ala	Ile	Gly	Glu	Val	Leu	Thr	Gln
		260				265							270		
Phe	Asn	Tyr	Met	Pro	Ala	Phe	Gly	Val	Ala	Thr	Ala	Thr	Val	Met	Leu
	275				280							285			
Leu	Ala	Arg	Ala	Val	Gly	Glu	Asp	Asp	Trp	Lys	Arg	Val	Ala	Ser	Leu
	290				295						300				
Ser	Lys	Gln	Thr	Phe	Trp	Leu	Ser	Leu	Phe	Leu	Met	Leu	Pro	Leu	Ser
305			310						315					320	
Phe	Ser	Ile	Tyr	Val	Leu	Gly	Val	Pro	Leu	Thr	His	Leu	Tyr	Thr	Thr
			325					330					335		
Asp	Ser	Leu	Ala	Val	Glu	Ala	Ser	Val	Leu	Val	Thr	Leu	Phe	Ser	Leu

			340					345				350			
Leu	Gly	Thr	Pro	Met	Thr	Thr	Gly	Thr	Val	Ile	Tyr	Thr	Ala	Val	Trp
		355					360					365			
Gln	Gly	Leu	Gly	Asn	Ala	Arg	Leu	Pro	Phe	Tyr	Ala	Thr	Ser	Ile	Gly
	370					375					380				
Met	Trp	Cys	Ile	Arg	Ile	Gly	Thr	Gly	Tyr	Leu	Met	Gly	Ile	Val	Leu
385					390					395					400
Gly	Trp	Gly	Leu	Pro	Gly	Ile	Trp	Ala	Gly	Ser	Leu	Leu	Asp	Asn	Gly
			405						410				415		
Phe	Arg	Trp	Leu	Phe	Leu	Arg	Tyr	Arg	Tyr	Gln	Arg	Tyr	Met	Ser	Leu
		420						425					430		
Lys	Gly														

(2) INFORMATION FOR SEQ ID NO:3248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...304

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3248:

Met	Glu	Asn	Leu	Val	Lys	Ser	Thr	Ser	Asp	Thr	Tyr	Ile	Leu	Glu	Glu
1			5						10					15	
Ile	Met	Ser	Phe	Ser	Asp	Leu	Lys	Leu	Phe	Ala	Leu	Ser	Ser	Asn	Lys
		20						25					30		
Glu	Leu	Ala	Glu	Arg	Val	Ala	Gln	Glu	Ile	Gly	Ile	Glu	Leu	Gly	Lys
	35					40						45			
Ser	Ser	Val	Arg	Gln	Phe	Ser	Asp	Gly	Glu	Ile	Gln	Val	Asn	Ile	Glu
	50					55					60				
Glu	Ser	Ile	Arg	Gly	Lys	His	Val	Phe	Ile	Leu	Gln	Ser	Thr	Ser	Ser
65				70					75						80
Pro	Val	Asn	Asp	Asn	Leu	Leu	Glu	Ile	Leu	Ile	Met	Val	Asp	Ala	Leu
		85						90						95	
Lys	Arg	Ala	Ser	Ala	Glu	Ser	Val	Asn	Val	Val	Met	Pro	Tyr	Tyr	Gly
	100							105					110		
Tyr	Ala	Arg	Gln	Asp	Arg	Lys	Ala	Arg	Ala	Arg	Glu	Pro	Ile	Thr	Ser
	115					120						125			
Lys	Leu	Val	Ala	Asn	Met	Leu	Glu	Val	Ala	Gly	Val	Asp	Arg	Leu	Leu
	130					135					140				
Thr	Ile	Asp	Leu	His	Ala	Ala	Gln	Ile	Gln	Gly	Phe	Phe	Asp	Ile	Pro
145				150					155						160
Val	Asp	His	Leu	Met	Gly	Ala	Pro	Leu	Ile	Ala	Asp	Tyr	Phe	Glu	Arg
		165						170						175	
Arg	Gly	Met	Val	Gly	Ser	Asp	Tyr	Val	Val	Val	Ser	Pro	Asp	His	Gly

Glu	Glu	Asn	Arg	Asn	Lys	Leu	Leu	Asn	Asp	Leu	Lys	Glu	Lys	Gln	Pro
				165					170					175	
Lys	Val	Ile	Val	Val	Asn	Asp	Lys	Val	Val	Val	Trp	Ser	Glu	Val	Glu
			180					185					190		
Thr	Leu	Leu	Lys	Glu	Asn	Tyr	Gln	Gln	Val	Lys	Thr	Asp	Tyr	Ser	Glu
		195					200					205			
Phe	Lys	Val	Tyr	Lys	Ile	Lys									
	210					215									

(2) INFORMATION FOR SEQ ID NO:3250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 643 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...643

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3250:

Asn	Arg	Phe	Gln	Thr	Arg	Thr	Lys	Cys	Tyr	Ile	Arg	Arg	Phe	Leu	Gln
1				5					10					15	
Met	Asn	Asn	Gln	Glu	Ile	Ala	Lys	Lys	Val	Ile	Asp	Ala	Leu	Gly	Gly
			20					25					30		
Arg	Glu	Asn	Val	Asn	Ser	Val	Ala	His	Cys	Ala	Thr	Arg	Leu	Arg	Val
		35				40					45				
Met	Val	Lys	Asp	Glu	Glu	Lys	Ile	Asn	Lys	Glu	Val	Ile	Glu	Asn	Leu
	50					55				60					
Glu	Lys	Val	Gln	Gly	Ala	Phe	Phe	Asn	Ser	Gly	Gln	Tyr	Gln	Ile	Ile
65				70					75					80	
Phe	Gly	Thr	Gly	Thr	Val	Asn	Lys	Met	Tyr	Asp	Glu	Val	Val	Val	Leu
			85					90					95		
Gly	Leu	Pro	Thr	Ser	Ser	Lys	Asp	Asp	Met	Lys	Ala	Glu	Val	Ala	Lys
		100					105					110			
Gln	Gly	Asn	Trp	Phe	Gln	Arg	Ala	Ile	Arg	Thr	Phe	Gly	Asp	Val	Phe
		115				120					125				
Val	Pro	Ile	Ile	Pro	Val	Ile	Val	Ala	Thr	Gly	Leu	Phe	Met	Gly	Val
	130				135					140					
Arg	Gly	Leu	Phe	Asn	Ala	Leu	Glu	Met	Pro	Leu	Pro	Gly	Asp	Phe	Ala
145				150					155					160	
Thr	Tyr	Thr	Gln	Ile	Leu	Thr	Asp	Thr	Ala	Phe	Ile	Ile	Leu	Pro	Gly
			165					170					175		
Leu	Val	Val	Trp	Ser	Thr	Phe	Arg	Val	Phe	Gly	Gly	Asn	Pro	Ala	Val
		180					185					190			
Gly	Ile	Val	Leu	Gly	Met	Met	Leu	Val	Ser	Gly	Ser	Leu	Pro	Asn	Ala
	195					200					205				
Trp	Ala	Val	Ala	Gln	Gly	Gly	Glu	Val	Thr	Ala	Met	Asn	Phe	Phe	Gly
	210					215					220				

Phe	Ile	Pro	Val	Val	Gly	Leu	Gln	Gly	Ser	Val	Leu	Pro	Ala	Phe	Ile
225					230					235					240
Ile	Gly	Val	Val	Gly	Ala	Lys	Phe	Glu	Lys	Ala	Val	Arg	Lys	Val	Val
				245					250						255
Pro	Asp	Val	Ile	Asp	Leu	Leu	Val	Thr	Pro	Phe	Val	Thr	Leu	Leu	Val
			260					265							270
Met	Ser	Ile	Leu	Gly	Leu	Phe	Val	Ile	Gly	Pro	Val	Phe	His	Val	Val
		275					280						285		
Glu	Asn	Tyr	Ile	Leu	Ile	Ala	Thr	Lys	Ala	Ile	Leu	Ser	Ile	Pro	Phe
	290					295					300				
Gly	Leu	Gly	Gly	Phe	Leu	Ile	Gly	Gly	Val	His	Gln	Leu	Ile	Val	Val
305					310					315					320
Ser	Gly	Val	His	His	Ile	Phe	Asn	Leu	Leu	Glu	Val	Gln	Leu	Leu	Ala
				325					330						335
Ala	Asp	His	Ala	Asn	Pro	Phe	Asn	Ala	Ile	Ile	Thr	Ala	Ala	Met	Thr
			340					345						350	
Ala	Gln	Gly	Ala	Ala	Thr	Val	Ala	Val	Gly	Val	Lys	Thr	Lys	Asn	Pro
		355					360						365		
Lys	Leu	Lys	Thr	Leu	Ala	Phe	Pro	Ala	Ala	Leu	Ser	Ala	Phe	Leu	Gly
	370					375					380				
Ile	Thr	Glu	Pro	Ala	Ile	Phe	Gly	Val	Asn	Leu	Arg	Phe	Arg	Lys	Pro
385					390					395					400
Phe	Phe	Leu	Ser	Leu	Ile	Ala	Gly	Ala	Ile	Gly	Gly	Gly	Leu	Ala	Ser
				405						410					415
Ile	Leu	Gly	Leu	Ala	Gly	Thr	Gly	Asn	Gly	Ile	Thr	Ile	Ile	Pro	Gly
			420					425						430	
Thr	Met	Leu	Tyr	Val	Gly	Asn	Gly	Gln	Leu	Pro	Gln	Tyr	Leu	Leu	Met
		435					440					445			
Val	Ala	Val	Ser	Phe	Ala	Leu	Gly	Phe	Ala	Leu	Thr	Tyr	Met	Phe	Gly
	450					455					460				
Tyr	Glu	Asp	Glu	Val	Asp	Ala	Thr	Ala	Ala	Ala	Lys	Gln	Ala	Glu	Val
465					470					475					480
Ala	Glu	Glu	Lys	Glu	Glu	Val	Ala	Pro	Ala	Ala	Leu	Gln	Asn	Glu	Thr
				485					490						495
Leu	Val	Thr	Pro	Ile	Val	Gly	Asp	Val	Val	Ala	Leu	Ala	Asp	Val	Asn
			500					505					510		
Asp	Pro	Val	Phe	Ser	Ser	Gly	Ala	Met	Gly	Gln	Gly	Ile	Ala	Val	Lys
		515					520						525		
Pro	Ser	Gln	Gly	Val	Val	Tyr	Ala	Pro	Ala	Asp	Ala	Glu	Val	Ser	Ile
	530					535						540			
Ala	Phe	Pro	Thr	Gly	His	Ala	Phe	Gly	Leu	Lys	Thr	Arg	Asn	Gly	Ala
545					550					555					560
Glu	Val	Leu	Ile	His	Val	Gly	Ile	Asp	Thr	Val	Ser	Met	Asn	Gly	Asp
				565					570						575
Gly	Phe	Glu	Ala	Lys	Val	Ala	Gln	Gly	Asn	Lys	Val	Lys	Ala	Gly	Asp
			580					585					590		
Val	Leu	Gly	Thr	Phe	Asp	Ser	Asn	Lys	Ile	Ala	Ala	Ala	Gly	Leu	Asp
		595					600						605		
Asp	Thr	Thr	Met	Val	Ile	Val	Thr	Asn	Thr	Ala	Asp	Tyr	Ala	Ser	Val
	610					615						620			
Ala	Pro	Val	Ala	Thr	Gly	Ser	Val	Ala	Lys	Gly	Asp	Ala	Val	Ile	Glu
625					630					635					640
Val	Lys	Ile													

(2) INFORMATION FOR SEQ ID NO:3251:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1972 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1972
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3251:

Ile	Leu	Phe	Gln	Gly	Gly	Ile	Met	Glu	Lys	Tyr	Phe	Gly	Glu	Lys	Gln
1			5					10					15		
Glu	Arg	Phe	Ser	Phe	Arg	Lys	Leu	Ser	Val	Gly	Leu	Val	Ser	Ala	Thr
		20				25						30			
Ile	Ser	Ser	Leu	Phe	Phe	Met	Ser	Val	Leu	Ala	Ser	Ser	Ser	Val	Asp
	35					40					45				
Ala	Gln	Glu	Thr	Ala	Gly	Val	His	Tyr	Lys	Tyr	Val	Ala	Asp	Ser	Glu
	50				55					60					
Leu	Ser	Ser	Glu	Glu	Lys	Lys	Gln	Leu	Val	Tyr	Asp	Ile	Pro	Thr	Tyr
65			70					75						80	
Val	Glu	Asn	Asp	Asp	Glu	Thr	Tyr	Tyr	Leu	Val	Tyr	Lys	Leu	Asn	Ser
		85						90					95		
Gln	Asn	Gln	Leu	Ala	Glu	Leu	Pro	Asn	Thr	Gly	Ser	Lys	Asn	Glu	Arg
		100						105					110		
Gln	Ala	Leu	Val	Ala	Gly	Ala	Ser	Leu	Ala	Ala	Leu	Gly	Ile	Leu	Ile
	115					120						125			
Phe	Ala	Val	Ser	Lys	Lys	Lys	Val	Lys	Asn	Lys	Thr	Val	Leu	His	Leu
	130					135					140				
Val	Leu	Val	Ala	Gly	Ile	Gly	Asn	Gly	Val	Leu	Val	Ser	Val	His	Ala
145			150					155						160	
Leu	Glu	Asn	His	Leu	Leu	Leu	Asn	Tyr	Asn	Thr	Asp	Tyr	Glu	Leu	Thr
		165						170					175		
Ser	Gly	Glu	Lys	Leu	Pro	Leu	Pro	Lys	Glu	Ile	Ser	Gly	Tyr	Thr	Tyr
		180						185					190		
Ile	Gly	Tyr	Ile	Lys	Glu	Gly	Lys	Thr	Thr	Ser	Asp	Phe	Glu	Val	Ser
	195					200						205			
Asn	Gln	Glu	Lys	Ser	Ala	Ala	Thr	Pro	Thr	Lys	Gln	Gln	Lys	Val	Asp
	210				215						220				
Tyr	Asn	Val	Thr	Pro	Asn	Phe	Val	Asp	His	Pro	Ser	Thr	Val	Gln	Ala
225			230					235						240	
Ile	Gln	Glu	Gln	Thr	Pro	Val	Ser	Ser	Thr	Lys	Pro	Thr	Glu	Val	Gln
		245						250					255		
Val	Val	Glu	Lys	Pro	Phe	Ser	Thr	Glu	Leu	Ile	Asn	Pro	Arg	Lys	Glu
		260						265				270			
Glu	Lys	Gln	Ser	Ser	Asp	Ser	Gln	Glu	Gln	Leu	Ala	Glu	His	Lys	Asn
	275					280					285				
Leu	Glu	Thr	Lys	Lys	Glu	Glu	Lys	Ile	Ser	Pro	Lys	Glu	Lys	Thr	Gly
	290					295					300				

Val	Asn	Thr	Leu	Asn	Pro	Gln	Asp	Glu	Val	Leu	Ser	Gly	Gln	Leu	Asn
305					310					315					320
Lys	Pro	Glu	Leu	Leu	Tyr	Arg	Glu	Glu	Thr	Ile	Glu	Ile	Lys	Ile	Asp
				325					330						335
Phe	Gln	Glu	Glu	Ile	Gln	Glu	Asn	Pro	Asp	Leu	Val	Glu	Gly	Ile	Val
			340					345					350		
Arg	Val	Lys	Gln	Glu	Gly	Lys	Leu	Gly	Lys	Lys	Val	Glu	Ile	Val	Arg
		355					360					365			
Ile	Phe	Ser	Val	Asn	Lys	Glu	Glu	Val	Ser	Arg	Glu	Ile	Val	Ser	Thr
	370					375					380				
Ser	Thr	Thr	Ala	Pro	Ile	Pro	Arg	Ile	Val	Glu	Lys	Gly	Thr	Lys	Lys
385					390					395					400
Thr	Gln	Val	Ile	Lys	Glu	Gln	Pro	Glu	Thr	Gly	Val	Glu	His	Lys	Asp
				405					410						415
Val	Gln	Ser	Gly	Ala	Ile	Val	Glu	Pro	Ala	Ile	Gln	Pro	Glu	Leu	Pro
			420					425					430		
Glu	Ala	Val	Val	Ser	Asp	Lys	Gly	Val	Pro	Glu	Val	Gln	Pro	Ala	Leu
		435					440					445			
Ser	Lys	Ala	Val	Ile	Thr	Asp	Lys	Gly	Glu	Thr	Glu	Val	Gln	Pro	Glu
	450					455					460				
Ser	Pro	Asp	Thr	Val	Val	Ser	Asp	Lys	Gly	Glu	Pro	Glu	Gln	Val	Ala
465					470					475					480
Pro	Leu	Pro	Glu	Tyr	Lys	Gly	Asn	Ile	Glu	Gln	Val	Lys	Pro	Glu	Thr
				485					490						495
Pro	Val	Glu	Lys	Thr	Lys	Glu	Gln	Gly	Pro	Glu	Lys	Thr	Glu	Glu	Val
			500					505					510		
Pro	Val	Lys	Pro	Thr	Glu	Glu	Thr	Pro	Val	Asn	Pro	Asn	Glu	Gly	Thr
		515					520					525			
Thr	Glu	Gly	Thr	Ser	Ile	Gln	Glu	Ala	Glu	Asn	Pro	Val	Gln	Pro	Ala
	530					535					540				
Glu	Glu	Ser	Thr	Thr	Asn	Ser	Glu	Lys	Val	Ser	Pro	Asp	Thr	Ser	Ser
545					550					555					560
Glu	Asn	Thr	Gly	Glu	Glu	Ser	Ser	Asn	Pro	Ser	Asp	Ser	Thr	Thr	Ser
				565					570						575
Val	Gly	Glu	Ser	Asn	Lys	Pro	Glu	His	Asn	Asp	Ser	Lys	Asn	Glu	Asn
			580					585					590		
Ser	Glu	Lys	Thr	Val	Glu	Glu	Val	Pro	Val	Asn	Pro	Asn	Glu	Gly	Thr
		595					600					605			
Val	Glu	Gly	Thr	Ser	Asn	Gln	Glu	Thr	Glu	Lys	Pro	Val	Gln	Pro	Ala
	610					615					620				
Glu	Glu	Thr	Gln	Thr	Asn	Ser	Gly	Lys	Ile	Ala	Asn	Glu	Asn	Thr	Gly
625					630					635					640
Glu	Val	Ser	Asn	Lys	Pro	Ser	Asp	Ser	Lys	Pro	Pro	Val	Glu	Glu	Ser
				645					650					655	
Asn	Gln	Pro	Glu	Lys	Asn	Gly	Thr	Ala	Thr	Lys	Pro	Glu	Asn	Ser	Gly
			660					665					670		
Asn	Thr	Thr	Ser	Glu	Asn	Gly	Gln	Thr	Glu	Pro	Glu	Lys	Lys	Leu	Glu
		675					680					685			
Leu	Arg	Asn	Val	Ser	Asp	Ile	Glu	Leu	Tyr	Ser	Gln	Thr	Asn	Gly	Thr
	690					695					700				
Tyr	Arg	Gln	His	Val	Ser	Leu	Asp	Gly	Ile	Pro	Glu	Asn	Thr	Asp	Thr
705					710					715					720
Tyr	Phe	Val	Lys	Val	Lys	Ser	Ser	Ala	Phe	Lys	Asp	Val	Tyr	Ile	Pro
			725						730					735	
Val	Ala	Ser	Ile	Thr	Glu	Glu	Lys	Arg	Asn	Gly	Gln	Ser	Val	Tyr	Lys
			740					745					750		
Ile	Thr	Ala	Lys	Ala	Glu	Lys	Leu	Gln	Gln	Glu	Leu	Glu	Asn	Lys	Tyr

Gly	Asn	Thr	Gly	Leu	Leu	Tyr	Thr	Pro	Asn	Gln	Phe	Leu	Tyr	Asp	Arg	1220	1225	1230
Asp	Ser	Ile	Val	Lys	Glu	Val	Leu	Pro	Glu	Leu	Gln	Lys	Leu	Asp	Tyr	1235	1240	1245
Gln	Ser	Asp	Ala	Ile	Arg	Lys	Thr	Leu	Gly	Ile	Ser	Pro	Ala	Val	Lys	1250	1255	1260
Leu	Thr	Glu	Leu	Tyr	Leu	Glu	Glu	Gln	Phe	Ser	Lys	Thr	Lys	Gln	Asn	1265	1270	1275
Leu	Gly	Gly	Ser	Leu	Lys	Lys	Leu	Leu	Ser	Ala	Asp	Ala	Gly	Leu	Ala	1285	1290	1295
Ser	Asp	Asn	Ser	Val	Thr	Arg	Gly	Tyr	Leu	Val	Asp	Lys	Ile	Lys	Asn	1300	1305	1310
Asn	Lys	Glu	Ala	Leu	Leu	Leu	Gly	Leu	Thr	Tyr	Leu	Glu	Arg	Trp	Tyr	1315	1320	1325
Asn	Phe	Asn	Tyr	Gly	Gln	Val	Asn	Val	Lys	Asp	Leu	Val	Met	Tyr	His	1330	1335	1340
Pro	Asp	Phe	Phe	Gly	Lys	Gly	Asn	Thr	Ser	Pro	Leu	Asp	Thr	Leu	Ile	1345	1350	1355
Glu	Leu	Gly	Lys	Ser	Gly	Phe	Asn	Asn	Leu	Leu	Ala	Lys	Asn	Asn	Val	1365	1370	1375
Asp	Thr	Tyr	Gly	Ile	Ser	Leu	Ala	Ser	His	His	Gly	Thr	Thr	Asp	Leu	1380	1385	1390
Phe	Ser	Ala	Leu	Glu	Thr	Tyr	Arg	Lys	Val	Phe	Leu	Pro	Asn	Thr	Ser	1395	1400	1405
Asn	Asn	Asp	Trp	Phe	Lys	Lys	Gln	Thr	Lys	Ala	Phe	Ile	Val	Glu	Glu	1410	1415	1420
Lys	Ser	Thr	Ile	Ala	Glu	Val	Lys	Ala	Lys	Gln	Lys	Gln	Ala	Gly	Thr	1425	1430	1435
Lys	Tyr	Ser	Ile	Gly	Val	Tyr	Asp	Arg	Ile	Thr	Ser	Asn	Thr	Trp	Lys	1445	1450	1455
Tyr	Arg	Asn	Met	Val	Leu	Pro	Leu	Leu	Thr	Leu	Pro	Glu	Arg	Ser	Val	1460	1465	1470
Phe	Val	Ile	Ser	Thr	Leu	Ser	Ser	Leu	Gly	Phe	Gly	Ala	Tyr	Asp	Arg	1475	1480	1485
Tyr	Arg	Asn	Ser	Glu	His	Lys	Ala	Gly	Lys	Asp	Leu	Asn	Asn	Phe	Val	1490	1495	1500
Glu	Glu	Asn	Ala	Ser	Glu	Thr	Ala	Lys	Arg	Gln	Arg	Asp	His	Tyr	Asp	1505	1510	1515
Tyr	Trp	Tyr	Arg	Ile	Leu	Asp	Asn	Glu	Gly	Arg	Glu	Lys	Leu	Tyr	Arg	1525	1530	1535
Thr	Ile	Leu	Leu	Tyr	Asp	Ala	Tyr	Lys	Phe	Gly	Asp	Asp	Thr	Thr	Ser	1540	1545	1550
Gly	Lys	Ala	Thr	Val	Glu	Ala	Lys	Phe	Asp	Ser	Ser	Asn	Pro	Ala	Met	1555	1560	1565
Lys	Asn	Phe	Phe	Gly	Pro	Val	Gly	Asn	Lys	Val	Val	His	Asn	His	His	1570	1575	1580
Gly	Ala	Tyr	Ala	Thr	Gly	Asp	Gly	Val	Tyr	Tyr	Met	Ser	Tyr	Arg	Met	1585	1590	1595
Leu	Asp	Lys	Asp	Gly	Ala	Ile	Thr	Tyr	Thr	His	Glu	Met	Thr	His	Asp	1605	1610	1615
Ser	Asp	Gln	Asp	Ile	Tyr	Leu	Gly	Gly	Tyr	Gly	Arg	Arg	Ser	Gly	Leu	1620	1625	1630
Gly	Pro	Glu	Phe	Phe	Ala	Lys	Gly	Leu	Leu	Gln	Ala	Pro	Asp	His	Pro	1635	1640	1645
Tyr	Asp	Ala	Thr	Ile	Thr	Ile	Thr	Ile	Asn	Ser	Ile	Leu	Lys	His	Ser	1650	1655	1660
Lys	Ser	Asp	Ser	Leu	Glu	Gly	Ser	Arg	Leu	Gln	Val	Leu	Asp	Pro	Thr			

1665		1670		1675		1680
Glu Arg Phe Gln Asn Ser Ala Asp Leu Gln Asn Tyr Val His Asn Met						
	1685		1690		1695	
Phe Asp Leu Ile Tyr Met Leu Glu Tyr Leu Glu Gly Gln Ser Ile Val						
	1700		1705		1710	
Lys Lys Leu Asn Val Ser Gln Lys Met Glu Ala Leu Arg Lys Ile Glu						
	1715		1720		1725	
Asn Gln Tyr Leu Thr Asp Pro Ala Asp Gly Asn Glu Val Tyr Ala Thr						
	1730		1735		1740	
Asn Val Val Lys Glu Leu Thr Glu Glu Glu Ala Arg Asn Leu Asn Ser						
1745		1750		1755		1760
Phe Asp Ser Leu Ile Asp Asn Asn Ile Leu Ser Ala Arg Glu Tyr Lys						
	1765		1770		1775	
Ala Gly Thr Tyr Glu Arg Asn Gly Tyr Phe Thr Ile Lys Leu Phe Ala						
	1780		1785		1790	
Pro Ile Phe Ser Ala Leu Ser Ser Glu Lys Gly Thr Pro Gly Asp Leu						
	1795		1800		1805	
Met Gly Arg Arg Ile Ala Tyr Glu Leu Leu Ala Ala Lys Gly Phe Lys						
	1810		1815		1820	
Asp Gly Met Val Pro Tyr Ile Ser Asn Gln Tyr Glu Gly Ile Ala Lys						
1825		1830		1835		1840
Gln Asn Gly Gln Thr Ile Asn Leu Tyr Gly Lys Lys Gln Gly Leu Val						
	1845		1850		1855	
Thr Asp Lys Leu Val Leu Glu Lys Ile Phe Ser Gly Lys Tyr Pro Ser						
	1860		1865		1870	
Trp Thr Ala Phe Lys Lys Ala Met Tyr Gln Glu Arg Ile Ala Gln Phe						
	1875		1880		1885	
Asp His Leu Thr Lys Val Ile Phe Lys Asp Pro Thr Lys Pro Trp Pro						
	1890		1895		1900	
Ser Tyr Gly Thr Lys Thr Ile Asn Asn Val Asp Glu Leu Gln Ala Leu						
1905		1910		1915		1920
Met Asp Gln Ala Val Leu Lys Asp Ala Glu Gly Pro Arg Trp Ser Asn						
	1925		1930		1935	
Tyr Asn Pro Glu Ile Asp Ser Ala Val His Lys Leu Lys Arg Ala Ile						
	1940		1945		1950	
Phe Lys Ala Tyr Leu Asp Gln Thr Asn Asp Phe Arg Ser Ser Ile Phe						
	1955		1960		1965	
Glu Asn Lys Lys						
1970						

(2) INFORMATION FOR SEQ ID NO:3252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...293

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3252:

Ser	His	Leu	His	Met	Asn	Pro	Asp	Pro	Glu	Ala	Leu	Gly	Phe	Gln	Val
1				5					10					15	
Gly	Leu	Lys	Ala	Leu	Leu	Glu	His	Gln	Val	Pro	Gln	Lys	Thr	Ile	Lys
			20					25					30		
Ala	Val	Gly	Phe	Asp	Glu	Pro	Thr	Leu	Thr	Trp	Met	Ala	Glu	Met	Asp
		35					40					45			
Leu	Val	Glu	Asp	Arg	Ala	Tyr	Gln	Gly	Ala	Leu	Val	Ile	Val	Cys	Asp
	50					55					60				
Thr	Ala	Asn	Thr	Ala	Arg	Ile	Asp	Asp	Lys	Arg	Tyr	Ser	Gln	Gly	Asp
65					70					75					80
Phe	Leu	Ile	Lys	Ile	Asp	His	His	Pro	Asn	Asp	Asp	Val	Tyr	Gly	Asp
				85					90					95	
Leu	Ser	Trp	Val	Asp	Thr	Ser	Ser	Ser	Ser	Ala	Ser	Glu	Met	Ile	Thr
			100					105					110		
Leu	Phe	Ala	Gln	Thr	Thr	Gln	Leu	Ala	Leu	Ala	Asp	Arg	Asp	Ala	Glu
			115				120					125			
Leu	Leu	Phe	Ala	Gly	Ile	Val	Gly	Asp	Thr	Gly	Arg	Phe	Leu	Tyr	Pro
	130					135					140				
Ser	Thr	Thr	Ala	Arg	Thr	Leu	Arg	Leu	Ala	Ala	Tyr	Leu	Arg	Glu	His
145					150					155					160
Asn	Phe	Asp	Phe	Ala	Ala	Leu	Thr	Arg	Lys	Met	Asp	Thr	Met	Ser	Tyr
				165					170					175	
Lys	Ile	Ala	Lys	Leu	Gln	Gly	Tyr	Ile	Tyr	Asp	His	Leu	Glu	Val	Asp
			180					185					190		
Glu	Asn	Gly	Ala	Ala	Arg	Val	Ile	Leu	Ser	Gln	Lys	Ile	Leu	Lys	Gln
	195					200					205				
Tyr	Asn	Val	Thr	Asp	Ala	Glu	Thr	Ala	Thr	Ile	Val	Gly	Ala	Pro	Gly
	210					215					220				
Arg	Ile	Asp	Arg	Val	Ser	Leu	Trp	Gly	Ile	Phe	Val	Glu	Gln	Ala	Asp
225					230					235					240
Gly	His	Tyr	Arg	Val	Arg	Leu	Arg	Ser	Lys	Val	His	Pro	Ile	Asn	Glu
				245					250					255	
Ile	Ala	Lys	Glu	His	Asp	Gly	Gly	Gly	His	Pro	Leu	Ala	Ser	Gly	Ala
		260					265						270		
Asn	Ser	Tyr	Ser	Leu	Lys	Glu	Asn	Glu	Ile	Ile	Tyr	Gln	Lys	Leu	Lys
		275					280					285			
Asn	Leu	Leu	Lys	Asn											
															290

(2) INFORMATION FOR SEQ ID NO:3253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...294

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3253:

Tyr	Phe	Ile	Gln	Arg	Lys	Lys	Lys	Thr	Glu	Arg	Trp	Glu	Met	Ile	Met
1				5					10					15	
Asn	Thr	His	Ile	Asn	Gly	Ile	Ser	Lys	Lys	Gly	Lys	Val	Leu	Ile	Tyr
			20					25					30		
Gly	Tyr	Met	Leu	Leu	Thr	Ile	Leu	Ile	Ser	Ile	Phe	Pro	Ile	Ala	Trp
		35					40					45			
Ile	Phe	Leu	Ser	Ser	Leu	Lys	Ala	Asp	Pro	Met	Lys	Asn	Pro	Gly	Ile
	50					55					60				
Ser	Leu	Pro	Thr	Asp	Phe	Thr	Leu	Glu	Gly	Tyr	Ile	Asn	Val	Phe	Thr
65					70					75					80
Lys	Leu	His	Val	Phe	Thr	Tyr	Phe	Trp	Asn	Ser	Phe	Lys	Val	Val	Ser
				85					90					95	
Ile	Ser	Val	Ile	Ile	Ser	Ile	Val	Met	Ile	Ser	Met	Ser	Ser	Tyr	Val
			100					105					110		
Ile	Ala	Arg	Met	Glu	Phe	Arg	Gly	Lys	Lys	Leu	Val	Thr	Ser	Met	Leu
		115					120					125			
Tyr	Ser	Thr	Leu	Phe	Ile	Pro	Ala	Thr	Ala	Met	Thr	Phe	Pro	Val	Tyr
	130					135					140				
Arg	Leu	Val	Asn	Glu	Leu	Gly	Ile	Tyr	Asn	Thr	Pro	Val	Ala	Leu	Ile
145					150					155					160
Leu	Val	Tyr	Ser	Cys	Ser	Gly	Ile	Ala	Met	Ser	Phe	Phe	Ile	Ile	Lys
				165					170					175	
Asn	Tyr	Phe	Glu	Ile	Ile	Pro	Lys	Glu	Leu	Glu	Glu	Ala	Ala	Glu	Ile
			180					185					190		
Asp	Gly	Ala	Thr	Tyr	Ala	Gln	Thr	Phe	Trp	Lys	Val	Met	Leu	Pro	Ile
		195				200						205			
Ala	Arg	Pro	Gly	Ile	Leu	Thr	Ala	Ala	Val	Leu	Ala	Phe	Ile	Asn	Asn
	210					215					220				
Trp	Asn	Glu	Tyr	Tyr	Trp	Ala	Ser	Met	Leu	Val	Ile	Asp	Lys	Asn	Glu
225					230					235					240
Leu	Thr	Val	Pro	Ala	Leu	Leu	Gly	Gln	Phe	Thr	Thr	Ser	Phe	Asn	Thr
				245					250					255	
Asn	Tyr	Asn	Gly	Leu	Phe	Ser	Ala	Ile	Val	Val	Ile	Val	Leu	Pro	Pro
			260					265					270		
Ile	Ile	Leu	Phe	Ala	Phe	Thr	Ser	Lys	Tyr	Phe	Ile	Glu	Ala	Leu	Gly
		275					280					285			
Gly	Gly	Ala	Val	Lys	Gly										
															290

(2) INFORMATION FOR SEQ ID NO:3254:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...244

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3254:

Leu	Lys	Asn	Leu	Arg	Ile	Ala	Leu	Ile	Ser	Lys	Asp	Trp	Ile	Trp	Lys
1				5					10					15	
Val	Arg	Lys	Arg	Asn	Lys	Glu	Met	Thr	Lys	Arg	Ile	Pro	Asn	Leu	Gln
			20					25					30		
Val	Ala	Leu	Asp	His	Ser	Asp	Leu	Gln	Gly	Ala	Ile	Lys	Ala	Ala	Val
			35				40					45			
Ser	Val	Gly	Gln	Glu	Val	Asp	Ile	Ile	Glu	Ala	Gly	Thr	Val	Cys	Leu
	50					55					60				
Leu	Gln	Val	Gly	Ser	Glu	Leu	Ala	Glu	Val	Leu	Arg	Ser	Leu	Phe	Pro
65					70					75				80	
Asp	Lys	Ile	Ile	Val	Ala	Asp	Thr	Lys	Cys	Ala	Asp	Ala	Gly	Gly	Thr
				85					90					95	
Val	Ala	Lys	Asn	Asn	Ala	Val	Arg	Gly	Ala	Asp	Trp	Met	Thr	Cys	Ile
			100					105					110		
Cys	Cys	Ala	Thr	Ile	Pro	Thr	Met	Glu	Ala	Ala	Leu	Lys	Ala	Ile	Lys
		115					120					125			
Thr	Glu	Arg	Gly	Glu	Arg	Gly	Glu	Ile	Gln	Ile	Glu	Leu	Tyr	Gly	Asp
	130					135					140				
Trp	Thr	Phe	Glu	Gln	Ala	Gln	Leu	Trp	Leu	Asp	Ala	Gly	Ile	Ser	Gln
145					150					155				160	
Ala	Ile	Tyr	His	Gln	Ser	Arg	Asp	Ala	Leu	Leu	Ala	Gly	Glu	Thr	Trp
				165				170						175	
Gly	Glu	Lys	Asp	Leu	Asn	Lys	Val	Lys	Lys	Leu	Ile	Asp	Met	Gly	Phe
			180					185					190		
Arg	Val	Ser	Val	Thr	Gly	Gly	Leu	Asp	Val	Asp	Thr	Leu	Lys	Leu	Phe
		195					200					205			
Glu	Gly	Val	Asp	Ile	Phe	Thr	Phe	Ile	Ala	Gly	Arg	Gly	Ile	Thr	Glu
	210					215					220				
Ala	Ala	Asp	Pro	Ala	Gly	Ala	Ala	Arg	Ala	Phe	Lys	Asp	Glu	Ile	Lys
225					230					235				240	
Arg	Ile	Trp	Gly												

(2) INFORMATION FOR SEQ ID NO:3255:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...61

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3255:

```
Gly Cys Ile Gln Leu Pro Phe Leu Val Leu Asn Leu Leu Lys Leu Thr
1           5           10           15
Asp Gly Gly Thr Lys Gln Arg Ser Leu Leu Leu Gly Val Gly Ala Leu
          20           25           30
Leu Asp Val Ser Val Val Val His Gln Leu Ala Lys Pro Pro Ser Leu
          35           40           45
Phe Pro Arg Lys Ile Thr Asp His Asn Arg Leu Ile Leu
          50           55           60
```

(2) INFORMATION FOR SEQ ID NO:3256:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...61

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3256:

```
Gly Cys Ile Gln Leu Pro Phe Leu Val Leu Asn Leu Leu Lys Leu Thr
1           5           10           15
Asp Ala Gly Thr Lys Gln Arg Ser Leu Pro Leu Arg Ala Gly Asp Val
          20           25           30
Leu Asp Val Ser Val Val Val His Gln Leu Ala Lys Pro Pro Ser Leu
          35           40           45
Phe Pro Gly Lys Ile Thr Asp His Asn Lys Leu Asn Leu
          50           55           60
```

(2) INFORMATION FOR SEQ ID NO:3257:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 336 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3257:

Lys	Arg	Val	Gln	Phe	Glu	Leu	Phe	Phe	Cys	Tyr	Asn	Glu	Gly	Arg	Lys
1				5					10					15	
Ile	Arg	Gln	Glu	Ile	Asp	Met	Ser	Glu	Pro	Leu	Phe	Leu	Gln	Ser	Val
			20					25					30		
Met	Gln	Glu	Lys	Ile	Trp	Gly	Gly	Ala	Lys	Leu	Arg	Asp	Glu	Phe	Gly
		35				40						45			
Tyr	Asp	Ile	Pro	Ser	Glu	Lys	Ile	Gly	Glu	Tyr	Trp	Ala	Ile	Ser	Ala
	50					55					60				
His	Pro	Asn	Gly	Val	Ser	Lys	Val	Ala	Asn	Gly	Arg	Tyr	Glu	Gly	Thr
65					70				75						80
Asp	Leu	Ala	Thr	Leu	Tyr	Ala	Glu	His	Arg	Glu	Leu	Phe	Gly	Asn	Arg
			85						90					95	
Pro	Glu	Pro	Val	Phe	Pro	Leu	Leu	Thr	Lys	Ile	Leu	Asp	Ala	Asn	Asp
			100					105					110		
Trp	Leu	Ser	Val	Gln	Val	His	Pro	Asp	Asp	Ala	Tyr	Gly	Leu	Glu	His
		115				120						125			
Glu	Gly	Glu	Leu	Gly	Lys	Thr	Glu	Cys	Trp	Tyr	Ile	Ile	Ala	Ala	Asp
	130					135					140				
Glu	Gly	Ser	Glu	Ile	Ile	Tyr	Gly	His	Asn	Ala	Lys	Ser	Lys	Glu	Glu
145					150					155					160
Leu	Arg	Gln	Gln	Ile	Glu	Asp	Lys	Asn	Trp	Asp	Ala	Leu	Leu	Thr	Lys
			165					170						175	
Val	Pro	Val	Lys	Ala	Gly	Asp	Phe	Phe	Tyr	Val	Pro	Ser	Gly	Thr	Met
			180					185					190		
His	Ala	Ile	Gly	Ala	Gly	Ile	Leu	Ile	Leu	Glu	Thr	Gln	Gln	Ser	Ser
		195				200						205			
Asp	Thr	Thr	Tyr	Arg	Val	Tyr	Asp	Phe	Asp	Arg	Lys	Asp	Asp	Lys	Gly
	210					215					220				
Asn	Leu	Arg	Glu	Leu	His	Leu	Glu	Lys	Ser	Ile	Asp	Val	Leu	Asn	Ile
225					230					235					240
Gly	Glu	Pro	Ala	Asn	Ser	Arg	Pro	Val	Thr	Ile	Lys	Ala	Asp	Asp	Leu
			245						250					255	
Arg	Ser	Thr	Leu	Val	Ser	Asn	Asp	Phe	Phe	Ala	Val	Tyr	Lys	Trp	
		260				265						270			
Glu	Ile	Thr	Gly	Lys	Val	Asn	Phe	Glu	Lys	Thr	Ala	Asp	Tyr	Ser	Leu
		275				280						285			
Leu	Ser	Val	Leu	Ala	Gly	Gln	Gly	Gln	Leu	Thr	Val	Asp	Gly	Lys	Asn
	290					295					300				
Tyr	Pro	Ile	Gln	Lys	Gly	Arg	His	Phe	Ile	Leu	Pro	Ser	Asp	Val	Glu
305					310					315					320
Ser	Trp	Thr	Leu	Glu	Gly	Gln	Asp	Leu	Glu	Leu	Ile	Val	Ser	His	Pro
			325						330					335	

(2) INFORMATION FOR SEQ ID NO:3258:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 126 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...126
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3258:

```

Leu Leu Val Gln Ser Arg Glu Arg Asn Ile Met Ala Asn His Phe Arg
1      5      10      15
Thr Asp Arg Val Gly Met Glu Ile Lys Arg Glu Val Asn Glu Ile Leu
20     25     30
Gln Lys Lys Val Arg Asp Pro Arg Val Gln Gly Val Thr Ile Thr Asp
35     40     45
Val Gln Met Leu Gly Asp Leu Ser Val Ala Lys Val Tyr Tyr Thr Ile
50     55     60
Leu Ser Asn Leu Ala Ser Asp Asn Gln Lys Ala Gln Ile Gly Leu Glu
65      70      75      80
Lys Ala Thr Gly Thr Ile Lys Arg Glu Leu Gly Arg Asn Leu Lys Leu
85      90      95
Tyr Lys Ile Pro Asp Leu Thr Phe Val Lys Asp Glu Ser Ile Glu Tyr
100     105     110
Gly Asn Lys Ile Asp Glu Met Leu Arg Asn Leu Asp Lys Asn
115     120     125

```

(2) INFORMATION FOR SEQ ID NO:3259:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 650 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...650
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3259:

```

Lys Met Ser His Ile Ile Glu Leu Pro Glu Met Leu Ala Asn Gln Ile
1      5      10      15
Ala Ala Gly Glu Val Ile Glu Arg Pro Ala Ser Val Val Lys Glu Leu
20     25     30
Val Glu Asn Ala Ile Asp Ala Gly Ser Ser Gln Ile Ile Ile Glu Ile
35     40     45

```

Glu	Glu	Ala	Gly	Leu	Lys	Lys	Val	Gln	Ile	Thr	Asp	Asn	Gly	His	Gly
50						55					60				
Ile	Ala	His	Asp	Glu	Val	Glu	Leu	Ala	Leu	Arg	Arg	His	Ala	Thr	Ser
65					70					75					80
Lys	Ile	Lys	Asn	Gln	Ala	Asp	Leu	Phe	Arg	Ile	Arg	Thr	Leu	Gly	Phe
			85						90					95	
Arg	Gly	Glu	Ala	Leu	Pro	Ser	Ile	Ala	Ser	Val	Ser	Val	Leu	Thr	Leu
			100					105					110		
Leu	Thr	Ala	Val	Asp	Gly	Ala	Ser	His	Gly	Thr	Lys	Leu	Val	Ala	Arg
		115					120					125			
Gly	Gly	Glu	Val	Glu	Glu	Val	Ile	Pro	Ala	Thr	Ser	Pro	Val	Gly	Thr
	130					135					140				
Lys	Val	Cys	Val	Glu	Asp	Leu	Phe	Phe	Asn	Thr	Pro	Ala	Arg	Leu	Lys
145					150					155					160
Tyr	Met	Lys	Ser	Gln	Gln	Ala	Glu	Leu	Ser	His	Ile	Ile	Asp	Ile	Val
				165					170					175	
Asn	Arg	Leu	Gly	Leu	Ala	His	Pro	Glu	Ile	Ser	Phe	Ser	Leu	Ile	Ser
			180					185					190		
Asp	Gly	Lys	Glu	Met	Thr	Arg	Thr	Ala	Gly	Thr	Gly	Gln	Leu	Arg	Gln
		195					200					205			
Ala	Ile	Ala	Gly	Ile	Tyr	Gly	Leu	Val	Ser	Ala	Lys	Lys	Met	Ile	Glu
	210					215					220				
Ile	Glu	Asn	Ser	Asp	Leu	Asp	Phe	Glu	Ile	Ser	Gly	Phe	Val	Ser	Leu
225					230					235					240
Pro	Glu	Leu	Thr	Arg	Ala	Asn	Arg	Asn	Tyr	Ile	Ser	Leu	Phe	Ile	Asn
				245					250					255	
Gly	Arg	Tyr	Ile	Lys	Asn	Phe	Leu	Leu	Asn	Arg	Ala	Ile	Leu	Asp	Gly
			260					265					270		
Phe	Gly	Ser	Lys	Leu	Met	Val	Gly	Arg	Phe	Pro	Leu	Ala	Val	Ile	His
		275					280					285			
Ile	His	Ile	Asp	Pro	Tyr	Leu	Ala	Asp	Val	Asn	Val	His	Pro	Thr	Lys
	290					295					300				
Gln	Glu	Val	Arg	Ile	Ser	Lys	Glu	Lys	Glu	Leu	Met	Thr	Leu	Val	Ser
305					310					315					320
Glu	Ala	Ile	Ala	Asn	Ser	Leu	Lys	Glu	Gln	Thr	Leu	Ile	Pro	Asp	Ala
				325					330					335	
Leu	Glu	Asn	Leu	Ala	Lys	Ser	Thr	Val	Arg	Asn	Arg	Glu	Lys	Val	Glu
		340						345					350		
Gln	Thr	Ile	Leu	Pro	Leu	Lys	Glu	Asn	Thr	Leu	Tyr	Tyr	Glu	Lys	Thr
		355					360					365			
Glu	Pro	Ser	Arg	Pro	Ser	Gln	Thr	Glu	Val	Ala	Asp	Tyr	Gln	Val	Glu
	370					375					380				
Leu	Thr	Asp	Glu	Gly	Gln	Asp	Leu	Thr	Leu	Phe	Ala	Lys	Glu	Thr	Leu
385					390					395					400
Asp	Arg	Leu	Thr	Lys	Pro	Ala	Lys	Leu	His	Phe	Ala	Glu	Arg	Lys	Pro
				405					410					415	
Ala	Asn	Tyr	Asp	Gln	Leu	Asp	His	Pro	Glu	Leu	Asp	Leu	Ala	Ser	Ile
			420					425					430		
Asp	Lys	Ala	Tyr	Asp	Lys	Leu	Glu	Arg	Glu	Glu	Ala	Ser	Ser	Phe	Pro
		435					440					445			
Glu	Leu	Glu	Phe	Phe	Gly	Gln	Met	His	Gly	Thr	Tyr	Leu	Phe	Ala	Gln
	450					455					460				
Gly	Arg	Asp	Gly	Leu	Tyr	Ile	Ile	Asp	Gln	His	Ala	Ala	Gln	Glu	Arg
465					470					475					480
Val	Lys	Tyr	Glu	Glu	Tyr	Arg	Glu	Ser	Ile	Gly	Asn	Val	Asp	Gln	Ser
				485					490					495	
Gln	Gln	Gln	Leu	Leu	Val	Pro	Tyr	Ile	Phe	Glu	Phe	Pro	Ala	Asp	Asp

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 321 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...321
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3261:

Asn	Ser	Pro	His	Asp	Ile	Ile	Pro	Lys	Phe	Ala	Asn	Phe	Val	Ser	Phe	1	5	10	15
Tyr	Lys	Phe	Tyr	Cys	Phe	Cys	Gly	Thr	Ile	Glu	Thr	Met	Ala	Ser	Ile	20	25	30	
Thr	Leu	Thr	Pro	Ser	Glu	Lys	Asp	Ile	Gln	Ala	Phe	Leu	Glu	His	Tyr	35	40	45	
Gln	Thr	Ser	Leu	Ala	Pro	Ser	Lys	Asn	Pro	Tyr	Ile	Arg	Tyr	Phe	Leu	50	55	60	
Lys	Leu	Pro	Gln	Ala	Thr	Val	Ser	Ile	Tyr	Thr	Ser	Gly	Lys	Ile	Leu	65	70	75	80
Leu	Gln	Gly	Glu	Gly	Ala	Glu	Lys	Tyr	Ala	Ser	Phe	Phe	Gly	Tyr	Gln	85	90	95	
Ala	Val	Glu	Gln	Thr	Ser	Gly	Gln	Asn	Leu	Pro	Leu	Ile	Gly	Thr	Asp	100	105	110	
Glu	Val	Gly	Asn	Gly	Ser	Tyr	Phe	Gly	Gly	Leu	Ala	Val	Val	Ala	Ala	115	120	125	
Phe	Val	Thr	Pro	Asp	Gln	His	Asp	Phe	Leu	Arg	Lys	Leu	Gly	Val	Gly	130	135	140	
Asp	Ser	Lys	Thr	Leu	Thr	Asp	Gln	Lys	Ile	Arg	Gln	Ile	Ala	Pro	Ile	145	150	155	160
Leu	Lys	Glu	Lys	Ile	Gln	His	Gln	Ala	Leu	Leu	Leu	Ser	Pro	Ser	Lys	165	170	175	
Tyr	Asn	Glu	Val	Ile	Gly	Asp	Arg	Tyr	Asn	Ala	Val	Ser	Val	Lys	Val	180	185	190	
Ala	Leu	His	Asn	Gln	Ala	Ile	Tyr	Leu	Leu	Leu	Gln	Lys	Gly	Val	Gln	195	200	205	
Pro	Glu	Lys	Ile	Val	Ile	Asp	Ala	Phe	Thr	Ser	Ala	Lys	Asn	Tyr	Asp	210	215	220	
Lys	Tyr	Leu	Ala	Gln	Glu	Ala	Asn	Arg	Phe	Ser	Asn	Pro	Ile	Ser	Leu	225	230	235	240
Glu	Glu	Lys	Ala	Glu	Gly	Lys	Tyr	Leu	Ser	Val	Ala	Val	Ser	Ser	Val	245	250	255	
Ile	Ala	Arg	Asp	Leu	Phe	Leu	Glu	Asn	Leu	Glu	Asn	Leu	Gly	Arg	Glu	260	265	270	
Leu	Gly	Tyr	Gln	Leu	Pro	Ser	Gly	Ala	Gly	Thr	Ala	Ser	Asp	Lys	Val	275	280	285	
Ala	Ser	Gln	Ile	Leu	Gln	Ala	Tyr	Gly	Met	Gln	Gly	Leu	Asn	Phe	Cys	290	295	300	
Ala	Lys	Leu	His	Phe	Lys	Asn	Thr	Glu	Lys	Ala	Lys	Lys	Arg	Leu	Glu				

305
Arg

310

315

320

(2) INFORMATION FOR SEQ ID NO:3262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...234

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3262:

Lys	Gly	Thr	His	Met	Ser	Ile	Ile	Glu	Met	Arg	Asp	Val	Val	Lys	Lys
1				5				10						15	
Tyr	Asp	Asn	Gly	Thr	Thr	Ala	Leu	Arg	Gly	Val	Ser	Val	Ser	Val	Gln
			20					25						30	
Pro	Gly	Glu	Phe	Ala	Tyr	Ile	Val	Gly	Pro	Ser	Gly	Ala	Gly	Lys	Ser
			35					40						45	
Thr	Phe	Ile	Arg	Ser	Leu	Tyr	Arg	Glu	Val	Lys	Ile	Asp	Lys	Gly	Ser
			50					55						60	
Leu	Ser	Val	Ala	Gly	Phe	Asn	Leu	Val	Lys	Ile	Lys	Lys	Lys	Asp	Ile
65						70					75				80
Pro	Leu	Leu	Arg	Arg	Ser	Val	Gly	Val	Val	Phe	Gln	Asp	Tyr	Lys	Leu
						85					90				95
Leu	Pro	Lys	Lys	Thr	Val	Tyr	Glu	Asn	Ile	Ala	Tyr	Ala	Met	Glu	Val
								105						110	
Ile	Gly	Glu	Asn	Arg	Arg	Asn	Ile	Lys	Arg	Arg	Val	Met	Glu	Val	Leu
			115					120						125	
Asp	Leu	Val	Gly	Leu	Lys	His	Lys	Val	Arg	Ser	Phe	Pro	Asn	Glu	Leu
			130					135						140	
Ser	Gly	Gly	Glu	Gln	Gln	Arg	Ile	Ala	Ile	Ala	Arg	Ala	Ile	Val	Asn
145						150					155				160
Asn	Pro	Lys	Val	Leu	Ile	Ala	Asp	Glu	Pro	Thr	Gly	Asn	Leu	Asp	Pro
						165					170				175
Asp	Asn	Ser	Trp	Glu	Ile	Met	Asn	Leu	Leu	Glu	Arg	Ile	Asn	Leu	Gln
						180					185				190
Gly	Thr	Thr	Ile	Leu	Met	Ala	Thr	His	Asn	Ser	Gln	Ile	Val	Asn	Thr
								200						205	
Leu	Arg	His	Arg	Val	Ile	Ala	Ile	Glu	Asn	Gly	Arg	Val	Val	Arg	Asp
						215								220	
Glu	Ser	Lys	Gly	Glu	Tyr	Gly	Tyr	Asp	Asp						
225						230									

(2) INFORMATION FOR SEQ ID NO:3263:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3263:

Asn	Leu	Ala	His	Val	Gly	Tyr	Tyr	Ser	Lys	Leu	Ser	Phe	Phe	Phe	Phe
1				5					10					15	
Leu	Ile	Asn	Val	Trp	Tyr	Ala	Trp	Phe	Leu	Ala	Phe	Trp	Leu	Arg	Ala
			20					25					30		
Trp	Phe	Gly	Ile	Arg	Arg	Trp	Ser	Cys	Trp	Phe	Leu	Met	Leu	Trp	Ile
		35					40					45			
Phe	Arg	Leu	Arg	Ser	Phe	Trp	Phe	Ser	Gly	Gly	Ser				
		50				55					60				

(2) INFORMATION FOR SEQ ID NO:3264:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 574 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...574

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3264:

Asn	Pro	Ala	His	Thr	Asp	Leu	Leu	Arg	Cys	Phe	Tyr	Ser	Phe	Glu	Ala
1				5					10					15	
Lys	Ala	Arg	Gln	Ser	Leu	Ser	Leu	Tyr	Leu	His	Ala	Thr	Asp	Glu	Leu
			20					25					30		
Thr	Val	Glu	Gln	Val	Asp	Lys	Arg	Thr	Leu	Ala	Leu	Arg	Gln	Glu	Gly
		35					40					45			
Lys	Thr	Glu	Thr	Asn	Lys	Asn	Ser	Leu	Thr	Met	Phe	Thr	Ala	Leu	Gln
		50				55					60				
Met	Asn	Thr	Asp	Ile	Leu	Ala	Ile	Ser	Gln	Glu	Ala	Gly	Asp	Trp	Arg
65				70					75					80	

Ile	Asp	Leu	Val	Ser	Ser	Gln	Thr	Glu	Met	Gln	Leu	Ala	Thr	Ser	Phe
				85					90					95	
Ile	Ser	Pro	Ser	Gln	Ala	Leu	Ile	Asn	Leu	Pro	Gln	Glu	Asp	Phe	Asp
			100					105					110		
Ser	Cys	Lys	Ala	Ser	Ala	Gln	Ala	Asp	Trp	Glu	Asn	Leu	Leu	His	Arg
		115					120					125			
Phe	Asp	Val	Ile	Glu	Thr	Gly	Glu	Ala	Asn	Arg	Thr	Phe	Phe	Asp	His
	130					135					140				
Cys	Leu	Tyr	Arg	Leu	Phe	Leu	Phe	Pro	Gln	Thr	Phe	Tyr	Glu	Val	Asp
145					150					155					160
Glu	Ser	Gly	Gln	Ala	Ile	His	Met	Asp	Leu	Ala	Thr	Gly	Thr	Val	Lys
				165					170					175	
Pro	Gly	Val	Leu	Phe	Ser	Asn	Asn	Gly	Phe	Trp	Asp	Thr	Phe	Arg	Thr
			180					185					190		
Thr	Phe	Pro	Leu	Phe	Ala	Leu	Ile	Ile	Pro	Glu	His	Tyr	Gln	Arg	Phe
		195					200					205			
Leu	Glu	Gly	Phe	Leu	Asn	Ser	Tyr	Arg	Asp	Thr	Gly	Phe	Leu	Pro	Lys
	210					215					220				
Trp	Leu	Ala	Pro	Asp	Glu	Arg	Gly	Met	Met	Pro	Gly	Thr	Leu	Leu	Asp
225					230					235					240
Gly	Ile	Ile	Ala	Asp	Ser	Ala	Cys	Lys	Asp	Met	Ala	Pro	Asp	Leu	Glu
				245					250					255	
Gly	Glu	Leu	Phe	Gln	Ala	Met	Leu	Glu	Thr	Ala	Ser	Lys	Ala	Asp	Pro
		260						265					270		
Leu	Gly	Ile	Asn	Gly	Arg	His	Gly	Leu	Ala	Gln	Tyr	Gln	Glu	Leu	Gly
	275						280					285			
Tyr	Leu	Ser	Thr	Asp	His	His	Glu	Ser	Val	Ser	His	Thr	Leu	Asp	Tyr
	290					295					300				
Ala	Tyr	Ser	Asp	Phe	Cys	Ile	Ala	Ser	Cys	Ala	Lys	Lys	Leu	Glu	Asn
305					310					315					320
Ile	Glu	Ile	Ala	Glu	Thr	Tyr	Lys	Ala	Ala	Ser	Gln	Asn	Tyr	Arg	Gln
				325					330					335	
Leu	Phe	Asp	Ala	Glu	Thr	Gly	Tyr	Met	Arg	Ala	Arg	Asp	Asn	Gln	Gly
			340					345					350		
Asn	Phe	His	Pro	Asp	Phe	Ser	Pro	Tyr	Ser	Trp	Gly	Arg	Asp	Tyr	Ala
	355						360					365			
Glu	Cys	Ser	Ala	Ile	Gln	Ala	Thr	Leu	Gly	Val	Leu	His	Asp	Ile	Pro
	370					375					380				
Gly	Leu	Ile	Gln	Leu	Met	Gly	Gly	Lys	Glu	Thr	Phe	Ser	Asn	Tyr	Leu
385					390					395					400
Leu	Lys	Ala	Cys	Gln	Asp	Ala	Pro	Leu	Phe	Glu	Thr	Thr	Gly	Tyr	Gly
				405					410					415	
Tyr	Glu	Ile	His	Glu	Met	Ser	Glu	Met	Ala	Thr	Ala	Pro	Phe	Gly	Gln
			420					425					430		
Ile	Ala	Ile	Ser	Asn	Gln	Pro	Ser	Phe	His	Ile	Pro	Tyr	Leu	Phe	Arg
	435						440					445			
Tyr	Ser	Asp	Tyr	Pro	Asp	Tyr	Thr	Ala	Leu	Leu	Ile	Lys	Thr	Leu	Arg
	450					455					460				
Gln	Lys	Ala	Phe	His	Pro	Ser	Trp	Glu	Ala	Tyr	Pro	Gly	Asp	Glu	Asp
465					470					475					480
Asn	Gly	Ser	Leu	Ser	Ala	Trp	Tyr	Ile	Trp	Ser	Ala	Leu	Gly	Phe	Tyr
				485					490					495	
Pro	Thr	Cys	Pro	Gly	Lys	Pro	Ser	Tyr	Asp	Leu	Gly	Ile	Pro	Leu	Phe
			500					505				510			
Asp	His	Leu	Arg	Val	Tyr	Leu	Ala	Lys	Glu	Asp	Lys	Trp	Leu	Asp	Ile
	515						520					525			
His	Thr	Lys	Gln	Asn	His	Asn	His	Phe	Asn	Phe	Val	Lys	Glu	Cys	Arg

530		535		540											
Leu	Asp	Lys	Thr	Leu	Val	Ser	Thr	Ile	Gln	His	Gln	Asp	Leu	Leu	Lys
545		550		555		560									
Ala	Glu	Gln	Leu	Thr	Phe	Thr	Leu	Ser	Trp	Leu	Pro	Ser	His		
		565		570											

(2) INFORMATION FOR SEQ ID NO:3265:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 72 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...72

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3265:

Ile	Gly	Ala	His	Phe	Leu	Thr	Lys	Gln	Ala	Gly	Gly	Ser	Gly	Val	Leu
1				5				10						15	
Pro	Gly	Gly	Val	Pro	Gly	Val	Pro	Lys	Gly	Lys	Val	Thr	Ile	Ile	Gly
			20					25					30		
Asp	Gly	Val	Val	Gly	Thr	His	Ala	Ala	Arg	Ile	Ala	Leu	Gly	Leu	Gly
			35				40					45			
Ala	Gln	Val	Thr	Ile	Leu	Asp	Ile	Ser	Ala	Lys	Arg	Leu	Ser	Val	Leu
		50				55					60				
Lys	Glu	Val	Phe	Gly	Ser	Gln	Ile								
65						70									

(2) INFORMATION FOR SEQ ID NO:3266:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 63 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...63

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3266:

Cys	Leu	Ala	Gln	Ile	Ser	Ile	Leu	His	Phe	Asp	Phe	Leu	Ser	Ile	Asp
1				5					10					15	
Lys	His	Ser	His	Thr	Val	Phe	Asn	Thr	Leu	Arg	Lys	Ser	Leu	Gln	Thr
			20					25					30		
Thr	Leu	Ala	Leu	Ser	Ala	Thr	Ser	Lys	Gln	Cys	Phe	Glu	Gln	Leu	Ala
		35					40					45			
Ala	Ser	Phe	Leu	Val	Cys	Ser	Leu	Ile	Phe	Ile	Glu	Tyr	Lys	Val	
	50					55					60				

(2) INFORMATION FOR SEQ ID NO:3267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...140

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3267:

Pro	Met	Ala	Gln	Leu	Thr	Val	Gln	Ile	Val	Thr	Pro	Asp	Gly	Leu	Val
1				5					10					15	
Tyr	Asp	His	His	Ala	Ser	Tyr	Val	Ser	Val	Arg	Thr	Leu	Asp	Gly	Glu
			20					25					30		
Met	Gly	Ile	Leu	Pro	Arg	His	Glu	Asn	Met	Ile	Ala	Val	Leu	Ala	Val
		35					40					45			
Asp	Glu	Val	Lys	Val	Lys	Arg	Ile	Asp	Asp	Lys	Asp	His	Val	Asn	Trp
	50					55					60				
Ile	Ala	Val	Asn	Gly	Gly	Val	Ile	Glu	Ile	Ala	Asn	Asp	Met	Ile	Thr
65				70						75				80	
Ile	Val	Ala	Asp	Ser	Ala	Glu	Arg	Ala	Arg	Asp	Ile	Asp	Ile	Ser	Arg
			85					90					95		
Ala	Glu	Arg	Ala	Lys	Leu	Arg	Ala	Glu	Arg	Ala	Ile	Glu	Glu	Ala	Gln
			100					105					110		
Asp	Lys	His	Leu	Ile	Asp	Gln	Glu	Arg	Arg	Ala	Lys	Ile	Ala	Leu	Gln
		115					120					125			
Arg	Ala	Ile	Asn	Arg	Ile	Asn	Val	Gly	Asn	Arg	Leu				
	130					135					140				

(2) INFORMATION FOR SEQ ID NO:3268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...224

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3268:

Gln	Ile	Tyr	His	Leu	Gly	Gln	Pro	Ile	Phe	Arg	Ser	Phe	Gly	Gln	Phe
1				5					10					15	
Phe	Asn	Gly	Val	Leu	Phe	Thr	Leu	Ala	Leu	Ala	Ile	Gly	Ser	Phe	Ile
			20					25					30		
Leu	Ala	Met	Val	Leu	Gly	Ile	Phe	Phe	Gly	Ala	Arg	Ser	Thr	Ser	Lys
		35					40					45			
Arg	Pro	Ile	Leu	Arg	Ile	Leu	Ala	Arg	Ile	Phe	Val	Glu	Phe	Tyr	Gln
	50					55					60				
Asn	Thr	Pro	Leu	Leu	Val	Gln	Phe	Val	Ile	Val	Phe	Tyr	Gly	Leu	Pro
65				70						75				80	
Leu	Ile	Ser	Asp	His	Ile	Ile	Met	Ile	Pro	Ile	Tyr	Trp	Thr	Ala	Val
				85					90					95	
Leu	Cys	Val	Gly	Leu	Tyr	His	Gly	Ala	Tyr	Ile	Ala	Glu	Val	Ile	Arg
			100					105					110		
Ser	Gly	Ile	Gln	Ser	Ile	Pro	Ser	Gly	Gln	Met	Glu	Ala	Ala	Leu	Ser
		115					120					125			
Gln	Gly	Phe	Thr	Tyr	Ile	Ser	Ala	Met	Arg	Leu	Ile	Ile	Leu	Pro	Gln
	130					135					140				
Ala	Phe	Arg	Ile	Ile	Leu	Pro	Pro	Leu	Thr	Asn	Gln	Ile	Val	Asn	Leu
145					150					155				160	
Ile	Lys	Asn	Thr	Ser	Thr	Val	Ala	Ile	Ile	Ser	Gly	Val	Asp	Leu	Met
			165					170					175		
Phe	Val	Thr	Lys	Ser	Trp	Ser	Ala	Leu	Asn	Gly	Asn	Tyr	Ile	Pro	Ala
		180					185						190		
Phe	Leu	Gly	Ala	Ala	Leu	Leu	Tyr	Phe	Ala	Leu	Cys	Phe	Pro	Val	Ala
	195					200					205				
Gln	Phe	Gly	Arg	Lys	Met	Glu	Gln	Ala	Asn	Lys	Lys	Ala	Tyr	Ser	Leu
	210					215				220					

(2) INFORMATION FOR SEQ ID NO:3269:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 61 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...61

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3269:

Lys	Ala	Tyr	Gln	Gly	Arg	Lys	Ile	Gly	Ser	Gln	Leu	Leu	Ala	Thr	Leu
1				5				10						15	
Glu	Ser	Glu	Leu	Ala	Lys	Lys	Val	Gly	Tyr	Leu	Gln	Val	Lys	Thr	Val
			20					25					30		
Ala	Glu	Gly	Ser	Asn	Lys	Asp	Tyr	Asp	Arg	Thr	Asn	Asp	Phe	Tyr	Arg
		35					40					45			
Gly	Leu	Gly	Phe	Lys	Lys	Leu	Glu	Ile	Cys	Leu	Gln	Leu			
	50					55					60				

(2) INFORMATION FOR SEQ ID NO:3270:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 217 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...217

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3270:

Lys	Glu	Asp	Leu	Met	Lys	Ile	Ala	Leu	Ile	Asn	Glu	Asn	Ser	Gln	Ala
1				5				10						15	
Ser	Lys	Asn	His	Ile	Ile	Tyr	Asp	Ser	Leu	Lys	Glu	Ala	Thr	Asp	Lys
			20					25					30		
Lys	Gly	Tyr	Gln	Leu	Phe	Asn	Tyr	Gly	Met	Arg	Gly	Glu	Gly	Gly	Glu
		35					40					45			
Ser	Gln	Leu	Thr	Tyr	Val	Gln	Asn	Gly	Leu	Met	Ala	Ala	Ile	Leu	Leu
	50					55				60					
Asn	Thr	Lys	Ala	Val	Asp	Phe	Val	Val	Thr	Gly	Cys	Gly	Thr	Gly	Val
65					70				75					80	
Gly	Ala	Met	Leu	Ala	Leu	Asn	Ser	Phe	Pro	Gly	Val	Val	Cys	Gly	Leu
			85					90					95		
Ala	Val	Asp	Pro	Thr	Asp	Ala	Tyr	Leu	Tyr	Ser	Gln	Ile	Asn	Gly	Gly
		100						105					110		
Asn	Ala	Leu	Ser	Ile	Pro	Tyr	Ala	Lys	Gly	Phe	Gly	Trp	Gly	Ala	Glu
	115						120					125			
Leu	Thr	Leu	Lys	Leu	Met	Phe	Glu	Arg	Leu	Phe	Ala	Glu	Glu	Met	Gly
	130					135					140				
Gly	Gly	Tyr	Pro	Arg	Glu	Arg	Val	Ile	Pro	Glu	Gln	Arg	Asn	Ala	Arg
145					150				155					160	
Ile	Leu	Asn	Glu	Val	Lys	Gln	Ile	Thr	His	Asn	Asp	Leu	Met	Thr	Ile
			165					170					175		
Leu	Lys	Ile	Ile	Asp	Gln	Asp	Phe	Leu	Lys	Asp	Thr	Ile	Ser	Gly	Lys
		180						185					190		

Tyr	Phe	Gln	Glu	Tyr	Phe	Phe	Glu	Asn	Cys	Gln	Asp	Asp	Glu	Val	Ala
		195					200					205			
Ala	Tyr	Leu	Lys	Glu	Val	Leu	Ala	Lys							
	210					215									

(2) INFORMATION FOR SEQ ID NO:3271:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 88 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...88
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3271:

Tyr	Asn	Tyr	Gln	Lys	Thr	Lys	Gly	Val	His	Leu	Met	Val	Glu	Leu	Asn
1				5					10					15	
Leu	Lys	Asn	Ile	Tyr	Lys	Lys	Tyr	Pro	Asn	Ser	Glu	His	Tyr	Ser	Val
		20					25					30			
Glu	Asp	Phe	Asn	Leu	Asn	Ile	Lys	Asp	Lys	Glu	Phe	Ile	Val	Phe	Val
	35					40					45				
Gly	Pro	Ser	Gly	Cys	Gly	Lys	Ser	Thr	Thr	Leu	Arg	Met	Ile	Ala	Gly
	50				55					60					
Leu	Glu	Asp	Ile	Thr	Glu	Gly	Thr	Ala	Ser	Ile	Asp	Gly	Val	Val	Val
65				70					75					80	
Asn	Asp	Val	Ala	Pro	Lys	Asp	Gln								
			85												

(2) INFORMATION FOR SEQ ID NO:3272:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...113
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3272:

Asn	Asn	Tyr	Gln	Lys	Thr	Arg	Lys	Lys	Ile	Met	Ser	Leu	Thr	Ser	Lys
1				5					10					15	
Gln	Arg	Ala	Phe	Leu	Asn	Ser	Gln	Ala	His	Thr	Leu	Lys	Pro	Ile	Ile
			20					25					30		
Gln	Ile	Gly	Lys	Asn	Gly	Leu	Asn	Asp	Gln	Ile	Lys	Thr	Ser	Val	Arg
		35					40					45			
Gln	Ala	Leu	Asp	Ala	Arg	Glu	Leu	Ile	Lys	Val	Thr	Leu	Leu	Gln	Asn
	50					55					60				
Thr	Asp	Glu	Asn	Ile	His	Glu	Val	Ala	Glu	Ile	Leu	Glu	Glu	Glu	Ile
65					70					75					80
Gly	Val	Asp	Thr	Val	Gln	Lys	Ile	Gly	Arg	Ile	Leu	Ile	Leu	Phe	Lys
				85					90					95	
Gln	Ser	Ser	Lys	Lys	Glu	Asn	Arg	Lys	Ile	Ser	Lys	Lys	Val	Lys	Glu
			100					105					110		
Ile															

(2) INFORMATION FOR SEQ ID NO:3273:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 473 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...473

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3273:

Ser	Leu	Tyr	His	Lys	Arg	Gly	Asp	Trp	Asp	Arg	Met	Glu	Val	Lys	Ala
1				5					10					15	
Val	Phe	Phe	Asp	Ile	Asp	Gly	Thr	Leu	Val	Asn	Asn	Arg	Lys	Ser	Val
			20					25					30		
Leu	Lys	Ser	Thr	Lys	Asp	Ala	Ile	Lys	Ile	Val	Lys	Glu	Gln	Gly	Val
		35					40					45			
Leu	Val	Gly	Val	Ala	Thr	Gly	Arg	Gly	Pro	Phe	Phe	Val	Lys	Glu	Leu
	50					55				60					
Met	Asp	Asp	Leu	Asp	Leu	Asp	Phe	Ala	Val	Thr	Tyr	Asn	Gly	Gln	Tyr
65					70					75					80
Ile	Phe	Ser	Lys	Asp	Arg	Val	Leu	Phe	Thr	Ser	Pro	Ile	Ser	Lys	Leu
				85					90					95	
His	Leu	Arg	His	Leu	Ile	Ser	Tyr	Ala	Lys	Lys	Glu	Gly	Thr	Glu	Ile
			100					105					110		
Ala	Leu	Gly	Thr	Lys	Asp	Ala	Met	Leu	Gly	Ser	Lys	Ile	Met	Ser	Phe
		115					120					125			
Gly	Leu	Gly	Ser	Phe	Ser	Gln	Arg	Ile	Ser	Arg	Phe	Val	Pro	Ser	Val
	130					135				140					
Leu	Thr	Arg	Thr	Val	Ser	Gln	Ser	Phe	Asn	Arg	Met	Val	Ser	Lys	Val

145		150		155		160									
Val	Pro	Gln	Lys	Glu	Asp	Leu	Leu	His	Leu	Met	Asn	Gln	Pro	Ile	
		165						170					175		
Tyr	Gln	Val	Leu	Met	Leu	Met	Thr	Pro	Glu	Glu	Ser	Glu	Lys	Ala	Ala
		180						185					190		
Ala	Asp	Phe	Glu	Asp	Leu	Lys	Leu	Thr	Arg	Ser	Asn	Pro	Phe	Ala	Ser
		195					200					205			
Asp	Val	Ile	Asn	Gln	Gly	Asn	Ser	Lys	Leu	Glu	Gly	Ile	Arg	Arg	Val
		210				215					220				
Gly	Lys	Glu	Tyr	Gly	Phe	Asp	Leu	Asn	Gln	Val	Met	Ala	Phe	Gly	Asp
225					230					235				240	
Ser	Asp	Asn	Asp	Leu	Glu	Met	Leu	Ala	Gly	Val	Gly	Met	Ser	Val	Ala
		245						250					255		
Met	Gly	Asn	Gly	Ser	Ser	Ser	Val	Lys	Glu	Ala	Ala	Lys	His	Ile	Thr
		260					265						270		
Thr	Ser	Asn	Gln	Gln	Asp	Gly	Ile	His	Lys	Ala	Leu	Glu	His	Phe	Gly
		275				280						285			
Val	Leu	Ser	Ser	Glu	Lys	Val	Phe	Val	Ser	Arg	Asp	Tyr	His	Phe	Asn
	290				295						300				
Lys	Val	Lys	Thr	Phe	His	His	Met	Met	Asp	Glu	Arg	Thr	Gln	Glu	Glu
305				310					315					320	
Pro	Arg	Ala	Trp	Asp	Leu	Glu	Gly	Ala	Thr	His	Arg	Ala	Gly	Phe	Lys
		325					330						335		
Ile	Glu	Glu	Leu	Val	Glu	Phe	Val	Arg	Ala	Ala	Ser	Pro	Ser	Glu	Glu
		340					345					350			
Asp	Phe	Gly	Gln	Gly	Val	Trp	Gln	Phe	His	Gln	Ala	Leu	Asp	Lys	Ala
	355				360						365				
Ala	Asp	Lys	Val	Ala	Lys	Lys	Thr	Pro	Ala	Gln	Gln	Asp	Leu	Ile	Gly
	370				375				380						
Gln	Val	Asp	Ala	Leu	Ile	Asp	Thr	Leu	Tyr	Phe	Thr	Tyr	Gly	Ser	Phe
385				390					395					400	
Val	Leu	Met	Gly	Val	Asp	Pro	Glu	Arg	Ile	Phe	Asp	Ile	Val	His	Gln
		405					410					415			
Ala	Asn	Met	Gly	Lys	Ile	Phe	Pro	Asp	Gly	Lys	Ala	His	Phe	Asp	Pro
		420					425					430			
Val	Thr	His	Lys	Ile	Leu	Lys	Pro	Asp	Asn	Trp	Glu	Glu	Lys	Tyr	Ala
	435						440				445				
Pro	Glu	Pro	Ala	Ile	Lys	Lys	Glu	Leu	Gln	Arg	Gln	Leu	Lys	Ala	Tyr
	450				455				460						
Glu	Arg	His	Lys	Glu	Arg	Asn	Lys	Ser							
465				470											

(2) INFORMATION FOR SEQ ID NO:3274:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 237 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...237

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3274:

```

Arg Val Asp Leu Met Ala Tyr Ile Glu Met Lys His Cys Tyr Lys Arg
1          5          10          15
Tyr Gln Val Gly Asp Thr Glu Ile Val Ala Asn Arg Asp Val Asn Phe
          20          25          30
Glu Ile Glu Lys Gly Glu Leu Val Ile Ile Leu Gly Ala Ser Gly Ala
          35          40          45
Gly Lys Ser Thr Val Leu Asn Leu Leu Gly Gly Met Asp Thr Asn Asp
          50          55          60
Glu Gly Glu Ile Trp Ile Asp Gly Val Asn Ile Ala Asp Tyr Ser Ser
65          70          75          80
His Gln Arg Thr Asn Tyr Arg Arg Asn Asp Val Gly Phe Val Phe Gln
          85          90          95
Phe Tyr Asn Leu Val Ser Asn Leu Thr Ala Lys Glu Asn Val Glu Leu
          100         105         110
Ala Ser Glu Ile Val Thr Asp Ala Leu Asn Pro Asp Gln Val Leu Thr
          115         120         125
Asp Val Gly Leu Ala His Arg Leu Asn Asn Phe Pro Ala Gln Leu Ser
130         135         140
Gly Gly Glu Gln Gln Arg Val Ser Ile Ala Arg Ala Val Ala Lys Asn
145         150         155         160
Pro Lys Ile Leu Leu Cys Asp Glu Pro Thr Gly Ala Leu Asp Tyr Gln
          165         170         175
Thr Gly Lys Gln Val Leu Lys Ile Leu Gln Asp Met Ser Arg Gln Lys
          180         185         190
Gly Ala Thr Val Ile Ile Val Thr His Asn Gly Ala Leu Ala Pro Ile
          195         200         205
Ala Asp Arg Val Ile His Met His Asp Ala Ser Val Lys Asp Val Val
210         215         220
Leu Asn Gln His Pro Gln Asp Ile Asp Ser Leu Glu Tyr
225         230         235

```

(2) INFORMATION FOR SEQ ID NO:3275:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 188 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...188

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3275:

```

Asn Val Asn Gln Pro Trp Ser Ser Leu Val Val Val Lys Ile Gln Gln

```

1		5		10		15									
Pro	Ala	Phe	Ser	Arg	Ala	His	Gly	Ser	Met	Lys	Gln	Ser	Lys	Leu	Ser
		20		25		30									
Pro	Leu	Ala	Tyr	Gly	Asn	Ile	Ile	Thr	Ser	Lys	Phe	Lys	Leu	Leu	Glu
	35			40		45									
Lys	Ser	Pro	Arg	Asn	Arg	Gly	Ile	Arg	His	Pro	Tyr	Pro	Arg	Tyr	Val
	50			55		60									
Ser	Ala	Gly	Thr	Asn	His	Cys	Ser	Thr	Thr	Thr	Leu	Arg	Arg	Phe	His
65				70		75									80
Ile	Ser	Tyr	Ile	Ser	Asp	Lys	Leu	Cys	Val	Glu	Ser	Lys	Ser	Leu	Lys
				85		90									95
Leu	Tyr	Leu	Phe	Ser	Tyr	Arg	Asn	His	Gly	Asp	Phe	His	Glu	Asn	Cys
				100		105									110
Ile	Asn	Thr	Ile	Gly	Lys	Asp	Leu	Val	Asn	Leu	Val	Asp	Leu	Arg	Tyr
	115			120		125									
Leu	Glu	Ile	Gly	Gly	Asn	Leu	Phe	Arg	Ala	Val	Ala	Cys	Gln	Ser	Thr
	130			135		140									
Pro	Ile	Thr	Ile	Thr	Val	Ser	Lys	Glu	Ile	Ser	Met	Arg	Xaa	Trp	Gln
145				150		155									160
Asn	Asn	Ala	Phe	Ser	Asn	Thr	Thr	Phe	Ile	Gln	Arg	Lys	Leu	Thr	Thr
				165		170									175
Ala	Lys	Val	Ile	Leu	Asn	Glu	Asn	Gln	Arg	Ala	Asn				
			180			185									

(2) INFORMATION FOR SEQ ID NO:3276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3276:

Lys	Glu	Asn	His	Leu	Met	Ser	Lys	Tyr	Leu	Leu	Lys	Leu	Leu	Val	Tyr
1		5		10		15									
Cys	Phe	Ser	Ala	Leu	Thr	Phe	Gly	Ser	Leu	Phe	Leu	Ile	Ile	Gly	Phe
		20		25		30									
Ile	Leu	Ile	Lys	Gly	Leu	Pro	His	Leu	Ser	Leu	Ser	Leu	Phe	Ser	Trp
	35			40		45									
Thr	Tyr	Thr	Ser	Glu	Asn	Ile	Ser	Leu	Met	Pro	Ala	Ile	Ile	Ser	Thr
	50			55		60									
Val	Ile	Leu	Val	Phe	Gly	Ala	Leu	Leu	Leu	Ala	Leu	Pro	Ile	Gly	Ile
65				70		75									80
Phe	Ala	Gly	Phe	Tyr	Leu	Val	Glu	Tyr	Thr	Lys	Lys	Asp	Ser	Leu	Cys
				85		90									95
Val	Lys	Ile	Met	Arg	Leu	Ala	Ser	Asp	Thr	Leu	Ser	Gly	Ile	Pro	Ser

		100						105					110				
Ile	Val	Phe	Gly	Leu	Phe	Gly	Met	Leu	Phe	Phe	Val	Val	Phe	Leu	Gly		
		115						120					125				
Phe	Gln	Tyr	Ser	Leu	Leu	Ser	Gly	Ile	Leu	Thr	Ser	Val	Ile	Met	Val		
		130						135					140				
Leu	Pro	Val	Ile	Ile	Arg	Ser	Thr	Glu	Glu	Ala	Leu	Leu	Ser	Val	Ser		
145					150					155					160		
Asp	Ser	Met	Arg	Gln	Ala	Ser	Tyr	Gly	Leu	Gly	Ala	Gly	Lys	Leu	Arg		
			165							170				175			
Thr	Val	Phe	Arg	Ile	Val	Leu	Pro	Val	Ala	Met	Pro	Gly	Ile	Leu	Ala		
		180							185				190				
Gly	Val	Ile	Leu	Ala	Ile	Gly	Arg	Ile	Val	Gly	Glu	Thr	Ala	Ala	Leu		
		195					200					205					
Met	Tyr	Thr	Leu	Gly	Thr	Ser	Thr	Asn	Thr	Pro	Ser	Ser	Leu	Met	Ser		
	210					215				220							
Ser	Gly	Arg	Ser	Leu	Ala	Leu	His	Met	Tyr	Met	Leu	Ser	Ser	Glu	Gly		
225					230					235					240		
Leu	His	Val	Asn	Glu	Ala	Tyr	Ala	Thr	Gly	Val	Ile	Leu	Ile	Ile	Thr		
			245						250					255			
Val	Leu	Met	Ile	Asn	Thr	Leu	Ser	Ser	Leu	Leu	Ser	Arg	Lys	Leu	Val		
			260					265					270				
Lys	Gly	Ala	Ser														
		275															

(2) INFORMATION FOR SEQ ID NO:3277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...65

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3277:

Arg	Leu	Arg	Gln	Asn	Phe	Ser	Gly	Tyr	Phe	Phe	His	Thr	Phe	Ile	Glu
1				5					10					15	
Ala	Trp	Gly	Gln	Asn	Val	Phe	His	Lys	Ala	Gln	Lys	Phe	Ser	His	Arg
			20					25					30		
Asn	Leu	Lys	Ile	Gly	Glu	Asp	Ile	Asp	His	His	Gln	Lys	Gln	Gly	Glu
		35				40					45				
Asn	Arg	Asn	Gln	Pro	Ile	Val	Gly	Tyr	Cys	Asp	Thr	Gly	Gln	Leu	Thr
	50					55					60				
Ile															
65															

(2) INFORMATION FOR SEQ ID NO:3278:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 63 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...63

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3278:

Cys	Arg	Arg	Gln	Ser	Val	Leu	Ala	Gly	Ser	Lys	Leu	Gly	Arg	Ala	Ile
1			5					10					15		
Glu	Tyr	Ser	Leu	Lys	Tyr	Glu	Glu	Thr	Phe	Lys	Thr	Ile	Leu	Lys	Asp
		20						25				30			
Gly	His	Leu	Val	Leu	Ser	Asn	Asn	Leu	Ala	Glu	Arg	Ala	Ile	Lys	Ser
	35					40					45				
Leu	Val	Met	Gly	Arg	Ser	Lys	Arg	Ile	Gln	Trp	Thr	Leu	Leu	Ala	
50					55					60					

(2) INFORMATION FOR SEQ ID NO:3279:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 323 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...323

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3279:

Pro	Leu	Cys	Leu	Val	Pro	Ala	Cys	Pro	Val	Gly	Leu	Ser	Ser	Tyr	Gln
1			5					10					15		
Tyr	Ser	Gln	Leu	Leu	Gln	His	Phe	Pro	Glu	Asn	His	Trp	Pro	Ile	Leu
		20						25				30			
Leu	Phe	Val	Gly	Ile	Thr	Ser	Val	Leu	Leu	Leu	Leu	Trp	Gly	Gly	Ile
	35					40					45				
Ala	Thr	Tyr	Met	Glu	Ala	Pro	Asp	Lys	Leu	Phe	Leu	Leu	Val	Gly	Glu
50					55					60					
Glu	Glu	Ile	Lys	Leu	His	Leu	Lys	Arg	Gln	Thr	Gly	Ile	Ser	Leu	Val
65				70					75				80		

Phe	Trp	Leu	Phe	Val	Gln	Thr	Leu	Phe	Leu	Leu	Leu	Phe	Ala	Pro	Leu
				85					90					95	
Phe	Leu	Ala	Met	Gly	Tyr	Gly	Leu	Pro	Val	Phe	Leu	Leu	Tyr	Val	Leu
			100					105					110		
Leu	Leu	Gly	Val	Gly	Lys	Tyr	Phe	His	Phe	Arg	Gln	Lys	Ala	Ser	Lys
		115					120					125			
Phe	Phe	Thr	Glu	Thr	Gly	Leu	Asp	Trp	Asp	Tyr	Leu	Ile	Ser	Gln	Glu
		130				135					140				
Ser	Lys	Arg	Lys	Gln	Val	Leu	Leu	Arg	Phe	Phe	Ala	Leu	Phe	Thr	Gln
145					150					155					160
Val	Lys	Gly	Ile	Ser	Asn	Ser	Val	Lys	Arg	Arg	Ala	Tyr	Leu	Asp	Phe
				165					170					175	
Ile	Leu	Lys	Ala	Val	Gln	Lys	Val	Pro	Gly	Lys	Ile	Trp	Gln	Asn	Leu
			180					185					190		
Tyr	Leu	Arg	Ser	Tyr	Leu	Arg	Asn	Gly	Asp	Leu	Phe	Ala	Leu	Ser	Leu
		195					200					205			
Arg	Leu	Leu	Leu	Leu	Ser	Val	Leu	Ala	Gln	Val	Phe	Ile	Glu	Gln	Ala
		210				215					220				
Trp	Ile	Ala	Thr	Ala	Val	Val	Val	Leu	Phe	Asn	Tyr	Leu	Leu	Leu	Phe
225					230					235					240
Gln	Leu	Leu	Ala	Leu	Tyr	His	Ala	Phe	Asp	Tyr	Gln	Tyr	Leu	Thr	Gln
				245					250					255	
Leu	Phe	Pro	Leu	Asp	Lys	Gly	Gln	Lys	Glu	Lys	Gly	Leu	Gln	Glu	Val
		260					265						270		
Val	Arg	Gly	Leu	Thr	Ser	Phe	Val	Leu	Leu	Val	Glu	Val	Val	Val	Gly
		275					280					285			
Leu	Ile	Thr	Phe	Gln	Glu	Lys	Leu	Ala	Leu	Leu	Ala	Leu	Leu	Gly	Ala
		290				295					300				
Gly	Leu	Val	Leu	Leu	Val	Leu	Tyr	Leu	Pro	Tyr	Gln	Val	Lys	Arg	Gln
305					310					315					320
Met	Gln	Asp													

(2) INFORMATION FOR SEQ ID NO:3280:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 68 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...68
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3280:

Gln	Glu	Phe	Gln	Phe	Ile	Trp	Ser	Phe	Gln	His	His	Phe	Phe	Pro	Ser
1				5					10					15	
Val	Ala	Gly	Pro	Gly	Pro	Asp	Val	Leu	Val	Trp	Gln	Phe	Leu	Pro	Asn
			20					25					30		

Pro Leu Asn Lys Trp Gln Glu Asn Pro Ser Ile Lys Lys Arg Leu Pro
35 40 45
Ser Gln Gln Ser Gln Thr Leu Asn Ile Gly Leu Ser Lys Ile Cys His
50 55 60
Asp Leu Leu Phe
65

(2) INFORMATION FOR SEQ ID NO:3281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...239

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3281:

Thr Lys Ile Gln Lys Lys Leu Lys His Ser Leu Lys Gln Leu His Gln
1 5 10 15
Asn Phe Leu His Gln Ile Leu Leu Lys Gln Val Ser Leu Leu Thr Ala
20 25 30
Leu Asp Leu Thr Thr Val Leu Ala Val Ala Lys Gly Ser Asn Leu Lys
35 40 45
Val Ala Ala Gln Asn Cys Tyr Phe Glu Asn Ala Gly Ala Phe Thr Gly
50 55 60
Glu Thr Ser Pro Gln Val Leu Lys Glu Ile Gly Thr Asp Tyr Val Val
65 70 75 80
Ile Gly His Ser Glu Arg Arg Asp Tyr Phe His Glu Thr Asp Glu Asp
85 90 95
Ile Asn Lys Lys Ala Lys Ala Ile Phe Ala Asn Gly Met Leu Pro Ile
100 105 110
Ile Cys Cys Gly Glu Ser Leu Glu Thr Tyr Glu Ala Gly Lys Ala Ala
115 120 125
Glu Phe Val Gly Ala Gln Val Ser Ala Ala Leu Ala Gly Leu Thr Ala
130 135 140
Glu Gln Val Ala Ala Ser Val Ile Ala Tyr Glu Pro Ile Trp Ala Ile
145 150 155 160
Gly Thr Gly Lys Ser Ala Ser Gln Asp Asp Ala Gln Lys Met Cys Lys
165 170 175
Val Val Arg Asp Val Val Ala Ala Asp Phe Gly Gln Glu Val Ala Asp
180 185 190
Lys Val Arg Val Gln Tyr Gly Gly Ser Val Lys Pro Glu Asn Val Ala
195 200 205
Ser Tyr Met Ala Cys Pro Asp Val Asp Gly Ala Leu Val Gly Gly Ala
210 215 220
Ser Leu Glu Ala Glu Ser Phe Leu Ala Leu Leu Asp Phe Val Lys
225 230 235

(2) INFORMATION FOR SEQ ID NO:3282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...235

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3282:

Arg	Arg	Ile	His	Leu	Met	Val	Lys	Leu	Val	Phe	Ala	Arg	His	Gly	Glu	
1				5					10					15		
Ser	Glu	Trp	Asn	Lys	Ala	Asn	Leu	Phe	Thr	Gly	Trp	Ala	Asp	Val	Asp	
			20					25					30			
Leu	Ser	Glu	Lys	Gly	Thr	Gln	Gln	Ala	Ile	Asp	Ala	Gly	Lys	Leu	Ile	
			35				40					45				
Lys	Glu	Ala	Gly	Ile	Glu	Phe	Asp	Gln	Ala	Tyr	Thr	Ser	Val	Leu	Lys	
	50					55				60						
Arg	Ala	Ile	Lys	Thr	Thr	Asn	Leu	Ala	Leu	Glu	Ala	Ser	Asp	Gln	Leu	
65					70					75					80	
Trp	Val	Pro	Val	Glu	Lys	Ser	Trp	Arg	Leu	Asn	Glu	Arg	His	Tyr	Gly	
				85				90						95		
Gly	Leu	Thr	Gly	Lys	Asn	Lys	Ala	Glu	Ala	Ala	Glu	Gln	Phe	Gly	Asp	
			100					105					110			
Glu	Gln	Val	His	Ile	Trp	Arg	Arg	Ser	Tyr	Asp	Val	Leu	Pro	Pro	Asn	
	115					120					125					
Met	Asp	Arg	Asp	Asp	Glu	His	Ser	Ala	His	Thr	Asp	Arg	Arg	Tyr	Ala	
	130					135					140					
Ser	Leu	Asp	Asp	Ser	Val	Ile	Pro	Asp	Ala	Glu	Asn	Leu	Lys	Val	Thr	
145					150					155					160	
Leu	Glu	Arg	Ala	Phe	Pro	Phe	Trp	Glu	Asp	Lys	Ile	Ala	Pro	Ala	Phe	
				165				170						175		
Lys	Asp	Gly	Lys	Asn	Val	Phe	Val	Gly	Ala	His	Gly	Asn	Ser	Ile	Arg	
			180					185					190			
Ala	Leu	Val	Lys	His	Ile	Lys	Gly	Leu	Ser	Asp	Asp	Glu	Ile	Met	Asp	
	195						200					205				
Val	Glu	Ile	Pro	Asn	Phe	Pro	Pro	Leu	Val	Phe	Glu	Phe	Asp	Glu	Lys	
	210				215						220					
Leu	Asn	Val	Val	Ser	Glu	Tyr	Tyr	Leu	Gly	Lys						
225					230					235						

(2) INFORMATION FOR SEQ ID NO:3283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 amino acids
- (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...286

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3283:

Arg	Met	Ile	Gln	Ile	Gly	Lys	Ile	Phe	Ala	Gly	Arg	Tyr	Arg	Ile	Val
1			5					10						15	
Lys	Gln	Ile	Gly	Arg	Gly	Gly	Met	Ala	Asp	Val	Tyr	Leu	Ala	Lys	Asp
		20					25						30		
Leu	Ile	Leu	Asp	Gly	Glu	Glu	Val	Ala	Val	Lys	Val	Leu	Arg	Thr	Asn
	35					40						45			
Tyr	Gln	Thr	Asp	Pro	Ile	Ala	Val	Ala	Arg	Phe	Gln	Arg	Glu	Ala	Arg
	50				55				60						
Ala	Met	Ala	Asp	Leu	Asp	His	Pro	His	Ile	Val	Arg	Ile	Thr	Asp	Ile
65					70				75						80
Gly	Glu	Glu	Asp	Gly	Gln	Gln	Tyr	Leu	Ala	Met	Glu	Tyr	Val	Ala	Gly
			85					90						95	
Leu	Asp	Leu	Lys	Arg	Tyr	Ile	Lys	Glu	His	Tyr	Pro	Leu	Ser	Asn	Glu
		100					105					110			
Glu	Ala	Val	Arg	Ile	Met	Gly	Gln	Ile	Leu	Leu	Ala	Met	Arg	Leu	Ala
		115				120						125			
His	Thr	Arg	Gly	Ile	Val	His	Arg	Asp	Leu	Lys	Pro	Gln	Asn	Ile	Leu
	130				135						140				
Leu	Thr	Pro	Asp	Gly	Thr	Ala	Lys	Val	Thr	Asp	Phe	Gly	Ile	Ala	Val
145				150					155						160
Ala	Phe	Ala	Glu	Thr	Ser	Leu	Thr	Gln	Thr	Asn	Ser	Met	Leu	Gly	Ser
			165					170					175		
Val	His	Tyr	Leu	Ser	Pro	Glu	Gln	Ala	Arg	Gly	Ser	Lys	Ala	Thr	Val
		180					185					190			
Gln	Ser	Asp	Ile	Tyr	Ala	Met	Gly	Ile	Ile	Phe	Tyr	Glu	Met	Leu	Thr
	195				200						205				
Gly	His	Ile	Pro	Tyr	Asp	Gly	Asp	Ser	Ala	Val	Thr	Ile	Ala	Leu	Gln
	210				215						220				
His	Phe	Gln	Lys	Pro	Leu	Pro	Ser	Val	Ile	Ala	Glu	Asn	Pro	Ser	Val
225				230					235						240
Pro	Gln	Ala	Leu	Glu	Asn	Val	Ile	Ile	Lys	Ala	Thr	Ala	Lys	Lys	Leu
			245					250					255		
Thr	Asn	Arg	Tyr	Arg	Ser	Val	Ser	Glu	Met	Tyr	Val	Asp	Leu	Ser	Ser
		260					265					270			
Ser	Leu	Ser	Tyr	Asn	Arg	Arg	Asn	Glu	Ser	Lys	Leu	Ile	Phe		
		275				280						285			

(2) INFORMATION FOR SEQ ID NO:3284:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 362 amino acids
 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...362

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3284:

Ala	Phe	Ser	His	Val	Asn	Ile	Asn	Thr	Lys	Ser	Leu	Val	Glu	Leu	Leu
1				5				10					15		
His	Ile	Ile	Glu	Cys	Phe	His	Lys	Thr	His	Phe	Thr	Lys	Ile	Ser	Cys
			20					25					30		
Phe	Phe	Gln	Glu	Glu	Thr	His	Thr	Met	Leu	Leu	Ile	Phe	Leu	Ser	Ser
		35					40					45			
Leu	Ala	Ile	Leu	Arg	Gln	Val	Trp	Tyr	Asn	Lys	Asn	Met	Arg	Ile	Gln
	50				55						60				
Gln	Leu	His	Tyr	Ile	Ile	Lys	Ile	Val	Glu	Thr	Gly	Ser	Met	Asn	Glu
65				70					75					80	
Ala	Ala	Lys	Gln	Leu	Phe	Ile	Thr	Gln	Pro	Ser	Leu	Ser	Asn	Ala	Val
			85					90					95		
Arg	Asp	Leu	Glu	Asn	Glu	Met	Gly	Ile	Glu	Ile	Phe	Ile	Arg	Asn	Pro
		100					105					110			
Lys	Gly	Ile	Thr	Leu	Thr	Arg	Asp	Gly	Met	Glu	Phe	Leu	Ser	Tyr	Ala
	115					120					125				
Arg	Gln	Val	Val	Glu	Gln	Thr	Gln	Leu	Leu	Glu	Glu	Arg	Tyr	Lys	Asn
	130				135						140				
Pro	Val	Ala	His	Arg	Glu	Leu	Phe	Ser	Val	Ser	Ser	Gln	His	Tyr	Ala
145				150					155					160	
Phe	Val	Val	Asn	Ala	Phe	Val	Ser	Leu	Leu	Lys	Lys	Ser	Asp	Met	Glu
			165					170					175		
Lys	Tyr	Glu	Leu	Phe	Leu	Arg	Glu	Thr	Arg	Thr	Trp	Glu	Ile	Ile	Asp
	180						185					190			
Asp	Val	Lys	Asn	Phe	Arg	Ser	Glu	Val	Gly	Val	Leu	Phe	Leu	Asn	Ser
	195					200					205				
Tyr	Asn	Arg	Asp	Val	Leu	Thr	Lys	Met	Leu	Asp	Asp	Asn	His	Leu	Leu
	210				215					220					
Ala	His	His	Leu	Phe	Thr	Ala	Gln	Pro	His	Ile	Phe	Val	Ser	Lys	Thr
225				230					235					240	
Asn	Pro	Leu	Ala	Lys	Lys	Asp	Lys	Val	Lys	Leu	Ser	Asp	Leu	Glu	Asn
			245					250					255		
Phe	Pro	Tyr	Leu	Ser	Tyr	Asp	Gln	Gly	Thr	His	Asn	Ser	Phe	Tyr	Phe
	260						265					270			
Ser	Glu	Glu	Ile	Leu	Ser	Gln	Glu	His	His	Lys	Lys	Ser	Ile	Val	Val
	275					280					285				
Ser	Asp	Arg	Ala	Thr	Leu	Phe	Asn	Leu	Leu	Ile	Gly	Leu	Asp	Gly	Tyr
	290				295					300					
Thr	Ile	Ala	Thr	Gly	Ile	Leu	Asn	Ser	Asn	Leu	Asn	Gly	Asp	Asn	Ile
305				310					315					320	
Val	Ser	Ile	Pro	Leu	Asp	Ile	Asp	Asp	Pro	Ile	Glu	Leu	Val	Tyr	Ile
			325					330					335		

Gln His Glu Lys Thr Ser Leu Ser Lys Met Gly Glu Arg Phe Ile Asp
 340 345 350
 Tyr Leu Leu Glu Glu Val Gln Phe Asp Ser
 355 360

(2) INFORMATION FOR SEQ ID NO:3285:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 75 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...75
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3285:

Leu Tyr Ser Gln Ile Arg Pro Arg Phe Trp Arg Phe Ala Leu Gln Ile
 1 5 10 15
 Leu Leu Trp Asp Ser Leu Met Ile Leu Ser Leu Val Ser Leu Ser Asp
 20 25 30
 Ile Pro Leu Phe Leu Gln Gly Thr Leu Leu Ile Leu Gly His Leu Ile
 35 40 45
 Pro Ser Tyr Arg Ile Cys Gln Ser Leu Lys Arg Asp Phe Pro Gln Ala
 50 55 60
 Tyr Gln Glu Pro Ile Ser Phe Trp Ser Ile Leu
 65 70 75

(2) INFORMATION FOR SEQ ID NO:3286:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 71 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...71
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3286:

Glu	Arg	Ser	Gln	Leu	Arg	Leu	Leu	Lys	Ser	Tyr	Phe	Arg	Glu	Phe	Ser
1			5					10					15		
Leu	Trp	Ile	Gly	Lys	Ile	Ile	Tyr	His	Leu	Glu	Leu	Gly	Ser	Arg	Phe
		20					25					30			
Gln	Lys	Leu	Asn	Val	Leu	Ser	Pro	Asn	Phe	Thr	Met	Ser	Pro	Val	Phe
	35					40					45				
Arg	Leu	Phe	Leu	Arg	Lys	Leu	Leu	Ser	Arg	Asn	Cys	Arg	Asn	Thr	Met
	50				55						60				
Leu	Ala	Gln	Lys	Gly	Phe	Leu									
65					70										

(2) INFORMATION FOR SEQ ID NO:3287:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 62 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...62
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3287:

Val	Ser	Ser	Gln	Phe	Ala	Ile	Ile	Ala	Val	Cys	Leu	Ile	Phe	Gln	Ala
1			5					10				15			
Pro	Ala	Cys	Phe	Gly	Ser	Glu	Leu	Val	Gly	Ile	Val	Ala	Asn	Ser	Ile
		20					25					30			
Arg	Met	Phe	Cys	Val	Arg	Glu	Ile	Ser	Ala	Val	Gly	His	Phe	Leu	Thr
	35					40					45				
Ser	Phe	Ile	Asp	Cys	Asn	Ile	Gly	Asn	Ser	Tyr	Leu	Val	Ser		
	50				55					60					

(2) INFORMATION FOR SEQ ID NO:3288:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 252 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...252

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3288:

Leu	Leu	Cys	Leu	Leu	Thr	Ile	Phe	Trp	Tyr	Asn	Ser	Arg	Glu	Lys	Gly
1				5					10					15	
Glu	His	Met	Lys	Lys	Ile	Leu	Ile	Val	Asp	Asp	Glu	Lys	Pro	Ile	Ser
			20					25					30		
Asp	Ile	Ile	Lys	Phe	Asn	Met	Thr	Lys	Glu	Gly	Tyr	Glu	Val	Val	Thr
			35				40					45			
Ala	Phe	Asn	Gly	Arg	Glu	Ala	Leu	Glu	Gln	Phe	Glu	Ala	Glu	Gln	Pro
			50			55				60					
Asp	Ile	Ile	Ile	Leu	Asp	Leu	Met	Leu	Pro	Glu	Ile	Asp	Gly	Leu	Glu
65				70					75					80	
Val	Ala	Lys	Thr	Ile	Arg	Lys	Thr	Ser	Ser	Val	Pro	Ile	Leu	Met	Leu
				85				90					95		
Ser	Ala	Lys	Asp	Ser	Glu	Phe	Asp	Lys	Val	Ile	Gly	Leu	Glu	Leu	Gly
			100					105				110			
Ala	Asp	Asp	Tyr	Val	Thr	Lys	Pro	Phe	Ser	Asn	Arg	Glu	Leu	Gln	Ala
			115				120					125			
Arg	Val	Lys	Ala	Leu	Leu	Arg	Arg	Ser	Gln	Pro	Met	Pro	Val	Asp	Gly
						135					140				
Gln	Glu	Ala	Asp	Ser	Lys	Pro	Gln	Pro	Ile	Gln	Ile	Gly	Asp	Leu	Glu
145				150					155					160	
Ile	Val	Pro	Asp	Ala	Tyr	Val	Ala	Lys	Lys	Tyr	Gly	Glu	Glu	Leu	Asp
				165				170						175	
Leu	Thr	His	Arg	Glu	Phe	Glu	Leu	Leu	Tyr	His	Leu	Ala	Ser	His	Thr
			180					185					190		
Gly	Gln	Val	Ile	Thr	Arg	Glu	His	Leu	Leu	Glu	Thr	Val	Trp	Gly	Tyr
			195				200					205			
Asp	Tyr	Phe	Gly	Asp	Val	Arg	Thr	Val	Asp	Val	Thr	Val	Arg	Arg	Leu
			210			215					220				
Arg	Glu	Lys	Ile	Glu	Asp	Thr	Pro	Ser	Arg	Pro	Glu	Tyr	Ile	Leu	Thr
225				230						235				240	
Arg	Arg	Gly	Val	Gly	Tyr	Tyr	Met	Arg	Asn	Asn	Ala				
				245					250						

(2) INFORMATION FOR SEQ ID NO:3289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...367

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3289:

Asn Val Ala Gln Val Ile Ser Leu Pro Ala Thr Gln Thr Gln Gln Lys

1				5				10					15				
Leu	Lys	Gln	Asn	Ser	Val	Gly	Lys	Gln	Ser	Thr	Ser	Pro	Lys	Cys			
			20					25				30					
Val	Lys	Thr	His	Gly	Val	Gly	Lys	Ala	Ser	Ile	Gln	Met	Asp	Leu	Lys		
		35					40					45					
Thr	Lys	Met	Met	Ile	Ser	Ile	Ile	Val	Pro	Cys	Leu	Asn	Glu	Glu	Glu		
		50				55					60						
Val	Leu	Pro	Leu	Phe	Tyr	Gln	Ala	Leu	Glu	Ala	Leu	Leu	Pro	Asp	Leu		
65					70					75					80		
Glu	Thr	Glu	Ile	Glu	Tyr	Val	Phe	Val	Asp	Asp	Gly	Ser	Ser	Asp	Gly		
			85						90					95			
Thr	Leu	Glu	Leu	Leu	Lys	Ala	Tyr	Arg	Glu	Gln	Asn	Pro	Ala	Val	His		
			100					105					110				
Tyr	Ile	Ser	Phe	Ser	Arg	Asn	Phe	Gly	Lys	Glu	Ala	Ala	Leu	Tyr	Ala		
		115				120						125					
Gly	Leu	Gln	Tyr	Ala	Thr	Gly	Asp	Leu	Val	Val	Val	Met	Asp	Ala	Asp		
		130				135					140						
Leu	Gln	Asp	Pro	Pro	Ser	Met	Leu	Phe	Glu	Met	Lys	Asn	Val	Leu	Asp		
145					150					155					160		
Lys	Asn	Val	Asp	Leu	Asp	Cys	Val	Gly	Thr	Arg	Arg	Thr	Ser	Arg	Glu		
			165					170						175			
Gly	Glu	Pro	Phe	Arg	Ser	Phe	Cys	Ala	Val	Leu	Phe	Tyr	Arg	Leu			
		180					185					190					
Met	Gln	Lys	Ile	Ser	Pro	Val	Ala	Leu	Pro	Ser	Gly	Val	Arg	Asp	Phe		
		195				200						205					
Arg	Met	Met	Arg	Arg	Ser	Val	Val	Asp	Ala	Ile	Leu	Ser	Leu	Thr	Glu		
		210				215					220						
Ser	Asn	Arg	Phe	Ser	Lys	Gly	Leu	Phe	Ala	Trp	Val	Gly	Phe	Lys	Thr		
225					230				235						240		
His	Tyr	Leu	Asp	Tyr	Pro	Asn	Val	Glu	Arg	Gln	Ala	Gly	Lys	Thr	Ser		
			245					250						255			
Trp	Ser	Phe	Arg	Gln	Leu	Phe	Phe	Tyr	Ser	Ile	Glu	Gly	Ile	Val	Asn		
		260					265						270				
Phe	Ser	Asp	Phe	Pro	Leu	Thr	Ile	Ala	Phe	Val	Ala	Gly	Leu	Leu	Ser		
		275					280					285					
Cys	Phe	Leu	Ser	Leu	Leu	Met	Thr	Phe	Phe	Val	Val	Val	Arg	Thr	Leu		
		290				295					300						
Ile	Leu	Gly	Asn	Pro	Thr	Ser	Gly	Trp	Thr	Ser	Leu	Met	Ala	Val	Ile		
305					310					315					320		
Leu	Phe	Leu	Gly	Gly	Ile	Gln	Leu	Leu	Thr	Ile	Gly	Ile	Leu	Gly	Lys		
			325						330					335			
Tyr	Ile	Ser	Lys	Ile	Tyr	Leu	Glu	Thr	Lys	Lys	Arg	Pro	Leu	Tyr	Leu		
		340						345					350				
Ile	Lys	Glu	Lys	Ser	Asp	Asp	Arg	Leu	Lys	Lys	Ile	Glu	Phe	Ile			
		355					360						365				

(2) INFORMATION FOR SEQ ID NO:3290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...241

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3290:

Arg	Val	Tyr	Gln	Ser	Lys	Arg	Ser	Ala	His	Arg	Arg	Leu	Tyr	Phe	Arg
1				5					10					15	
Thr	Val	Arg	Ile	Arg	Lys	Glu	Lys	Pro	Met	Arg	Asn	Gln	Phe	Asp	Leu
			20					25					30		
Glu	Leu	His	Glu	Leu	Glu	Gln	Ser	Phe	Leu	Gly	Leu	Gly	Gln	Leu	Val
		35					40					45			
Leu	Glu	Thr	Ala	Ser	Lys	Ala	Leu	Leu	Ala	Leu	Ala	Ser	Lys	Asp	Lys
		50				55					60				
Glu	Met	Ala	Glu	Leu	Ile	Ile	Asn	Lys	Asp	His	Ala	Ile	Asn	Gln	Gly
65					70					75				80	
Gln	Ser	Ala	Ile	Glu	Leu	Ala	Cys	Ala	Arg	Leu	Leu	Ala	Leu	Gln	Gln
			85						90					95	
Pro	Gln	Val	Ser	Asp	Leu	Arg	Phe	Val	Ile	Ser	Ile	Met	Ser	Ser	Cys
			100					105					110		
Ser	Asp	Leu	Glu	Arg	Met	Gly	Asp	His	Met	Ala	Gly	Ile	Ala	Lys	Ala
		115				120						125			
Val	Leu	Gln	Leu	Lys	Glu	Asn	Gln	Leu	Ala	Pro	Asp	Glu	Glu	Gln	Leu
		130				135					140				
His	Gln	Met	Gly	Lys	Leu	Ser	Leu	Ser	Met	Leu	Ala	Asp	Leu	Leu	Val
145					150					155					160
Ala	Phe	Pro	Leu	His	Gln	Ala	Ser	Lys	Ala	Ile	Ser	Ile	Ala	Gln	Lys
				165					170					175	
Asp	Glu	Gln	Ile	Asp	Gln	Tyr	Tyr	Tyr	Ala	Leu	Ser	Lys	Glu	Ile	Ile
			180					185					190		
Gly	Leu	Met	Lys	Asp	Gln	Glu	Thr	Ser	Ile	Pro	Asn	Gly	Thr	Gln	Tyr
		195					200					205			
Leu	Tyr	Ile	Ile	Gly	His	Leu	Glu	Arg	Phe	Ala	Asp	Tyr	Ile	Ala	Asn
	210				215						220				
Ile	Cys	Glu	Arg	Leu	Val	Tyr	Leu	Glu	Thr	Gly	Glu	Leu	Val	Asp	Leu
225					230					235					240
Asn															

(2) INFORMATION FOR SEQ ID NO:3291:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 117 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...117

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3291:

Glu	Ser	Tyr	His	Gly	Ser	Arg	Val	Thr	Met	Tyr	Phe	Pro	Thr	Ser	Ser
1				5					10					15	
Ala	Leu	Ile	Glu	Phe	Leu	Ile	Leu	Ala	Val	Leu	Glu	Gln	Gly	Asp	Ser
			20					25					30		
Tyr	Gly	Tyr	Glu	Ile	Ser	Gln	Thr	Ile	Lys	Leu	Ile	Ala	Asn	Ile	Lys
		35					40					45			
Glu	Ser	Thr	Leu	Tyr	Pro	Ile	Leu	Lys	Lys	Leu	Glu	Gly	Asn	Ser	Phe
	50					55					60				
Leu	Thr	Thr	Tyr	Ser	Arg	Glu	Phe	Gln	Gly	Arg	Met	Arg	Lys	Tyr	Tyr
65					70					75					80
Ser	Leu	Thr	Asn	Gly	Gly	Ile	Glu	Gln	Leu	Leu	Thr	Leu	Lys	Asp	Glu
			85					90						95	
Trp	Thr	Leu	Tyr	Thr	Asp	Thr	Ile	Asn	Gly	Ile	Ile	Glu	Gly	Ser	Ile
		100						105					110		
Arg	His	Asp	Lys	Asn											
		115													

(2) INFORMATION FOR SEQ ID NO:3292:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 572 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...572

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3292:

Met	Ser	Tyr	Gln	Glu	Asn	Tyr	Gln	Lys	Trp	Val	Asp	Phe	Val	Glu	Leu
1				5					10					15	
Pro	Asp	Tyr	Leu	Arg	Gln	Asp	Leu	Glu	Asn	Met	Asp	Glu	Lys	Thr	Lys
			20					25					30		
Glu	Asp	Ala	Phe	Tyr	Thr	Asn	Leu	Glu	Phe	Gly	Thr	Ala	Gly	Met	Arg
		35					40					45			
Gly	Leu	Val	Gly	Ala	Gly	Thr	Asn	Arg	Ile	Asn	Ile	Tyr	Val	Val	Arg
	50					55					60				
Gln	Ala	Thr	Glu	Gly	Leu	Ala	Arg	Leu	Ile	Glu	Ser	Lys	Gly	Gly	Asn
65					70					75					80
Glu	Lys	Glu	Arg	Gly	Val	Ala	Ile	Ala	Tyr	Asp	Ser	Arg	His	Phe	Ser
			85					90						95	
Pro	Glu	Phe	Ala	Phe	Glu	Ser	Ala	Ala	Val	Leu	Ala	Lys	His	Gly	Ile
		100						105					110		
Lys	Ser	Tyr	Val	Phe	Glu	Ser	Leu	Arg	Pro	Thr	Pro	Glu	Leu	Ser	Phe

(2) INFORMATION FOR SEQ ID NO:3293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...148

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3293:

Gln	Arg	Tyr	Gln	Asn	Ile	Met	Val	Ala	Ile	Asp	Gly	Ser	Lys	Glu	Ala
1			5						10					15	
Asp	Leu	Ala	Phe	Val	Lys	Gly	Val	His	Ser	Ala	Leu	Arg	Asn	Asp	Ala
			20					25					30		
Lys	Leu	Thr	Ile	Ala	His	Val	Ile	Asp	Thr	Arg	Ala	Leu	Gln	Ser	Val
			35				40					45			
Ser	Thr	Phe	Asp	Ala	Glu	Val	Tyr	Glu	Glu	Leu	Gln	Val	Asp	Ala	Glu
			50				55				60				
Ser	Leu	Met	Lys	Glu	Tyr	Glu	Lys	Arg	Ala	Lys	Asp	Ala	Gly	Val	Ala
65					70					75				80	
Asp	Val	His	Ile	Val	Ile	Glu	Met	Gly	Asn	Pro	Lys	Thr	Leu	Leu	Ala
				85					90					95	
Arg	Thr	Ile	Pro	Asp	Ala	Glu	Glu	Val	Asp	Leu	Ile	Leu	Val	Gly	Ala
			100					105					110		
Thr	Gly	Leu	Asn	Ala	Phe	Glu	Arg	Leu	Leu	Val	Gly	Ser	Ser	Ser	Glu
			115				120					125			
Tyr	Ile	Leu	Arg	His	Ala	Lys	Val	Asp	Leu	Leu	Val	Val	Arg	Glu	Gln
			130				135				140				
Glu	Lys	Thr	Leu												
145															

(2) INFORMATION FOR SEQ ID NO:3294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...89

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3294:

Arg	Leu	His	Gln	Gln	Thr	Ser	Arg	Tyr	Arg	Ile	Met	Met	Leu	Ser	Ser
1			5					10					15		
Leu	Ile	Trp	Ile	Ser	Leu	Ile	Gln	Asn	Thr	Arg	Glu	Asn	Met	Val	Ala
			20				25					30			
Lys	Lys	Lys	Ile	Leu	Phe	Phe	Met	Trp	Ser	Phe	Pro	Leu	Gly	Gly	Gly
		35				40					45				
Ala	Glu	Lys	Ile	Leu	Ser	Thr	Ile	Val	Ser	Asn	Leu	Asp	Pro	Glu	Lys
	50				55					60					
Tyr	Asp	Ile	Asp	Ile	Leu	Glu	Met	Glu	His	Phe	Asp	Lys	Gly	Tyr	Glu
65				70				75						80	
Ser	Phe	Pro	Lys	His	Val	Arg	Ile	Leu							
			85												

(2) INFORMATION FOR SEQ ID NO:3295:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 291 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...291

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3295:

Pro	Tyr	His	Gln	Lys	Lys	Asn	Ala	Ser	Thr	Val	Met	Asn	Phe	Thr	Leu
1			5					10					15		
Ile	Asn	Trp	Arg	Ile	Arg	Met	Gln	Tyr	Leu	Glu	Lys	Lys	Glu	Ile	Lys
			20				25					30			
Glu	Ile	Gln	Leu	Ala	Leu	Leu	Asp	Tyr	Ile	Asp	Glu	Thr	Cys	Lys	Lys
		35				40					45				
Tyr	Asp	Ile	Pro	Tyr	Phe	Leu	Ser	Tyr	Gly	Thr	Met	Leu	Gly	Ala	Ile
	50				55				60						
Arg	His	Lys	Gly	Met	Ile	Pro	Trp	Asp	Asp	Asp	Ile	Asp	Ile	Ser	Leu
65				70				75						80	
Tyr	Arg	Glu	Asp	Tyr	Glu	Arg	Leu	Leu	Lys	Ile	Ile	Glu	Glu	Glu	Asn
			85				90					95			
His	Pro	Arg	Tyr	Lys	Val	Leu	Ser	Tyr	Asp	Thr	Ser	Ser	Trp	Tyr	Phe
			100				105					110			
His	Asn	Phe	Ala	Ser	Ile	Leu	Asp	Thr	Ser	Thr	Val	Ile	Glu	Asp	His
	115				120						125				
Val	Lys	Tyr	Lys	Arg	His	Asp	Thr	Ser	Leu	Phe	Ile	Asp	Val	Phe	Pro
	130				135				140						
Ile	Asp	Arg	Phe	Thr	Asp	Leu	Ser	Ile	Val	Asp	Lys	Ser	Tyr	Lys	Tyr

145		150		155		160									
Val	Ala	Leu	Arg	Gln	Leu	Ala	Tyr	Ile	Lys	Lys	Ser	Arg	Ala	Val	His
		165		170		175									
Gly	Asp	Ser	Lys	Leu	Lys	Asp	Phe	Leu	Arg	Leu	Cys	Ser	Trp	Tyr	Ala
		180		185		190									
Leu	Arg	Phe	Val	Asn	Pro	Arg	Tyr	Phe	Tyr	Lys	Lys	Ile	Asp	Gln	Leu
		195		200		205									
Val	Lys	Asn	Ala	Val	Thr	Asn	Thr	Pro	Gln	Tyr	Glu	Gly	Gly	Val	Gly
		210		215		220									
Ile	Gly	Lys	Glu	Gly	Met	Lys	Glu	Ile	Phe	Pro	Val	Asp	Thr	Phe	Lys
225				230		235									240
Glu	Leu	Ile	Leu	Thr	Glu	Phe	Glu	Gly	Arg	Met	Leu	Pro	Val	Pro	Lys
				245		250									255
Lys	Tyr	Asp	Gln	Phe	Leu	Thr	Gln	Met	Tyr	Gly	Asp	Tyr	Met	Thr	Pro
		260		265		270									
Pro	Ser	Lys	Glu	Met	Gln	Glu	Trp	Tyr	Ser	His	Ser	Ile	Lys	Ala	Tyr
		275		280		285									
Arg	Lys	Ser													
		290													

(2) INFORMATION FOR SEQ ID NO:3296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...291

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3296:

Thr	Ile	Asn	Gln	Leu	Ser	Asn	Arg	Glu	Glu	Phe	Leu	Gln	Phe	Arg	Asn
1			5					10					15		
Glu	Leu	Gln	Leu	Glu	Ile	Ser	Asn	Arg	Lys	Arg	Val	Ser	Met	Lys	Ile
		20				25					30				
Asn	Lys	Lys	Tyr	Leu	Val	Gly	Ser	Ala	Ala	Ala	Leu	Ile	Leu	Ser	Val
		35				40					45				
Cys	Ser	Tyr	Glu	Leu	Gly	Leu	Tyr	Gln	Ala	Arg	Thr	Val	Lys	Glu	Asn
		50				55					60				
Asn	Arg	Val	Ser	Tyr	Ile	Asp	Gly	Lys	Gln	Ala	Thr	Gln	Lys	Thr	Glu
65				70				75							80
Asn	Leu	Thr	Pro	Asp	Glu	Val	Ser	Lys	Arg	Glu	Gly	Ile	Asn	Ala	Glu
				85				90						95	
Gln	Ile	Val	Ile	Lys	Ile	Thr	Asp	Gln	Gly	Tyr	Val	Thr	Ser	His	Gly
		100				105						110			
Asp	His	Tyr	His	Tyr	Tyr	Asn	Gly	Lys	Val	Pro	Tyr	Asp	Ala	Ile	Phe
		115				120						125			
Ser	Glu	Glu	Leu	Leu	Met	Lys	Asp	Pro	Asn	Tyr	Lys	Leu	Lys	Asp	Glu

130		135		140											
Asp	Ile	Val	Asn	Glu	Val	Lys	Gly	Gly	Tyr	Val	Ile	Lys	Val	Asp	Gly
145		150		155		160									
Lys	Tyr	Tyr	Val	Tyr	Leu	Lys	Asp	Ala	Ala	His	Ala	Asp	Asn	Val	Arg
		165		170		175									
Thr	Lys	Glu	Glu	Ile	Asn	Arg	Gln	Lys	Gln	Glu	His	Ser	Pro	His	Arg
		180		185		190									
Glu	Lys	Leu	Asp	Ser	Lys	Lys	Thr	Lys	Phe	Pro	Leu	Pro	Trp	Gly	Pro
		195		200		205									
Phe	Ala	Arg	Asp	Ala	Ile	Leu	Gln	Met	Met	Val	Ile	Ser	Leu	Met	Leu
		210		215		220									
Leu	Ile	Ser	Tyr	Arg	Ile	Leu	Val	Met	Leu	Ile	Ser	Phe	Leu	Met	Glu
225				230		235									
Ile	Ile	Thr	Ile	Thr	Phe	Leu	Arg	Met	Ser	Tyr	Gln	Leu	Ala	Ser	Trp
		245		250		255									
Leu	Leu	Gln	Lys	Pro	Ser	Tyr	Leu	Val	Gly	Glu	Ile	Cys	Gln	Ile	Gln
		260		265		270									
Glu	Pro	Ile	Ala	Asp	Lys	Ile	Ala	Ile	Thr	Leu	Gln	Glu	Gln	Thr	Gly
		275		280		285									
Tyr	Leu	Leu													
290															

(2) INFORMATION FOR SEQ ID NO:3297:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 78 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...78
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3297:

Tyr	Lys	Asn	Gln	Ala	Glu	Glu	Asp	Lys	Pro	Leu	Ser	Asp	Lys	Tyr	Ile
1		5		10		15									
Phe	Glu	Lys	Ile	Leu	Gly	Lys	Thr	Tyr	Ala	Ala	Phe	Lys	Lys	Asp	Gln
		20		25		30									
Ile	Asn	Glu	Arg	Val	Glu	Lys	Leu	Gly	Lys	Leu	Lys	Pro	Ile	Thr	Ile
		35		40		45									
Asn	Tyr	Asn	Gly	Lys	Ser	Glu	Val	Ile	Asp	Ser	Lys	Glu	Lys	Leu	Gln
		50		55		60									
Glu	Leu	Met	Asn	Lys	Ala	Val	Lys	Asp	Glu	Val	Ala	Gln	Ile		
65				70		75									

(2) INFORMATION FOR SEQ ID NO:3298:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 392 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...392

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3298:

Cys	Tyr	Cys	Gln	Ile	Pro	Asn	Ser	Gly	Ile	Leu	Gly	Gln	Tyr	Phe	Ile
1			5					10						15	
Asn	Met	Lys	Glu	Ile	Phe	Met	Ala	Lys	Lys	Gly	Thr	Leu	Thr	Gly	Leu
		20					25					30			
Leu	Leu	Phe	Gly	Ile	Phe	Phe	Gly	Ala	Gly	Asn	Leu	Ile	Phe	Pro	Pro
	35					40					45				
Ser	Leu	Gly	Ala	Leu	Ser	Gly	Glu	His	Phe	Leu	Pro	Ala	Ile	Ala	Gly
	50				55					60					
Phe	Val	Phe	Ser	Gly	Val	Gly	Ile	Ala	Val	Leu	Thr	Leu	Ile	Ile	Gly
65				70					75						80
Thr	Leu	Asn	Pro	Lys	Gly	Tyr	Ile	Tyr	Glu	Ile	Ser	Ala	Lys	Ile	Ala
		85						90						95	
Pro	Trp	Phe	Ala	Thr	Leu	Tyr	Leu	Ser	Val	Leu	Tyr	Leu	Ser	Ile	Gly
	100						105					110			
Pro	Phe	Phe	Ala	Thr	Pro	Arg	Thr	Ala	Thr	Thr	Ala	Tyr	Glu	Val	Gly
	115					120					125				
Ile	Ser	Pro	Leu	Leu	Ser	Asp	Ala	Asn	Lys	Gly	Leu	Gly	Leu	Ile	Val
	130				135					140					
Phe	Thr	Val	Leu	Tyr	Phe	Ala	Ala	Ala	Tyr	Leu	Ile	Ser	Leu	Asn	Pro
145				150					155					160	
Ser	Lys	Ile	Leu	Asp	Arg	Ile	Gly	Arg	Ile	Leu	Thr	Pro	Val	Phe	Ala
		165					170							175	
Ile	Leu	Ile	Val	Ile	Leu	Val	Val	Leu	Gly	Ala	Ile	Lys	Tyr	Gly	Gly
	180					185					190				
Thr	Ser	Pro	Gln	Thr	Ala	Ser	Ser	Ala	Tyr	Gln	Ala	Ser	Ala	Phe	Gly
	195					200					205				
Thr	Gly	Phe	Leu	Glu	Gly	Tyr	Asn	Thr	Leu	Asp	Ala	Leu	Ala	Ser	Val
	210				215					220					
Ala	Phe	Ile	Val	Ile	Ala	Val	Gln	Thr	Leu	Lys	Gln	Leu	Gly	Phe	Ser
225				230					235					240	
Ser	Lys	Lys	Lys	Tyr	Ile	Ser	Thr	Ile	Trp	Val	Val	Gly	Ile	Val	Val
		245					250							255	
Ala	Leu	Ala	Phe	Ser	Ala	Leu	Tyr	Ile	Gly	Leu	Gly	Phe	Leu	Gly	Asn
		260				265						270			
His	Phe	Pro	Val	Pro	Ala	Glu	Ala	Met	Lys	Gly	Gly	Thr	Pro	Gly	Val
	275				280							285			
Tyr	Ile	Leu	Ser	Gln	Ala	Thr	Gln	Glu	Ile	Phe	Gly	Ser	Thr	Ala	Gln
	290				295						300				
Leu	Phe	Leu	Ala	Ala	Met	Val	Thr	Val	Thr	Cys	Phe	Thr	Thr	Thr	Val
305				310						315					320
Gly	Leu	Ile	Val	Ser	Thr	Ala	Glu	Phe	Phe	Asn	Glu	Arg	Phe	Ala	Gln

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          325          330          335
Ile Ser Tyr Lys Val Tyr Ala Thr Ala Phe Thr Leu Ile Gly Phe Ala
          340          345          350
Ile Gly Xaa Ser Xaa Xaa Asn Xaa Xaa Xaa Xaa Phe Xaa Lys Asn
          355          360          365
Ile Asn Ser Leu Val Lys Asn Val His Xaa Pro Lys Ile Tyr Asn Phe
          370          375          380
Pro Pro Leu Pro Pro Phe Leu Xaa
385          390

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(2) INFORMATION FOR SEQ ID NO:3299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...224

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3299:

```

Leu Ala Cys Gln Ser His Arg His Met Trp Phe Leu Ala Leu Arg Ser
1          5          10          15
Gly Ile Leu Met Lys Thr Lys Leu Ile Phe Trp Gly Ser Met Leu Phe
          20          25          30
Leu Leu Ser Leu Ser Ile Leu Leu Thr Ile Tyr Leu Ala Trp Ile Phe
          35          40          45
Tyr Pro Met Glu Ile Gln Trp Leu Asn Leu Thr Asn Arg Val Tyr Leu
          50          55          60
Lys Pro Glu Thr Ile Gln Tyr Asn Phe His Ile Leu Met Asn Tyr Leu
          65          70          75          80
Thr Asn Pro Phe Ser Gln Val Leu Gln Met Pro Asp Phe Arg Ser Ser
          85          90          95
Ala Ala Gly Leu His His Phe Ala Val Val Lys Asn Leu Phe His Leu
          100          105          110
Val Gln Leu Val Ala Leu Val Thr Leu Pro Ser Phe Tyr Val Phe Val
          115          120          125
Asn Arg Ile Val Lys Lys Asp Phe Leu Ser Leu Tyr Arg Lys Ser Leu
          130          135          140
Leu Ala Leu Val Val Leu Pro Val Met Ile Gly Leu Gly Gly Val Leu
          145          150          155          160
Ile Gly Phe Asp Gln Phe Phe Thr Leu Phe His Gln Ile Leu Phe Val
          165          170          175
Gly Asp Asp Thr Trp Leu Phe Asp Pro Ala Lys Asp Pro Val Ile Met
          180          185          190
Ile Leu Pro Glu Thr Phe Phe Leu His Ala Phe Leu Leu Phe Phe Ala
          195          200          205
Leu Tyr Glu Asn Phe Phe Gly Tyr Leu Cys Val Lys Ser Arg Arg Lys

```


210

215

220

(2) INFORMATION FOR SEQ ID NO:3300:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 231 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3300:

```

Gly Ser Ser Gln Ser Val Gly Asp Thr Tyr Ile Gln His Ser Thr Gly
1          5          10          15
Val Pro Asp Gly Lys Glu Gly Phe Ala Ala Phe Phe Ala Asp Phe Phe
20          25          30
Glu Arg His Pro Glu Arg Gln Ile Lys Ile Val Arg Thr Ile Glu Asp
35          40          45
Gly Asn Leu Val Phe Val His Val His Gln Tyr Leu Asn Gly Gly Glu
50          55          60
Ala Gln Trp Val Thr Thr Asp Thr Phe Arg Glu Asp Glu Asn Gly Cys
65          70          75          80
Ile Val Glu His Trp Asp Val Ile Asp Tyr Tyr Arg Thr Pro Glu Asn
85          90          95
Asp Gln Leu Asp Gln Ile Phe Gly Asp Phe Glu Ile Lys Asp Leu Asp
100         105         110
Lys Lys Ala Glu Asn Lys Lys Leu Val Arg Arg Phe Leu Thr Glu Ile
115         120         125
Phe Gln Asn Gly Glu Leu Glu Gln Trp Ser Asp Tyr Val Ala Asp Asp
130         135         140
Leu Ile Gln His Asn His Glu Ile Gly Gln Gly Ser Ala Ala Tyr Lys
145         150         155         160
Asn Tyr Val Ala Glu Tyr Ser Val Thr Phe Asp Phe Val Phe Gln Leu
165         170         175
Leu Gly Gln Gly Asn Tyr Val Val Ser Tyr Gly Gln Thr Gln Ile Asp
180         185         190
Gly Val Ala Tyr Ala Gln Tyr Asp Ile Phe Arg Leu Glu Asn Gly Lys
195         200         205
Ile Val Glu His Trp Asp Asn Lys Glu Val Met Pro Lys Val Glu Asp
210         215         220
Leu Thr Asn Arg Gly Lys Phe
225         230

```

(2) INFORMATION FOR SEQ ID NO:3301:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 165 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...165

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3301:

Phe	Ser	Ser	Leu	Ile	Lys	Glu	Ala	Glu	Asn	Glu	Leu	Gln	Arg	Ser	Ile
1			5					10						15	
Arg	Cys	Thr	Ile	Ile	Leu	Ser	Leu	Val	Leu	Ile	Ser	Leu	Ala	His	Ser
		20						25					30		
Phe	Gly	Ser	Val	Ser	Ile	Ile	Ala	His	Thr	Ile	His	Gln	Lys	Phe	Asn
	35						40					45			
Leu	Lys	Val	Pro	Asn	Tyr	Arg	Gln	Glu	Glu	Asp	Trp	Ala	Arg	Met	Gly
	50					55				60					
Leu	Pro	Ile	Thr	Arg	Lys	Glu	Ile	Ser	Asn	Trp	His	Ile	Lys	Ala	Ser
65					70					75					80
Gln	Tyr	Tyr	Leu	Glu	Ser	Leu	Tyr	Asn	Leu	Leu	Arg	Glu	Lys	Leu	Leu
			85					90					95		
Glu	Gln	Pro	Leu	Leu	His	Ala	Asp	Glu	Thr	Ser	Tyr	Arg	Val	Leu	Glu
		100						105					110		
Ser	Asp	Ser	His	Leu	Thr	Tyr	Tyr	Trp	Thr	Phe	Leu	Ser	Gly	Lys	Ala
	115						120					125			
Glu	Asn	Gln	Ala	Ile	Thr	Leu	Tyr	His	His	Asp	Gln	Arg	Arg	Ser	Gly
	130					135				140					
Leu	Val	Val	Gln	Glu	Phe	Leu	Gly	Asp	Tyr	Ser	Gly	Tyr	Val	His	Cys
145					150					155					160
Asp	Met	Leu	Arg	Gln											
				165											

(2) INFORMATION FOR SEQ ID NO:3302:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 191 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...191

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3302:

Thr	Tyr	Ser	Leu	Ile	Cys	Leu	Gln	Gly	Gly	Asn	Met	Gln	Glu	Ser	Asn
1				5					10					15	
Lys	Arg	Leu	Lys	Thr	Lys	Arg	Thr	Ile	Glu	Asn	Ala	Met	Val	Gln	Leu
			20					25					30		
Leu	Met	Glu	Gln	Pro	Phe	Asp	Lys	Ile	Ser	Thr	Val	Lys	Leu	Val	Glu
		35					40					45			
Lys	Ala	Gly	Ile	Ser	Arg	Ser	Ser	Phe	Tyr	Thr	His	Tyr	Lys	Asp	Lys
	50					55					60				
Tyr	Asp	Met	Ile	Glu	His	Tyr	Gln	Ser	Lys	Leu	Phe	His	Thr	Phe	Glu
65					70					75					80
Tyr	Ile	Phe	Gln	Lys	His	Ala	His	His	Lys	Arg	Asp	Ala	Ile	Leu	Glu
			85						90					95	
Val	Phe	Glu	Tyr	Leu	Glu	Ser	Glu	Pro	Leu	Leu	Ala	Val	Leu	Leu	Ser
			100					105					110		
Glu	Asn	Gly	Thr	Lys	Glu	Ile	Gln	Asn	Phe	Leu	Arg	Asn	Lys	Leu	His
		115					120					125			
Ile	Met	Leu	Ser	Thr	Asp	Leu	Gln	Lys	Arg	Phe	Met	Gln	Leu	Asn	Leu
	130					135					140				
Asn	Thr	Thr	Glu	Leu	Glu	Tyr	Ser	Ser	Ile	Tyr	Leu	Thr	His	Ala	Leu
145					150					155					160
Phe	Gly	Val	Cys	Gln	Thr	Trp	Ile	Ala	His	Gly	Lys	Lys	Glu	Ser	Ser
			165						170					175	
Gln	Glu	Ile	Thr	Asp	Phe	Leu	Met	Lys	Met	Leu	Gly	Asp	Thr	Asn	
			180					185					190		

(2) INFORMATION FOR SEQ ID NO:3303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...75

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3303:

Met	Phe	Leu	His	His	Phe	Thr	Glu	Ile	Tyr	Asp	Thr	Phe	Ala	Pro	Phe
1				5					10					15	
Leu	Pro	Leu	Leu	Ser	Lys	Gln	Lys	Asn	Arg	Lys	Pro	Glu	Pro	Ala	Val
			20					25					30		
Lys	Glu	Gln	Phe	Arg	Lys	Phe	Pro	Phe	Tyr	Leu	Phe	Asn	Cys	Asn	Gln
		35				40						45			
Ala	Ile	Trp	Leu	Tyr	Cys	Glu	Leu	Trp	Leu	Val	Cys	His	Ala	Thr	Val
	50					55					60				

Trp Phe Glu Val Val Pro Ala Cys Ser Val Arg
65 70 75

(2) INFORMATION FOR SEQ ID NO:3304:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 65 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...65
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3304:

Ile Leu Leu Gln Thr Val Lys Glu Asn Val Leu Arg Leu Arg Phe Gly
1 5 10 15
Leu Asp Asp Gly Lys Met Arg Thr Leu Glu Asp Val Gly Lys Val Phe
20 25 30
Asn Val Thr Arg Glu Arg Ile Arg Gln Ile Glu Ala Lys Ala Leu Arg
35 40 45
Lys Leu Arg Gln Pro Ser Arg Ser Lys Pro Leu Arg Asp Phe Ile Glu
50 55 60
Asp
65

(2) INFORMATION FOR SEQ ID NO:3305:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 344 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...344
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3305:

Ile Gly Ser Leu Thr Ile Ile Leu Leu Lys Gln Val Thr Leu Lys Arg
1 5 10 15
Asn Arg Leu Arg Lys Gln Phe Ser Ile Lys Thr Ser Val Arg Leu Ser

(A) NAME/KEY: misc_feature
(B) LOCATION 1...109

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3306:

Gly	Gly	Ser	Leu	Met	Ile	Gln	Pro	Ala	Ser	Leu	Glu	Glu	Leu	Ala	Ser
1				5					10					15	
Leu	Val	Glu	Lys	Asp	Gly	Lys	Lys	Val	Phe	Leu	Phe	Val	Ala	Asp	Trp
			20					25					30		
Cys	Gly	Asp	Cys	Arg	Tyr	Ile	Tyr	Pro	Ala	Leu	Pro	Glu	Ile	Glu	Glu
		35					40					45			
Ser	Asn	Pro	Glu	Phe	Thr	Phe	Ile	Arg	Val	Asp	Arg	Asp	Gln	Tyr	Ile
	50					55				60					
Asp	Leu	Ala	Lys	Leu	Trp	Asp	Val	Tyr	Gly	Ile	Pro	Ser	Leu	Val	Val
65					70				75					80	
Leu	Glu	Lys	Asp	Lys	Glu	Ile	Gly	Arg	Phe	Val	Asn	Arg	Asp	Arg	Lys
			85					90					95		
Ser	Lys	Gln	Gln	Ile	Asn	Asp	Phe	Leu	Ala	Gly	Leu	Lys			
			100					105							

(2) INFORMATION FOR SEQ ID NO:3307:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3307:

Lys	Leu	Leu	Gln	Cys	Arg	Lys	Arg	Lys	Glu	Ala	Leu	Met	Thr	Ser	Leu
1				5					10					15	
Tyr	Asp	Phe	Ser	Val	Leu	Asn	Gln	Asn	Asn	Gln	Ala	Thr	Pro	Leu	Asp
			20					25					30		
Ser	Tyr	Arg	Gly	Lys	Val	Leu	Leu	Ile	Val	Asn	Thr	Ala	Thr	Gly	Cys
		35					40					45			
Gly	Leu	Thr	Pro	Gln	Tyr	Gln	Gly	Leu	Gln	Glu	Leu	Tyr	Glu	Arg	Tyr
	50					55				60					
Gln	Asp	Gln	Gly	Phe	Glu	Ile	Leu	Asp	Phe	Pro	Cys	Asn	Gln	Phe	Met
65					70				75					80	
Gly	Gln	Ala	Pro	Gly	Ser	Ala	Glu	Glu	Ile	Asn	Ala	Phe	Cys	Ser	Leu
			85					90					95		
His	Phe	Gln	Thr	Thr	Phe	Pro	Arg	Phe	Ala	Lys	Ile	Lys	Val	Asn	Gly
		100						105					110		
Lys	Glu	Ala	Asp	Pro	Leu	Tyr	Val	Trp	Leu	Lys	Asp	His	Lys	Ser	Gly
		115					120					125			
Pro	Leu	Gly	Lys	Arg	Ile	Glu	Trp	Asn	Phe	Ala	Lys	Phe	Leu	Ile	Ser

130		135		140
Arg Asp Gly Gln Val Phe Glu Arg Phe Ser Ser Lys Thr Asp Pro Lys				
145		150		155
Gln Ile Glu Glu Ala Ile Gln Thr Leu Leu				160
	165		170	

(2) INFORMATION FOR SEQ ID NO:3308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...331

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3308:

Ser	Leu	Ser	Leu	Cys	Ala	Tyr	Ala	Leu	Asn	Gln	His	Arg	Ala	Gln	Glu
1			5						10					15	
Asn	Lys	Asp	Asn	Asn	Arg	Val	Ser	Tyr	Val	Asp	Gly	Ser	Gln	Ser	Ser
			20					25					30		
Gln	Lys	Ser	Glu	Asn	Leu	Thr	Pro	Asp	Gln	Val	Ser	Gln	Lys	Glu	Gly
			35				40					45			
Ile	Gln	Ala	Glu	Gln	Ile	Val	Ile	Lys	Ile	Thr	Asp	Gln	Gly	Tyr	Val
			50			55				60					
Thr	Ser	His	Gly	Asp	His	Tyr	His	Tyr	Tyr	Asn	Gly	Lys	Val	Pro	Tyr
65					70				75					80	
Asp	Ala	Leu	Phe	Ser	Glu	Glu	Leu	Leu	Met	Lys	Asp	Pro	Asn	Tyr	Gln
				85				90						95	
Leu	Lys	Asp	Ala	Asp	Ile	Val	Asn	Glu	Val	Lys	Gly	Gly	Tyr	Ile	Ile
			100					105					110		
Lys	Val	Asp	Gly	Lys	Tyr	Tyr	Val	Tyr	Leu	Lys	Asp	Ala	Ala	His	Ala
			115				120					125			
Asp	Asn	Val	Arg	Thr	Lys	Asp	Glu	Ile	Asn	Arg	Gln	Lys	Gln	Glu	His
			130			135					140				
Val	Lys	Asp	Asn	Glu	Lys	Val	Asn	Ser	Asn	Val	Ala	Val	Ala	Arg	Ser
145					150					155				160	
Gln	Gly	Arg	Tyr	Thr	Thr	Asn	Asp	Gly	Tyr	Val	Phe	Asn	Pro	Ala	Asp
				165				170						175	
Ile	Ile	Glu	Asp	Thr	Gly	Asn	Ala	Tyr	Ile	Val	Pro	His	Gly	Gly	His
			180				185					190			
Tyr	His	Tyr	Ile	Pro	Lys	Ser	Asp	Leu	Ser	Ala	Ser	Glu	Leu	Ala	Ala
			195			200						205			
Ala	Lys	Ala	His	Leu	Ala	Gly	Lys	Asn	Met	Gln	Pro	Ser	Gln	Leu	Ser
			210			215				220					
Tyr	Ser	Ser	Thr	Ala	Ser	Asp	Asn	Asn	Thr	Gln	Ser	Val	Ala	Lys	Gly
225					230					235				240	
Ser	Thr	Ser	Lys	Pro	Ala	Asn	Lys	Ser	Glu	Asn	Leu	Gln	Ser	Leu	Leu

(2) INFORMATION FOR SEO ID NO:3309:

(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: YES

(A) ORGANISM: *Streptococcus pneumoniae*

(B) LOCATION 1...296

2297

	195					200				205					
Ile	Tyr	Glu	Glu	Tyr	Gln	Arg	Gly	Thr	Ile	Ser	Glu	Leu	Leu	Glu	Ser
	210					215					220				
Ile	Ala	Glu	Thr	Ser	Leu	Lys	Gly	Glu	Cys	Leu	Leu	Ile	Val	Glu	Gly
225					230					235					240
Ala	Ser	Gln	Asp	Val	Glu	Glu	Lys	Asp	Glu	Glu	Asp	Leu	Phe	Leu	Glu
				245					250					255	
Ile	Gln	Ala	Arg	Ile	Gln	Gln	Gly	Met	Lys	Lys	Asn	Gln	Ala	Ile	Lys
			260					265					270		
Glu	Val	Ala	Lys	Ile	Tyr	Gln	Trp	Asn	Lys	Ser	Gln	Leu	Tyr	Ala	Ala
		275					280					285			
Tyr	His	Asp	Trp	Glu	Glu	Lys	Gln								
	290					295									

(2) INFORMATION FOR SEQ ID NO:3310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...280

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3310:

Lys	Glu	Ser	Leu	Met	Thr	Val	Val	Lys	Val	Glu	Lys	Leu	Ser	Lys	Lys
1				5					10					15	
Ile	Lys	Asp	Lys	Glu	Ile	Leu	Arg	Asn	Ile	Ser	Phe	Glu	Ile	Asn	Asp
			20					25					30		
Gly	Glu	Cys	Val	Ala	Leu	Ile	Gly	Pro	Asn	Gly	Ala	Gly	Lys	Thr	Thr
		35					40					45			
Leu	Leu	Asp	Cys	Leu	Leu	Gly	Asp	Lys	Leu	Val	Thr	Ser	Gly	Gln	Val
	50					55				60					
Ser	Ile	Gln	Gly	Leu	Pro	Val	Thr	Ser	Ser	Lys	Leu	Asp	Tyr	Thr	Arg
65					70					75					80
Ala	Tyr	Leu	Pro	Gln	Glu	Asn	Ile	Ile	Val	Gln	Lys	Leu	Lys	Val	Lys
				85					90					95	
Glu	Leu	Ile	Ala	Phe	Phe	Gln	Arg	Ile	Tyr	Pro	Asn	Pro	Leu	Ser	Asn
			100					105					110		
Gln	Glu	Ile	Asp	Gln	Leu	Leu	Gln	Phe	Val	Lys	Gln	Gln	Lys	Glu	Gln
		115					120					125			
Leu	Ala	Glu	Lys	Leu	Ser	Gly	Gly	Gln	Lys	Arg	Leu	Phe	Ser	Phe	Ile
	130					135					140				
Leu	Thr	Leu	Ile	Gly	Arg	Pro	Lys	Ile	Val	Phe	Leu	Asp	Glu	Pro	Thr
145					150					155				160	
Ala	Ser	Met	Asp	Thr	Ser	Thr	Arg	Gln	Arg	Phe	Trp	Glu	Ile	Val	Gln
				165					170					175	

Glu	Leu	Lys	Ala	Gln	Gly	Val	Thr	Ile	Leu	Tyr	Ser	Ser	His	Tyr	Ile
			180					185					190		
Glu	Glu	Val	Glu	His	Thr	Ala	Asp	Arg	Ile	Leu	Leu	Leu	Asn	Lys	Gly
		195					200					205			
Glu	Leu	Ile	Arg	Asp	Thr	Thr	Pro	Leu	Ala	Met	Arg	Ser	Glu	Glu	Ile
		210				215					220				
Glu	Lys	His	Phe	Ile	Leu	Pro	Ile	Ala	Tyr	Lys	Glu	Val	Val	Glu	Gln
225					230					235					240
Ser	Asn	Leu	Val	Glu	Asn	Trp	Thr	Leu	Lys	Gln	Asp	Ser	Leu	Gln	Val
			245						250					255	
Val	Thr	Arg	Glu	Ala	Asp	Ala	Phe	Trp	Glu	Leu	Leu	Ala	Gln	Ala	Gly
			260					265					270		
Cys	Arg	Met	Gln	Arg	Asn	Arg	Ser								
		275					280								

(2) INFORMATION FOR SEQ ID NO:3311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...108

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3311:

Pro	Glu	Ile	Gln	Tyr	Trp	Leu	Gly	Gln	Phe	Ser	Arg	Gln	Lys	Glu	Gly
1			5					10					15		
Arg	Asp	Leu	Gln	Glu	Ile	Phe	Ala	Arg	Phe	Thr	Asn	Phe	Asn	Phe	Cys
		20					25					30			
Arg	Trp	Val	Thr	Ser	Gln	Val	Ala	Ile	Asp	Ser	Ser	His	Lys	Lys	Gln
		35				40						45			
Arg	Tyr	Lys	Val	Cys	Phe	Ser	Asp	Ala	Ala	Tyr	Ala	Cys	Arg	Leu	Phe
		50				55				60					
Phe	Asn	Gly	Ser	Leu	Ser	Ser	Leu	Gln	Leu	Lys	Asn	Tyr	Leu	Lys	Lys
65				70					75					80	
Gln	Leu	Ser	Ile	Ile	Arg	Pro	Asn	Arg	Lys	Tyr	Ser	Arg	Lys	Ile	Lys
			85				90						95		
Ala	Gln	Ser	Val	Val	Asp	Phe	Ile	Tyr	Arg	Val	Thr				
			100				105								

(2) INFORMATION FOR SEQ ID NO:3312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...64
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3312:

Ala	Glu	Ile	Gln	Glu	Met	Arg	Glu	Asp	Phe	Tyr	Glu	Lys	Val	Ser	Thr
1				5					10					15	
Ser	Ile	Gln	Asn	Lys	Cys	Ser	Leu	Leu	Leu	Leu	Ile	Phe	Arg	Ile	Trp
		20						25					30		
Ser	Phe	Ser	Ala	Asp	Ala	Tyr	Arg	Pro	Lys	Leu	Leu	Ala	Ile	Phe	Phe
		35					40					45			
Pro	Asp	Trp	Gln	Phe	Arg	Leu	Asp	Ser	Lys	Tyr	Leu	Glu	Phe	Thr	Ile
	50					55					60				

(2) INFORMATION FOR SEQ ID NO:3313:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 172 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...172
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3313:

Arg	Arg	Ile	His	Met	Ser	Leu	Leu	Asp	Ile	Ala	Lys	Ser	Ile	Lys	Lys
1				5					10					15	
Glu	Gly	Phe	Asp	Pro	Arg	Lys	Asp	Ser	Ala	Asn	Gly	Pro	Ala	Pro	Ile
		20						25					30		
Pro	Ala	Gly	Thr	Tyr	Pro	Val	Val	Leu	Lys	Lys	Ala	Thr	Phe	Asn	Val
		35					40					45			
Ser	Asp	Lys	Gly	Trp	Glu	Ser	Leu	Gly	Tyr	Gln	Phe	Glu	Ile	Arg	Gly
	50					55					60				
Gly	Asp	Tyr	Ser	Gly	Arg	Ser	Glu	Phe	Ala	Thr	Phe	Gly	Thr	Leu	Thr
65					70				75					80	
Glu	Trp	Asn	Gly	Lys	Asn	Leu	Asp	Trp	Ala	Val	Glu	Arg	Thr	Met	Lys
			85						90					95	
Phe	Phe	Ile	Lys	Ala	Leu	Val	Leu	Ala	Gly	Asp	Ser	Met	Gln	Gly	Asn
			100					105					110		

Glu	Glu	Asp	Gly	Lys	Ala	Leu	Glu	Glu	Ala	Leu	Gln	Arg	Lys	Ala	Val
		115					120					125			
Gly	Ser	Tyr	Tyr	Asn	Leu	Val	Ile	Ser	Val	Thr	Lys	Gly	Lys	Asp	Gly
		130				135					140				
Arg	Glu	Phe	Arg	Asn	Tyr	Asp	Leu	Glu	Glu	Glu	Ala	Gln	Pro	Leu	
145					150					155				160	
Thr	Glu	Ala	Asp	Ile	Asp	Glu	Asp	Asp	Leu	Pro	Phe				
			165						170						

(2) INFORMATION FOR SEQ ID NO:3314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...132

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3314:

Ser	Cys	Ser	His	Leu	Ile	Ser	Ile	His	Tyr	Arg	Arg	Arg	Lys	Arg	Met
1				5					10					15	
Ile	Leu	Arg	His	Leu	Gly	Ile	Ser	Pro	Thr	Asn	Asp	Leu	Val	Ala	Lys
			20					25					30		
Lys	Ile	Phe	Ser	Asn	Pro	Glu	Ile	Thr	Cys	Gln	Phe	Ile	Arg	Asp	Met
		35				40						45			
Leu	Asp	Leu	Pro	Ala	Lys	Asn	Val	Thr	Ile	Leu	Glu	Gly	Ser	Asn	Ile
	50					55					60				
His	Val	Leu	Pro	Ser	Met	Pro	Tyr	Ser	Val	Gln	Asp	Phe	Tyr	Thr	Ser
65				70						75				80	
Ile	Asp	Val	Leu	Ala	Glu	Leu	Asp	Asn	Gly	Thr	Gln	Val	Ile	Ile	Glu
			85						90					95	
Ile	Gln	Val	His	His	Gln	Asn	Phe	Phe	Ile	Asn	His	Leu	Trp	Ala	Tyr
			100					105					110		
Leu	Cys	Ser	Gln	Val	Asn	Gln	Asn	Leu	Glu	Lys	Ile	His	Gln	Arg	Glu
		115					120					125			
Gly	Asp	Thr	His												
		130													

(2) INFORMATION FOR SEQ ID NO:3315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3315:

```
Phe Ile Ser His Lys Val Glu Val Phe Tyr His Ile Val Phe Thr Pro
1           5           10           15
Lys Tyr Arg Arg Lys Val Ile Tyr Asn Gln Tyr Arg Ser Ser Leu Gly
          20           25           30
Glu Ile Phe His Arg Leu Cys Ser Tyr Lys Gly Val Glu Met Ile Glu
          35           40           45
Gly His Leu Met Pro Asp His Val His Met Leu Val Ser Ile Pro Ser
          50           55           60
Arg Leu Ser Val Ser Ser Phe Met Gly Tyr Leu Lys Gly Lys Ser Ala
65          70           75           80
Leu Met Met Phe Asp Lys His Ala Asn Leu Lys Tyr Lys Phe Gly Asn
          85           90           95
Arg His Phe Trp Ala Glu Gly Tyr Tyr Val Ser Pro Val Gly Leu Asn
          100          105          110
Glu Ala Thr Ile Lys Lys Tyr Ser Gln Asp
          115          120
```

(2) INFORMATION FOR SEQ ID NO:3316:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 104 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3316:

```
Gly Leu Ser His Ile Thr Gln Lys Lys Lys Glu Gln Lys Glu Ser Gln
1           5           10           15
Thr Met Ala Ser Lys Asp Phe His Val Val Ala Glu Thr Gly Ile His
          20           25           30
Ala Arg Pro Ala Thr Leu Leu Val Gln Thr Ala Ser Lys Phe Ala Ser
          35           40           45
Asp Ile Thr Leu Glu Tyr Lys Gly Lys Ser Val Asn Leu Lys Ser Ile
          50           55           60
Met Gly Val Met Ser Leu Gly Val Gly Gln Gly Ala Asp Val Thr Ile
```

65		70		75		80								
Ser	Ala	Glu	Gly	Ala	Asp	Ala	Asp	Ala	Ile	Ala	Ala	Ile	Ser	Glu
			85					90					95	
Thr	Met	Glu	Lys	Glu	Gly	Leu	Ala							
			100											

(2) INFORMATION FOR SEQ ID NO:3317:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 82 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...82

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3317:

Pro	His	Gly	Leu	His	Gly	Asn	Glu	Pro	Ser	Pro	Leu	Pro	Trp	Met	Asn
1				5					10					15	
Lys	Lys	Thr	Leu	Pro	Asn	Asn	Pro	Ala	Thr	Ser	Lys	Asp	Ser	His	Gly
			20					25					30		
Val	Ala	Ala	Pro	Asn	Cys	Ser	Ala	Asn	Ser	Arg	Leu	Lys	Thr	Thr	Pro
			35				40					45			
Glu	Lys	Ala	Pro	Ile	Thr	Ile	Ile	Pro	Ser	Arg	Pro	Thr	Phe	Thr	Thr
			50			55					60				
Pro	Pro	Arg	Ser	Glu	Lys	Thr	Pro	Pro	Ile	Leu	Val	Lys	Met	Arg	Gly
65					70					75					80
Ala	Glu														

(2) INFORMATION FOR SEQ ID NO:3318:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 328 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...328

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3318:

Phe	Phe	Thr	Gln	Ser	Leu	His	Glu	Ser	Gly	Ile	Asn	Leu	Tyr	Lys	Asp
1				5					10					15	
Leu	Leu	Asp	Tyr	Lys	Cys	Ser	Lys	Pro	Thr	Gln	Glu	Lys	Tyr	Ile	Glu
			20					25					30		
Ile	Lys	Val	Ile	Ile	Met	Lys	Phe	Lys	Lys	Met	Leu	Thr	Leu	Ala	Ala
		35					40					45			
Ile	Gly	Leu	Ser	Gly	Phe	Gly	Leu	Val	Ala	Cys	Gly	Asn	Gln	Ser	Ala
	50					55					60				
Ala	Ser	Lys	Gln	Ser	Ala	Ser	Gly	Thr	Ile	Glu	Val	Ile	Ser	Arg	Glu
65					70					75				80	
Asn	Gly	Ser	Gly	Thr	Arg	Gly	Ala	Phe	Thr	Glu	Ile	Thr	Gly	Ile	Leu
				85					90					95	
Lys	Lys	Asp	Gly	Asp	Lys	Lys	Ile	Asp	Asn	Thr	Ala	Lys	Thr	Ala	Val
			100					105					110		
Ile	Gln	Asn	Ser	Thr	Glu	Gly	Val	Leu	Ser	Ala	Val	Gln	Gly	Asn	Ala
		115					120					125			
Asn	Ala	Ile	Gly	Tyr	Ile	Ser	Leu	Gly	Ser	Leu	Thr	Lys	Ser	Val	Lys
	130					135					140				
Ala	Leu	Glu	Ile	Asp	Gly	Val	Lys	Ala	Ser	Arg	Asp	Thr	Val	Leu	Asp
145					150					155				160	
Gly	Glu	Tyr	Pro	Leu	Gln	Arg	Pro	Phe	Asn	Ile	Val	Trp	Ser	Ser	Asn
				165					170					175	
Leu	Ser	Lys	Leu	Gly	Gln	Asp	Phe	Ile	Ser	Phe	Ile	His	Ser	Lys	Gln
			180					185					190		
Gly	Gln	Gln	Val	Val	Thr	Asp	Asn	Lys	Phe	Ile	Glu	Ala	Lys	Thr	Glu
		195					200					205			
Thr	Thr	Glu	Tyr	Thr	Ser	Gln	His	Leu	Ser	Gly	Lys	Leu	Ser	Val	Val
	210					215					220				
Gly	Ser	Thr	Ser	Val	Ser	Ser	Leu	Met	Glu	Lys	Leu	Ala	Glu	Ala	Tyr
225					230					235				240	
Lys	Lys	Glu	Asn	Pro	Glu	Val	Thr	Ile	Asp	Ile	Thr	Ser	Asn	Gly	Ser
				245					250					255	
Ser	Ala	Gly	Ile	Thr	Ala	Val	Lys	Glu	Lys	Thr	Ala	Asp	Ile	Gly	Met
		260					265					270			
Val	Ser	Arg	Glu	Leu	Thr	Pro	Glu	Glu	Gly	Lys	Ser	Leu	Thr	His	Asp
		275					280					285			
Ala	Ile	Ala	Leu	Asp	Gly	Ile	Ala	Val	Val	Val	Asn	Asn	Asp	Asn	Lys
	290					295					300				
Ala	Ser	Gln	Val	Ser	Met	Ala	Glu	Leu	Ala	Asp	Val	Phe	Ser	Gly	Lys
305					310					315				320	
Leu	Thr	Thr	Trp	Asp	Lys	Ile	Lys								
				325											

(2) INFORMATION FOR SEQ ID NO:3319:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3319:

```
Leu Arg Thr His Gln Lys Asn Gln Val Thr Lys Asn His Leu Leu Gln
1          5          10          15
Asn Gln Val Cys Asn Gln Val Leu Asn Gln Arg Leu Asn Arg Ser Trp
          20          25          30
Lys Asn Gln Asn Gln Arg Leu Asn Arg Asn Gln Lys Asn Gln Asn Gln
          35          40          45
Arg Leu Asn Arg Ser Arg Lys Asn Gln Asn Gln Arg Leu Asn Arg Ser
          50          55          60
Arg Lys Asn Gln Asn Gln Arg Leu Asn Arg Ser Arg Lys Asn Gln Asn
65          70          75          80
Gln Arg Leu Asn Arg Ser Arg Lys Asn Gln Asn Gln Arg Leu Asn Arg
          85          90          95
Ser Arg Lys Asn Gln Asn Gln Arg Leu Asn Arg Ser Arg Lys Asn Gln
          100          105          110
Asn Gln Arg Leu Asn Arg Ser Arg Lys Asn Gln Asn Gln Arg Leu Asn
          115          120          125
Arg Ser Arg Lys Asn Gln Asn Gln Arg Leu Asn Arg Ser Arg Lys Asn
          130          135          140
Gln Asn Gln Arg Leu Asn Arg Asn Gln Lys Asn Gln Asn Gln Arg Leu
145          150          155          160
Asn Arg Asn Gln Lys Asn Gln Asn Gln Ile Ile Ala Ser His Lys Gln
          165          170          175
Met Ile Arg Ser His Gln Leu Gln Ile Ile
          180          185
```

(2) INFORMATION FOR SEQ ID NO:3320:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 144 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...144

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3320:

```
Pro Lys Ala His Ile Lys Leu Leu Ala Asn Gln Gln Lys His Ser Asp
1          5          10          15
Ala Gly Ala Thr Ile Glu Asp Glu Tyr Tyr Val Phe Ile Ala Glu Ser
          20          25          30
```


Lys	Ile	Asp	Gly	Lys	Lys	Glu	Val	Ile	Gln	Cys	Cys	Met	Gly	Ala	Ala
	35						40					45			
Arg	Asp	Phe	Leu	Glu	Leu	Ile	Asn	His	Lys	Gly	Leu	Pro	Phe	Phe	Asn
	50					55					60				
Pro	Leu	Val	Gly	Asp	Ser	His	Val	Asn	Asn	Arg	Gln	Glu	Tyr	Asp	Asn
65					70					75					80
Thr	Gly	Ser	Gly	Asn	Leu	Gln	Pro	Glu	Lys	Trp	Asn	Glu	Thr	Ala	Gln
				85					90					95	
Gln	Leu	Tyr	Asn	Ala	Ile	Met	Trp	Leu	Ile	Ile	Leu	Trp	Asn	Ala	Lys
			100					105					110		
Pro	Asp	Thr	Pro	Leu	Phe	Ile	Phe	Lys	Asp	Glu	Val	Ile	Lys	Tyr	Lys
		115					120					125			
Thr	Tyr	Glu	Pro	Phe	Glu	Ser	Ser	Ile	Lys	Leu	Val	Ser	Ile	Asn	Glu
	130					135					140				

(2) INFORMATION FOR SEQ ID NO:3321:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3321:

Lys	Met	Ala	His	Leu	Leu	Glu	Lys	Thr	Arg	Lys	Ile	Thr	Ser	Ile	Leu
1			5						10					15	
Lys	Arg	Ser	Glu	Gln	Leu	Gln	Asp	Glu	Leu	Pro	Tyr	Asn	Ala	Ile	
		20					25					30			
Thr	Arg	Gln	Leu	Ala	Asp	Ile	Ile	His	Cys	Asn	Ala	Cys	Ile	Ile	Asn
	35					40						45			
Ser	Lys	Gly	Arg	Leu	Leu	Gly	Tyr	Phe	Met	Arg	Tyr	Lys	Thr	Asn	Thr
	50					55					60				
Asp	Arg	Val	Lys	Gln	Phe	Phe	Gln	Thr	Lys	Ile	Phe	Pro	Asp	Asp	Tyr
65				70					75						80
Val	Gln	Gly	Ala	Asn	Met	Ile	Tyr	Glu	Thr	Glu	Ala	Asn	Leu	Pro	Val
			85						90					95	
Glu	His	Asp	Met	Ser	Ile	Phe	Pro	Val	Glu	Ser	Arg	Asp	Asp	Phe	Pro
		100						105					110		
Asp	Gly	Leu	Thr	Thr	Ile	Ala	Pro	Ile	His	Val	Ser	Gly	Ile	Arg	Leu
	115					120						125			
Gly	Ser	Leu	Ile	Ile	Trp	Arg	Asn	Asp	Lys	Lys	Phe	Glu	Asp	Glu	Asp
	130					135					140				
Leu	Val	Leu	Val	Glu	Ile	Ala	Ser	Thr	Val	Val	Gly	Ile	Gln	Leu	Leu
145					150					155					160
Asn	Phe	Gln	Arg	Glu	Asp	Glu	Lys	Asn	Ile	Arg	Arg	Arg	Thr	Ala	
			165					170					175		

Val Thr Met Ala Val Asn Thr Leu Ser Tyr Ser Glu Leu Arg Ala Val
180 185 190

(2) INFORMATION FOR SEQ ID NO:3322:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 191 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...191
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3322:

```

Ile Ile Gln Gln Asn Lys Lys Leu Val Lys Gln Lys Glu Glu Leu Phe
1      5      10      15
Trp Glu Ser Leu Lys Lys Trp Tyr Asn Glu Lys Lys Thr Ile Arg Arg
20      25      30
Glu Arg Met Arg Cys Pro Lys Cys Gly Ala Thr Lys Ser Ser Val Ile
35      40      45
Asp Ser Arg Gln Ala Glu Glu Gly Asn Thr Ile Arg Arg Arg Arg Glu
50      55      60
Cys Asp Glu Cys Gln His Arg Phe Thr Thr Tyr Glu Arg Val Glu Glu
65      70      75      80
Arg Thr Leu Val Val Val Lys Lys Asp Gly Thr Arg Glu Gln Phe Ser
85      90      95
Arg Asp Lys Ile Phe Asn Gly Ile Ile Arg Ser Ala Gln Lys Arg Pro

100      105      110
Val Ser Ser Asp Glu Ile Asn Met Val Val Asn Arg Ile Glu Gln Lys
115      120      125
Leu Arg Gly Arg Asn Glu Asn Glu Ile Gln Ser Glu Asp Ile Gly Ser
130      135      140
Leu Val Met Glu Glu Leu Ala Glu Leu Asp Glu Ile Thr Tyr Val Arg
145      150      155      160
Phe Ala Ser Val Tyr Arg Ser Phe Lys Asp Val Ser Glu Leu Glu Ser
165      170      175
Leu Leu Gln Gln Ile Thr Gln Ser Ser Lys Lys Lys Lys Glu Arg
180      185      190

```

(2) INFORMATION FOR SEQ ID NO:3323:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 710 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...710

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3323:

Leu	Ser	Lys	Gln	Lys	Glu	Val	Lys	Asn	Met	Asn	Asn	Asn	Phe	Asn	Asn
1				5				10						15	
Phe	Asn	Asn	Met	Asp	Asp	Leu	Phe	Asn	Gln	Leu	Met	Gly	Gly	Met	Arg
			20					25					30		
Gly	Tyr	Ser	Ser	Glu	Asn	Arg	Arg	Tyr	Leu	Ile	Asn	Gly	Arg	Glu	Val
		35					40					45			
Thr	Pro	Glu	Glu	Phe	Ala	His	Tyr	Arg	Ala	Thr	Gly	Gln	Leu	Pro	Gly
	50					55					60				
Asn	Ala	Glu	Thr	Asp	Val	Gln	Met	Pro	Gln	Gln	Ala	Ser	Gly	Met	Lys
65					70					75					80
Gln	Asp	Gly	Val	Leu	Ala	Lys	Leu	Gly	Arg	Asn	Leu	Thr	Ala	Glu	Ala
				85					90					95	
Arg	Glu	Gly	Lys	Leu	Asp	Pro	Val	Ile	Gly	Arg	Asn	Lys	Glu	Ile	Gln
			100					105					110		
Glu	Thr	Ser	Glu	Ile	Leu	Ser	Arg	Arg	Thr	Lys	Asn	Asn	Pro	Val	Leu
		115					120					125			
Val	Gly	Asp	Ala	Gly	Val	Gly	Lys	Thr	Ala	Val	Val	Glu	Gly	Leu	Ala
	130					135					140				
Gln	Ala	Ile	Val	Asn	Gly	Asp	Val	Pro	Ala	Ala	Ile	Lys	Asn	Lys	Glu
145					150					155					160
Ile	Ile	Ser	Ile	Asp	Ile	Ser	Gly	Leu	Glu	Ala	Gly	Thr	Gln	Tyr	Arg
				165					170					175	
Gly	Ser	Phe	Glu	Glu	Asn	Val	Gln	Asn	Leu	Val	Asn	Glu	Val	Lys	Glu
		180					185						190		
Ala	Gly	Asn	Ile	Ile	Leu	Phe	Phe	Asp	Glu	Ile	His	Gln	Ile	Leu	Gly
		195					200					205			
Ala	Gly	Ser	Thr	Gly	Gly	Asp	Ser	Gly	Ser	Lys	Gly	Leu	Ala	Asp	Ile
	210					215					220				
Leu	Lys	Pro	Ala	Leu	Ser	Arg	Gly	Glu	Leu	Thr	Val	Ile	Gly	Ala	Thr
225					230					235					240
Thr	Gln	Asp	Glu	Tyr	Arg	Asn	Thr	Ile	Leu	Lys	Asn	Ala	Ala	Leu	Ala
				245					250					255	
Arg	Arg	Phe	Asn	Glu	Val	Lys	Val	Asn	Ala	Pro	Ser	Ala	Glu	Asn	Thr
			260					265					270		
Phe	Asn	Ile	Leu	Gln	Gly	Ile	Arg	Asp	Leu	Tyr	Gln	Gln	His	His	Asn
		275					280					285			
Val	Ile	Leu	Pro	Asp	Glu	Val	Leu	Lys	Ala	Ala	Val	Asp	Tyr	Ser	Val
	290					295					300				
Gln	Tyr	Ile	Pro	Gln	Arg	Ser	Leu	Pro	Asp	Lys	Ala	Ile	Asp	Leu	Val
305					310					315					320
Asp	Val	Thr	Ala	Ala	His	Leu	Ala	Ala	Gln	His	Pro	Val	Thr	Asp	Val
				325					330					335	
His	Ala	Val	Glu	Arg	Glu	Ile	Glu	Thr	Glu	Lys	Asp	Lys	Gln	Glu	Lys
			340					345					350		
Ala	Val	Glu	Ala	Glu	Asp	Phe	Glu	Ala	Ala	Leu	Asn	Tyr	Lys	Thr	Arg

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3324:

```
Ile Tyr Lys His Ile Ala Pro Val Tyr Val Ile Ala Ile Val Asp Ser
1           5           10           15
Asn Tyr Phe Ser Asp Asp Leu Ala Phe His Ser Phe Ser Met Arg Glu
          20           25           30
Asp Thr Thr Gly Glu Val Leu Ala Ile Thr Asn Asn Gly Gln Glu Asn
          35           40           45
His Leu Val Lys Met Ala Phe Leu Glu Leu Lys Asn Thr Glu Lys Pro
          50           55           60
Ala Lys Thr Arg Phe Ala Ser His Gly Trp Ser Phe Ser Ala Thr Ser
65           70           75           80
Pro Leu Pro Ser Asn Arg Asn Glu Pro Leu Ala Lys Gln Ile Asn Cys
          85           90           95
Trp Thr Thr Arg Ala Gly Pro Arg Arg Thr Gly Lys Cys Leu Val Asn
          100          105          110
Tyr Ile Cys Glu Lys Asn Lys Ser Cys
          115          120
```

(2) INFORMATION FOR SEQ ID NO:3325:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 174 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3325:

```
Cys Ser Lys His Arg Phe Glu Val Ala Asp Arg Thr Asp Glu Val Ser
1           5           10           15
Ser Lys His Arg Phe Glu Val Ala Asp Arg Thr Asp Glu Val Ser Ser
          20           25           30
Lys His Arg Phe Glu Val Ala Asp Arg Thr Asp Glu Val Ser Ser Lys
          35           40           45
His Arg Phe Glu Val Ala Asp Arg Thr Asp Glu Val Ser Ser Lys His
          50           55           60
Arg Phe Glu Val Ala Asp Arg Thr Asp Glu Val Ser Ser Lys His Arg
65           70           75           80
```

Phe	Glu	Val	Ala	Asp	Arg	Thr	Asp	Glu	Val	Ser	Ser	Lys	His	Arg	Phe
				85					90					95	
Glu	Val	Ala	Asp	Arg	Thr	Asp	Glu	Val	Ser	Ser	Lys	His	Arg	Phe	Glu
			100					105					110		
Val	Ala	Asp	Arg	Thr	Asp	Glu	Val	Ser	Ser	Lys	His	Arg	Phe	Glu	Val
		115					120					125			
Ala	Asp	Arg	Thr	Asp	Glu	Val	Ser	Ser	Lys	His	Arg	Phe	Glu	Val	Ala
	130					135					140				
Asp	Arg	Thr	Asp	Glu	Val	Ser	Ser	Lys	His	Arg	Phe	Glu	Val	Ala	Asp
145					150					155				160	
Arg	Thr	Asp	Glu	Val	Ser	Asn	Ile	Tyr	Thr	Ala	Arg	Arg	Ser		
				165					170						

(2) INFORMATION FOR SEQ ID NO:3326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...235

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3326:

Met	Thr	Lys	Gln	Val	Leu	Leu	Val	Asp	Asp	Glu	Glu	His	Ile	Leu	Lys
1			5						10					15	
Leu	Leu	Asp	Tyr	His	Leu	Ser	Lys	Glu	Gly	Phe	Ser	Thr	Gln	Leu	Val
		20						25					30		
Thr	Asn	Gly	Arg	Lys	Ala	Leu	Ala	Glu	Thr	Glu	Pro	Phe	Asp		
	35					40				45					
Phe	Ile	Leu	Leu	Asp	Ile	Met	Leu	Pro	Gln	Leu	Asp	Gly	Met	Glu	Val
50					55				60						
Cys	Lys	Arg	Leu	Arg	Ala	Lys	Gly	Val	Lys	Thr	Pro	Ile	Met	Met	Val
65				70					75					80	
Ser	Ala	Lys	Ser	Asp	Glu	Phe	Asp	Lys	Val	Leu	Ala	Leu	Glu	Leu	Gly
			85					90					95		
Ala	Asp	Asp	Tyr	Leu	Thr	Lys	Pro	Phe	Ser	Pro	Arg	Glu	Leu	Leu	Ala
		100						105					110		
Arg	Val	Lys	Ala	Val	Leu	Arg	Arg	Thr	Lys	Gly	Glu	Gln	Glu	Gly	Asp
		115				120						125			
Asp	Ser	Asp	Asn	Ile	Ala	Asp	Asp	Ser	Trp	Leu	Phe	Gly	Thr	Leu	Lys
130					135						140				
Val	Tyr	Pro	Glu	Arg	His	Glu	Val	Tyr	Lys	Ala	Asn	Lys	Leu	Leu	Ser
145				150					155					160	
Leu	Thr	Pro	Lys	Glu	Phe	Glu	Leu	Leu	Leu	Tyr	Leu	Met	Lys	His	Pro
			165					170					175		
Asn	Met	Thr	Leu	Thr	Arg	Glu	Arg	Leu	Leu	Glu	Arg	Ile	Trp	Gly	Tyr

225		230		235		240									
Glu	Asp	Leu	Lys	Gly	Lys	Thr	Val	Gly	Val	Lys	Asn	Gly	Thr	Ala	Ser
		245		250		255									
Gln	Thr	Phe	Leu	Thr	Glu	Asn	Gln	Ser	Lys	Tyr	Gly	Tyr	Lys	Ile	Lys
		260		265		270									
Thr	Phe	Ala	Asp	Gly	Ser	Ser	Met	Tyr	Asp	Ser	Leu	Asn	Thr	Gly	Ala
		275		280		285									
Ile	Asp	Ala	Val	Met	Asp	Asp	Glu	Pro	Val	Leu	Lys	Tyr	Ser	Ile	Ser
		290		295		300									
Gln	Gly	Gln	Lys	Leu	Lys	Thr	Pro	Ile	Ser	Gly	Thr	Pro	Ile	Gly	Glu
305				310		315									320
Thr	Ala	Phe	Ala	Val	Lys	Lys	Gly	Ala	Asn	Pro	Glu	Leu	Ile	Glu	Met
				325		330									335
Phe	Asn	Asn	Gly	Leu	Ala	Asn	Leu	Lys	Ala	Asn	Gly	Glu	Phe	Gln	Lys
			340			345								350	
Ile	Leu	Asp	Lys	Tyr	Leu	Ala	Ser	Glu	Ser	Ser	Thr	Ala	Ser	Thr	Ser
		355		360		365									
Thr	Val	Asp	Glu	Thr	Thr	Leu	Trp	Gly	Leu	Leu	Gln	Asn	Asn	Tyr	Lys
		370		375		380									
Gln	Leu	Leu	Ser	Gly	Leu	Gly	Ile	Thr	Leu	Ala	Leu	Asp	Ser	Tyr	Leu
385				390		395									400
Ile	Cys	Tyr	Cys	His	Cys	His	Arg	Asn	Tyr	Leu	Arg	Tyr	Val		
			405			410									

(2) INFORMATION FOR SEQ ID NO:3328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...206

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3328:

Lys	Met	Lys	Gln	Glu	Arg	Phe	Pro	Leu	Val	Ser	Asp	Asp	Glu	Val	Met
1			5					10					15		
Leu	Thr	Glu	Met	Pro	Val	Met	Asn	Leu	Tyr	Asp	Glu	Ser	Asp	Leu	Ile
		20					25					30			
Ser	Asn	Ile	Lys	Gly	Glu	Tyr	Arg	Asp	Lys	Asn	Tyr	Leu	Glu	Trp	Ala
		35				40					45				
Pro	Ile	Thr	Glu	Glu	Lys	Pro	Val	Lys	Pro	Ile	Glu	Lys	Gln	Val	Glu
	50				55				60						
Lys	Pro	Lys	Lys	Ala	Pro	Leu	Gly	Val	Lys	Lys	Glu	Gly	Lys	Ser	Tyr
65			70					75						80	
Ala	Glu	Val	Ala	Arg	Glu	Glu	Ala	Arg	Ala	Asp	Leu	Lys	Lys	Lys	Arg
			85				90						95		
Ser	Ala	Asn	Tyr	Leu	Thr	Gln	Asp	Phe	Ser	Leu	Ala	Arg	Arg	His	Ser

			100					105				110				
Gln	Pro	Ser	Leu	Val	Arg	Gln	Gly	Asn	Gln	Pro	Thr	Ala	Pro	Phe	Gln	
			115					120				125				
Lys	Glu	Asn	Pro	Gly	Glu	Phe	Val	Lys	Tyr	Ser	Gln	Lys	Leu	Thr	Gln	
			130					135				140				
Ser	His	Tyr	Ile	Leu	Ala	Glu	Glu	Val	His	Ser	Ile	Pro	Thr	Lys	Asn	
145					150					155					160	
Glu	Glu	Val	Ser	Ala	Pro	Ala	Pro	Lys	Lys	Asn	Asn	Tyr	Asp	Phe	Leu	
				165						170				175		
Lys	Lys	Ser	Gln	Ile	Tyr	Asn	Lys	Lys	Ser	Lys	Gln	Thr	Glu	Gln	Glu	
			180					185					190			
Arg	Arg	Val	Ala	Gln	Glu	Leu	Asn	Leu	Thr	Arg	Met	Thr	Glu			
		195					200					205				

(2) INFORMATION FOR SEQ ID NO:3329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...158

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3329:

Leu	Pro	Glu	His	Thr	Phe	Tyr	Val	Asp	Asn	Leu	Phe	Val	Phe	Thr	Pro	
1			5					10					15			
Leu	Gln	Gln	Val	Lys	Thr	Met	Tyr	Tyr	Leu	Pro	Val	Asp	Phe	Tyr	Arg	
		20					25					30				
Tyr	Leu	Ile	Gly	Arg	Glu	Asp	Gln	Ser	Val	Asn	Glu	Gln	Val	Met	Ile	
		35				40					45					
Lys	Cys	Ile	Asp	Gln	Gln	Leu	Lys	Val	Asn	Arg	Leu	Leu	Val	Asp	Gln	
	50				55				60							
Leu	Asp	Leu	Ser	Gln	Val	Ser	His	Pro	Lys	Met	Arg	Glu	Tyr	Leu	Leu	
65				70				75						80		
Asn	His	Ile	Glu	Ile	Thr	Thr	Val	Ile	Ser	Ser	Thr	Leu	Leu	Asn	Arg	
		85				90								95		
Ser	Gly	Thr	Thr	Glu	His	Leu	Ala	Lys	Lys	Arg	Gln	Leu	Trp	Thr	Tyr	
		100				105						110				
Ile	Gln	Gln	Lys	Asn	Pro	Glu	Val	Phe	Gln	Ala	Ile	Arg	Lys	Thr	Met	
		115				120					125					
Leu	Ser	Arg	Leu	Thr	Lys	His	Ser	Val	Leu	Pro	Asp	Arg	Lys	Leu	Ser	
	130				135					140						
Asn	Val	Val	Tyr	Gln	Ile	Thr	Lys	Ser	Val	Tyr	Gly	Phe	Asn			
145					150					155						

(2) INFORMATION FOR SEQ ID NO:3330:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 86 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...86
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3330:

Val	Leu	Glu	His	Thr	Met	Glu	Val	Val	Met	Asp	Asn	Ile	Ile	Asp	Val
1				5					10					15	
Ser	Ile	Pro	Val	Ala	Glu	Val	Val	Asp	Lys	His	Pro	Glu	Val	Leu	Glu
			20					25					30		
Ile	Leu	Val	Glu	Leu	Gly	Phe	Lys	Pro	Leu	Ala	Asn	Pro	Leu	Met	Arg
		35				40					45				
Asn	Thr	Val	Gly	Arg	Lys	Val	Ser	Leu	Lys	Gln	Gly	Ser	Lys	Leu	Ala
		50				55				60					
Gly	Thr	Pro	Met	Asp	Lys	Ile	Val	Arg	Thr	Leu	Glu	Ala	Asn	Gly	Tyr
65					70				75						80
Glu	Val	Ile	Gly	Leu	Asp										
					85										

(2) INFORMATION FOR SEQ ID NO:3331:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 327 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...327
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3331:

Lys	Leu	Glu	His	Ser	Ser	Arg	Lys	His	Phe	Val	Lys	Ile	Val	Lys	Glu
1				5					10					15	
Pro	Gly	Leu	Lys	Gly	Ala	Leu	Arg	Ser	Phe	Ile	His	Pro	Glu	Lys	Gln
			20					25					30		
Thr	Phe	Glu	Ala	Val	Lys	Asp	Leu	Thr	Phe	Glu	Val	Pro	Lys	Gly	Gln
		35					40					45			

Ile	Leu	Gly	Phe	Ile	Gly	Ala	Asn	Gly	Ala	Gly	Lys	Ser	Thr	Thr	Ile
50						55					60				
Lys	Met	Leu	Thr	Gly	Ile	Leu	Lys	Pro	Thr	Ser	Gly	Phe	Cys	Arg	Ile
65					70					75					80
Asn	Gly	Lys	Ile	Pro	Gln	Asp	Asn	Arg	Gln	Asp	Tyr	Val	Lys	Asp	Ile
				85					90					95	
Gly	Val	Val	Phe	Gly	Gln	Arg	Thr	Gln	Leu	Trp	Trp	Asp	Leu	Ala	Leu
			100					105					110		
Gln	Glu	Thr	Tyr	Thr	Val	Leu	Lys	Glu	Ile	Tyr	Asp	Val	Pro	Asn	Ser
		115					120					125			
Leu	Phe	His	Lys	Arg	Met	Asp	Phe	Leu	Asn	Glu	Val	Leu	Asp	Leu	Lys
	130					135					140				
Asp	Phe	Ile	Lys	Asp	Pro	Val	Arg	Thr	Leu	Ser	Leu	Gly	Gln	Arg	Met
145					150					155					160
Arg	Ala	Asp	Ile	Ala	Ala	Ser	Leu	Leu	His	Asn	Pro	Lys	Val	Leu	Phe
				165					170					175	
Leu	Asp	Glu	Pro	Thr	Ile	Gly	Leu	Asp	Val	Ser	Val	Lys	Asp	Asn	Ile
			180					185					190		
Arg	Arg	Ala	Ile	Thr	Gln	Ile	Asn	Gln	Glu	Glu	Glu	Thr	Thr	Ile	Leu
		195					200						205		
Leu	Thr	Thr	His	Asp	Leu	Ser	Asp	Ile	Glu	Gln	Leu	Cys	Asp	Arg	Ile
	210					215					220				
Phe	Met	Ile	Asp	Lys	Gly	Gln	Glu	Ile	Phe	Asp	Gly	Thr	Val	Ser	Gln
225					230				235						240
Leu	Lys	Glu	Thr	Phe	Gly	Lys	Met	Lys	Thr	Leu	Ser	Phe	Glu	Leu	Leu
				245					250					255	
Pro	Gly	Gln	Ser	His	Leu	Val	Ser	His	Tyr	Glu	Gly	Leu	Ser	Asp	Met
			260					265					270		
Thr	Ile	Asp	Arg	Gln	Gly	Asn	Ser	Leu	Asn	Ile	Glu	Phe	Asp	Ser	Ser
	275						280					285			
Arg	Tyr	Gln	Ser	Ala	Asp	Ile	Ile	Lys	Gln	Thr	Leu	Ser	Asp	Phe	Glu
	290					295					300				
Ile	Arg	Asp	Leu	Lys	Met	Val	Asp	Thr	Asp	Ile	Glu	Asp	Ile	Ile	Arg
305					310					315					320
Arg	Phe	Tyr	Arg	Lys	Glu	Leu									
				325											

(2) INFORMATION FOR SEQ ID NO:3332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...188

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3332:

Gln	Asp	Arg	Gln	Thr	Ser	Leu	Ser	Gln	Pro	Lys	Asn	Phe	Ala	Asn	Arg
1				5					10					15	
Gly	Met	Ser	Phe	Glu	Lys	Met	Ile	Asn	Ala	Thr	Asn	Asp	Tyr	Tyr	Leu
			20					25					30		
Ser	Gln	Gly	Leu	Ala	Val	Ile	His	Lys	Lys	Pro	Thr	Pro	Ile	Gln	Ile
		35					40					45			
Val	Gln	Val	Asp	Tyr	Pro	Gln	Arg	Ser	Arg	Ala	Lys	Ile	Val	Glu	Ala
	50					55					60				
Tyr	Phe	Arg	Gln	Ala	Ser	Thr	Thr	Asp	Tyr	Ser	Gly	Val	Tyr	Asn	Gly
65					70				75					80	
Tyr	Tyr	Ile	Asp	Phe	Glu	Val	Lys	Glu	Thr	Lys	Gln	Lys	Arg	Ala	Ile
			85					90					95		
Pro	Met	Lys	Asn	Phe	His	Pro	His	Gln	Ile	Gln	His	Met	Glu	Gln	Val
			100					105					110		
Leu	Ala	Gln	Gln	Gly	Ile	Cys	Phe	Val	Leu	Leu	His	Phe	Ser	Ser	Gln
		115					120					125			
Gln	Glu	Thr	Tyr	Leu	Leu	Pro	Ala	Phe	Asp	Leu	Ile	Arg	Phe	Tyr	His
	130					135					140				
Gln	Asp	Lys	Gly	Gln	Lys	Ser	Met	Pro	Leu	Glu	Tyr	Ile	Arg	Glu	Tyr
145					150				155					160	
Gly	Tyr	Glu	Ile	Lys	Ala	Gly	Ala	Phe	Pro	Gln	Ile	Pro	Tyr	Leu	Asn
			165					170					175		
Val	Ile	Lys	Glu	His	Leu	Leu	Gly	Gly	Lys	Thr	Arg				
			180					185							

(2) INFORMATION FOR SEQ ID NO:3333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3333:

Thr	Ser	Arg	Gln	Arg	Arg	Ile	Asp	Met	Ala	Glu	Thr	Asn	Gln	Asn	Thr
1				5					10					15	
Asp	Asn	Leu	Leu	Asp	Leu	Thr	Lys	Ile	Thr	Glu	Pro	Phe	Glu	Leu	Ala
		20					25					30			
Ser	Ala	Leu	Arg	Tyr	Met	Lys	Glu	Asn	Gly	Glu	Phe	Ile	Arg	Cys	Lys
		35				40					45				
Asn	Val	Ser	Asp	Asp	Phe	Tyr	Met	Tyr	Arg	Asp	Val	Gln	Lys	Arg	Pro
	50				55					60					
Val	Ile	Val	Asn	Gly	Arg	Arg	Gln	Phe	Lys	Asp	Val	Glu	Thr	Val	Trp
65				70				75						80	
Ala	Phe	Asn	Gln	Trp	Gly	Gly	Thr	Ile	Ala	Thr	Ile	Asn	Val	Ala	Val

				85					90					95					
Leu	Leu	Asn	His	Glu	Phe	Tyr	Ile	Met	Lys	Phe	Asp	Ala	Glu	Gly	Asn				
				100					105					110					
Pro	Asp	Trp	Thr	Val	Pro	Thr	Val	Glu	Pro	Lys	Glu								
				115					120										

(2) INFORMATION FOR SEQ ID NO:3334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3334:

Asp	Lys	Arg	Gln	Glu	Arg	Gly	Leu	Asp	Val	Lys	Ile	Arg	Met	Arg	Asn				
1				5					10					15					
Thr	Ile	Gln	Phe	Asp	Glu	Gln	Leu	Glu	Val	Ile	Asp	Gln	Leu	Tyr	Asp				
			20					25					30						
Val	Glu	Val	His	Glu	Lys	Gly	Asp	Tyr	Ser	Tyr	Leu	Leu	Phe	Tyr	Asn				
			35				40					45							
Glu	Glu	Lys	Glu	Lys	Val	Val	Ile	Lys	Phe	His	Gly	Gln	Glu	Leu	Val				
			50			55					60								
Met	Ser	Arg	Phe	Ser	Asn	Pro	Lys	Thr	Ile	Met	Arg	Phe	Leu	Lys	Asp				
65				70					75				80						
Ser	Asp	Ser	Leu	Ala	Tyr	Ile	Pro	Thr	Pro	Met	Gly	Met	Gln	Glu	Phe				
			85						90				95						
Ile	Ile	Gln	Thr	Ser	Arg	Tyr	Gln	Val	Asp	Arg	Gln	Lys	Ile	Glu	Leu				
			100					105					110						
Ala	Tyr	Gln	Leu	Gln	Asn	Gln	Glu	Gly	His	Pro	Phe	Ala	Ser	Tyr	Gln				
			115				120					125							
Leu	Glu	Ile	Thr	Trp	Gly														
			130																

(2) INFORMATION FOR SEQ ID NO:3335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...279

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3335:

His	Cys	Gly	His	Glu	Phe	Ser	Gly	Glu	Ile	Ile	Asp	Val	Gly	Ser	Asp
1				5					10					15	
Val	Thr	Arg	Val	Lys	Val	Gly	Asp	Arg	Val	Ala	Val	Glu	Pro	Ile	Leu
			20					25					30		
Ala	Lys	Asn	Asn	Leu	Val	Gly	Asp	Tyr	Asn	Leu	Asp	Pro	Asn	Leu	Asn
		35					40					45			
Phe	Val	Gly	Leu	Ala	Ala	Asp	Gly	Gly	Phe	Ala	Lys	Tyr	Cys	Val	Leu
	50					55					60				
Asp	Gly	Asp	Leu	Val	His	Val	Ile	Pro	Asp	Ser	Leu	Ser	Tyr	Glu	Gln
65					70				75					80	
Ala	Ala	Leu	Thr	Glu	Pro	Ala	Ala	Val	Ala	Val	Tyr	Ala	Val	Arg	Gln
				85				90						95	
Ser	Ser	Leu	Lys	Ala	Gly	Asp	Thr	Ala	Val	Val	Phe	Gly	Leu	Gly	Pro
		100						105					110		
Ile	Gly	Leu	Leu	Ile	Val	Glu	Ala	Leu	Arg	Ala	Ala	Gly	Ala	Ser	Lys
	115					120						125			
Ile	Tyr	Ala	Val	Glu	Leu	Ser	Pro	Glu	Arg	Gln	Ala	Lys	Ala	Glu	Glu
	130					135					140				
Leu	Gly	Ala	Ile	Val	Val	Arg	Pro	Glu	Glu	Gly	Glu	Thr	Ala	Val	Glu
145					150					155					160
Ala	Ile	His	Arg	Leu	Thr	Asn	Gly	Gly	Val	Asp	Val	Ser	Tyr	Glu	Val
			165					170						175	
Thr	Gly	Val	Pro	Val	Val	Leu	Gly	Gln	Ala	Leu	Ala	Ala	Val	His	Lys
		180						185					190		
Ala	Gly	Glu	Cys	Met	Val	Val	Ser	Ile	Trp	Glu	Arg	Glu	Ala	Asn	Ile
	195						200					205			
Asn	Pro	Asn	Glu	Phe	Ala	Ile	Gln	Glu	Lys	Thr	Leu	Lys	Gly	Ile	Ile
	210					215					220				
Ala	Tyr	Arg	His	Ile	Phe	Pro	Lys	Val	Leu	Glu	Leu	Met	Glu	Gln	Gly
225				230						235				240	
Tyr	Phe	Ser	Ala	Glu	Lys	Leu	Val	Thr	Lys	Lys	Ile	Lys	Leu	Glu	Asn
			245						250					255	
Ile	Val	Glu	Glu	Gly	Phe	Ile	Glu	Leu	Thr	Gln	Asp	Lys	Ser	Gln	Ile
		260					265						270		
Lys	Ile	Leu	Val	Glu	Pro	Glu									
	275														

(2) INFORMATION FOR SEQ ID NO:3336:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...69

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3336:

```
Ala Met Leu Gln Val Ala Leu Leu Ile Gln Gln Leu Met Ile Leu Arg
1           5           10           15
Ile Asn Ala Gly Lys Ile Leu Ile Ser Gly Ser Val Phe Val Tyr Arg
          20           25           30
Tyr Ser Ser Val Val Leu Tyr Lys Asn Leu Tyr Asn Leu Met Thr Tyr
          35           40           45
Ala Val Ile Glu Thr Ile Leu Leu Gln Thr Ser Arg Leu Phe Cys Tyr
          50           55           60
Lys Phe Thr Cys Ser
65
```

(2) INFORMATION FOR SEQ ID NO:3337:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 326 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...326

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3337:

```
Lys Leu Leu Gln Gln Thr Leu Leu Gln Thr Cys Leu Glu Val Val Phe
1           5           10           15
Met Thr Asn Leu Ile Ala Thr Phe Gln Asp Arg Phe Gly Asp Trp Leu
          20           25           30
Thr Ala Leu Ser Gln His Leu Gln Leu Ser Leu Leu Thr Leu Leu Leu
          35           40           45
Ala Ile Leu Leu Ala Ile Pro Leu Ala Val Tyr Leu Arg Tyr His Glu
          50           55           60
Lys Leu Ala Asp Trp Val Leu Gln Ile Ala Gly Ile Phe Gln Thr Ile
65          70          75          80
Pro Ser Leu Ala Leu Leu Gly Leu Phe Ile Pro Leu Met Gly Ile Gly
          85          90          95
Thr Leu Pro Ala Leu Thr Ala Leu Val Ile Tyr Ala Ile Phe Pro Ile
          100         105         110
Leu Gln Asn Thr Ile Thr Gly Leu Lys Gly Ile Asp Pro Ser Leu Gln
          115         120         125
Glu Ala Gly Ile Ala Phe Gly Met Thr Arg Trp Glu Arg Leu Lys Lys
          130         135         140
```

Phe	Glu	Ile	Pro	Leu	Ala	Met	Pro	Val	Ile	Met	Ser	Gly	Ile	Arg	Thr
145					150					155					160
Ala	Ala	Val	Leu	Ile	Ile	Gly	Thr	Ala	Thr	Leu	Ala	Thr	Leu	Ile	Gly
				165					170					175	
Ala	Gly	Gly	Leu	Gly	Ser	Phe	Ile	Leu	Leu	Gly	Ile	Asp	Arg	Asn	Asn
			180					185					190		
Ala	Ser	Leu	Ile	Leu	Ile	Gly	Ala	Leu	Ser	Ser	Ala	Val	Leu	Ala	Ile
	195						200					205			
Ala	Phe	Asn	Phe	Leu	Leu	Lys	Val	Met	Glu	Lys	Ala	Lys	Leu	Arg	Thr
	210					215					220				
Ile	Phe	Ser	Gly	Phe	Ala	Leu	Val	Ala	Leu	Leu	Leu	Gly	Leu	Ser	Tyr
225					230					235					240
Ser	Pro	Ala	Leu	Leu	Ala	Gln	Lys	Glu	Lys	Glu	Asn	Leu	Ile	Ile	Ala
				245					250					255	
Gly	Lys	Ile	Gly	Pro	Glu	Pro	Glu	Ile	Leu	Ala	Asn	Met	Tyr	Lys	Leu
			260					265					270		
Leu	Ile	Glu	Glu	Asn	Thr	Ser	Met	Thr	Ala	Thr	Val	Thr	Pro	Asn	Phe
		275					280					285			
Gly	Thr	Thr	Ser	Phe	Leu	Tyr	Glu	Ala	Leu	Lys	Lys	Gly	Asp	Ile	Asp
	290					295					300				
Ile	Tyr	Pro	Glu	Phe	Thr	Gly	Thr	Val	Thr	Glu	Lys	Phe	Ala	Ser	Thr
305					310					315					320
Ile	Thr	Gln	Gly	Glu	Ser										
				325											

(2) INFORMATION FOR SEQ ID NO:3338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...149

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3338:

Tyr	Asn	Met	Gln	Lys	Leu	Gly	Gly	Gly	Arg	Met	Ile	Glu	Lys	Met	Glu
1				5					10					15	
Leu	Gly	Glu	Phe	Tyr	Lys	Glu	Leu	Arg	Leu	Ala	Arg	Lys	Leu	Lys	Gln
			20					25					30		
Thr	Asp	Val	Ala	Cys	Glu	Gly	Leu	Thr	Ala	Ser	Gln	Leu	Ser	Lys	Phe
	35					40					45				
Glu	Leu	Gly	Gln	Ser	Met	Leu	Ser	Ala	Asp	Lys	Leu	Ile	Leu	Ala	Ile
	50				55				60						
Gln	Gly	Ile	Asn	Val	Thr	Phe	Asp	Glu	Phe	Gly	His	Lys	Leu	Asn	Asn
65				70				75						80	
Tyr	Gln	Glu	Ser	Pro	His	Met	Arg	Ile	Gly	Arg	Lys	Val	Val	Asn	Arg
				85				90						95	

Phe	Ala	His	Gln	Asp	Ile	Ala	Ala	Leu	Glu	Gln	Leu	Leu	Glu	Glu	Val
			100					105					110		
Asp	Gln	Glu	Gln	Met	Ala	Gln	Thr	Tyr	Arg	Arg	Leu	Asn	Ala	Ile	Val
		115					120					125			
Ile	Lys	Asp	Ala	Ile	His	Ser	Leu	Asn	Lys	Ser	Tyr	Pro	Leu	Ala	Glu
	130					135					140				
Gly	Asp	Ser	Glu	Phe											
145															

(2) INFORMATION FOR SEQ ID NO:3339:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...196

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3339:

Asn	Trp	Ser	His	Arg	Gln	Glu	Arg	Lys	Arg	Lys	Cys	His	Tyr	Gln	Met
1				5					10					15	
Lys	Lys	Ile	Ala	Val	Phe	Ala	Ser	Gly	Asn	Gly	Ser	Asn	Phe	Gln	Val
			20					25					30		
Ile	Ala	Glu	Glu	Phe	Pro	Val	Glu	Phe	Val	Phe	Ser	Asp	His	Arg	Asp
		35					40					45			
Ala	Tyr	Val	Leu	Glu	Arg	Ala	Lys	Gln	Leu	Gly	Val	Leu	Ser	Tyr	Ala
	50					55					60				
Phe	Glu	Leu	Lys	Glu	Phe	Glu	Ser	Lys	Thr	Asp	Tyr	Glu	Ala	Ala	Leu
65					70					75					80
Val	Glu	Leu	Leu	Glu	Glu	His	Gln	Ile	Asp	Leu	Val	Cys	Leu	Ala	Gly
				85					90					95	
Tyr	Ile	Lys	Ile	Val	Gly	Pro	Thr	Leu	Leu	Ser	Ala	Tyr	Glu	Gly	Arg
			100					105					110		
Ile	Val	Asn	Ile	His	Pro	Ala	Tyr	Leu	Pro	Glu	Phe	Pro	Gly	Ala	His
		115					120					125			
Gly	Ile	Glu	Asp	Ala	Trp	Asn	Ala	Gly	Val	Gly	Gln	Ser	Gly	Val	Thr
	130					135					140				
Ile	His	Trp	Val	Asp	Ser	Gly	Val	Asp	Thr	Gly	Gln	Val	Ile	Lys	Gln
145					150					155					160
Val	Arg	Val	Pro	Arg	Leu	Ala	Asp	Asp	Thr	Ser	Asp	Arg	Cys	Glu	Ala
				165					170					175	
Arg	Ile	His	Glu	Ala	Glu	Tyr	Arg	Leu	Tyr	Pro	Glu	Val	Val	Lys	Ala
			180					185					190		
Leu	Phe	Thr	Asp												
			195												

(2) INFORMATION FOR SEQ ID NO:3340:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 945 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...945
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3340:

```

Gly Lys Ala His Asp Lys Ile Val Met His Gly Ala Arg Ala His Asn
1      5      10      15
Leu Lys Asn Ile Asp Val Glu Ile Pro Arg Asp Lys Leu Val Val Val
20     25     30
Thr Gly Leu Ser Gly Ser Gly Lys Ser Ser Leu Ala Phe Asp Thr Leu
35     40     45
Tyr Ala Glu Gly Gln Arg Arg Tyr Val Glu Ser Leu Ser Ala Tyr Ala
50     55     60
Arg Gln Phe Leu Gly Asn Met Glu Lys Pro Asp Val Asp Ala Ile Asp
65     70     75     80
Gly Leu Ser Pro Ala Ile Ser Ile Asp Gln Lys Thr Thr Ser Lys Asn
85     90     95
Pro Arg Ser Thr Val Gly Thr Thr Thr Glu Ile Asn Asp Tyr Leu Arg
100    105    110
Leu Leu Tyr Ala Arg Val Gly Thr Pro Tyr Cys Ile Asn Gly His Gly
115    120    125
Ala Ile Asn Ala Ser Ser Val Glu Gln Ile Val Asp Lys Val Leu Glu
130    135    140
Leu Pro Glu Arg Gln Arg Leu Gln Ile Leu Ala Pro Val Ile Arg Lys
145    150    155    160
Lys Lys Gly Gln His Lys Ser Val Ile Glu Lys Val Gln Lys Asp Gly
165    170    175
Tyr Val Arg Val Arg Val Asp Gly Glu Val Tyr Asp Val Thr Glu Val
180    185    190
Pro Glu Leu Ser Lys Ser Lys Gln His Asn Ile Asp Val Val Val Asp
195    200    205
Arg Ile Val Ile Lys Glu Gly Ile Arg Ser Arg Leu Phe Asp Ser Ile
210    215    220
Glu Ala Ala Leu Arg Ile Ala Glu Gly Tyr Val Ile Ile Asp Thr Met
225    230    235    240
Asp Asp Ser Glu Leu Leu Phe Ser Glu His Tyr Ala Cys Pro Val Cys
245    250    255
Gly Phe Thr Val Pro Glu Leu Glu Pro Arg Leu Phe Ser Phe Asn Ala
260    265    270
Pro Phe Gly Ser Cys Ser Glu Cys Asp Gly Leu Gly Ile Lys Leu Glu
275    280    285
Val Asp Thr Asp Leu Val Val Pro Asp Ala Ser Lys Thr Leu Arg Glu

```

290		295		300
Gly Ala Leu Ala Pro Trp Asn Pro Ile Ser Ser Asn Tyr Tyr Pro Asn				
305		310		320
Met Leu Glu Gln Ala Met Lys Val Phe Gly Val Ala Met Asp Lys Pro				
	325		330	335
Phe Glu Asp Leu Ser Glu Glu Asp Lys Asn Leu Ile Leu Tyr Gly Ser				
	340		345	350
Asp Gly Lys Glu Phe His Phe His Tyr Glu Asn Glu Phe Gly Gly Val				
	355		360	365
Arg Asp Ile Asp Ile Pro Phe Glu Gly Val Ile Asn Asn Ile Lys Arg				
	370		375	380
Arg Tyr His Glu Thr Asn Ser Asp Tyr Thr Arg Thr Gln Met Arg Leu				
385		390		400
Tyr Met Asn Glu Leu Thr Cys Gly Thr Cys Gln Gly Tyr Arg Leu Asn				
	405		410	415
Asp Gln Ala Leu Ser Val Arg Val Gly Gly Gln Gln Gly Pro His Ile				
	420		425	430
Gly Glu Ile Ser Asp Leu Ser Ile Ala Asp His Leu Asp Leu Val Ser				
	435		440	445
Gln Leu Thr Leu Ser Glu Asn Glu Ala Ile Ile Ala Arg Pro Ile Leu				
	450		455	460
Lys Glu Ile Lys Asp Arg Leu Thr Phe Leu Asn Asn Val Gly Leu Asn				
465		470		480
Tyr Leu Thr Leu Ser Arg Ser Ala Gly Thr Leu Ser Gly Gly Glu Ser				
	485		490	495
Gln Arg Ile Arg Leu Ala Thr Gln Ile Gly Ser Asn Leu Ser Gly Val				
	500		505	510
Leu Tyr Ile Leu Asp Glu Pro Ser Ile Gly Leu His Gln Arg Asp Asn				
	515		520	525
Asp Arg Leu Ile Ala Ser Leu Lys Lys Met Arg Asp Leu Gly Asn Thr				
	530		535	540
Leu Ile Val Val Glu His Asp Glu Asp Thr Met Arg Glu Ala Asp Tyr				
545		550		560
Leu Ile Asp Val Gly Pro Gly Ala Gly Val Phe Gly Gly Glu Ile Val				
	565		570	575
Ala Ala Gly Thr Pro Lys Gln Val Ala Arg Asn Ser Lys Ser Ile Thr				
	580		585	590
Gly Gln Tyr Leu Ser Gly Lys Arg Val Ile Pro Val Pro Glu Glu Arg				
	595		600	605
Arg Val Gly Asn Gly Arg Phe Ile Glu Val Ile Gly Ala Arg Glu Asn				
	610		615	620
Asn Leu Gln Asn Val Thr Ala Arg Phe Pro Leu Gly Lys Phe Ile Ala				
625		630		640
Val Thr Gly Val Ser Gly Ser Gly Lys Ser Thr Leu Ile Asn Ser Ile				
	645		650	655
Leu Lys Lys Ala Ile Ala Gln Lys Leu Asn Arg Asn Ser Asp Lys Pro				
	660		665	670
Gly Lys Phe Lys Thr Ile Thr Gly Ile Glu His Val Asp Arg Leu Ile				
	675		680	685
Asp Ile Asp Gln Ser Pro Ile Gly Arg Thr Pro Arg Ser Asn Pro Ala				
	690		695	700
Thr Tyr Thr Gly Val Phe Asp Asp Ile Arg Asp Leu Phe Ala Gln Thr				
705		710		720
Asn Glu Ala Lys Ile Arg Gly Tyr Lys Lys Gly Arg Phe Ser Phe Asn				
	725		730	735
Val Lys Gly Gly Arg Cys Glu Ala Cys Ser Gly Asp Gly Ile Ile Lys				
	740		745	750

Ile	Glu	Met	His	Phe	Leu	Pro	Asp	Val	Tyr	Val	Ala	Cys	Glu	Val	Cys
		755					760					765			
His	Gly	Thr	Arg	Tyr	Asn	Ser	Glu	Thr	Leu	Glu	Val	His	Tyr	Lys	Glu
		770				775					780				
Lys	Asn	Ile	Ser	Gln	Val	Leu	Asp	Met	Thr	Val	Asn	Asp	Ala	Val	Glu
785					790					795					800
Phe	Phe	Gln	His	Ile	Pro	Lys	Ile	Gln	Arg	Lys	Leu	Gln	Thr	Ile	Lys
				805					810					815	
Asp	Val	Gly	Leu	Gly	Tyr	Val	Thr	Leu	Gly	Gln	Pro	Ala	Thr	Thr	Leu
			820					825					830		
Ser	Gly	Gly	Glu	Ala	Gln	Arg	Met	Lys	Leu	Ala	Ser	Glu	Leu	His	Lys
		835					840					845			
Arg	Ser	Thr	Gly	Lys	Ser	Phe	Tyr	Ile	Leu	Asp	Glu	Pro	Thr	Thr	Gly
		850				855					860				
Leu	His	Thr	Glu	Asp	Ile	Ala	Arg	Leu	Leu	Lys	Val	Leu	Ala	Arg	Phe
865					870					875					880
Val	Asp	Asp	Gly	Asn	Thr	Val	Leu	Val	Ile	Glu	His	Asn	Leu	Asp	Val
				885					890					895	
Ile	Lys	Thr	Ala	Asp	His	Ile	Ile	Asp	Leu	Gly	Pro	Glu	Gly	Gly	Val
			900					905					910		
Gly	Gly	Gly	Thr	Ile	Ile	Val	Thr	Gly	Thr	Pro	Glu	Glu	Val	Ala	Ala
		915					920					925			
Asn	Glu	Ala	Ser	Tyr	Thr	Gly	His	Tyr	Leu	Lys	Gly	Lys	Leu	His	His
	930					935					940				
Glu															
945															

(2) INFORMATION FOR SEQ ID NO:3341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3341:

Glu	Gly	Ala	Gln	Ala	Ala	Met	Pro	Thr	Ala	Leu	Gly	Tyr	Val	Ser	Ile
1			5						10					15	
Gly	Leu	Ala	Cys	Gly	Thr	Ile	Gly	Ala	Pro	Tyr	Val	Thr	Pro	Val	Glu
		20						25					30		
Met	Gly	Leu	Met	Ser	Leu	Phe	Val	Tyr	Ala	Gly	Ser	Ala	Gln	Phe	Ala
		35				40					45				
Met	Leu	Ala	Leu	Ile	Val	Val	Gln	Ala	Pro	Val	Ala	Ala	Ile	Ala	Met
	50				55					60					
Thr	Val	Phe	Leu	Ile	Asn	Leu	Arg	Leu	Phe	Leu	Leu	Ser	Leu	His	Ala
65					70				75						80

Ser	Thr	Tyr	Phe	Arg	His	Thr	Ser	Leu	Trp	Tyr	Asn	Ile	Gly	Met	Ser
				85					90					95	
Ser	Ile	Leu	Thr	Asp	Glu	Thr	Tyr	Gly	Val	Leu	Met	Gly	Glu	Leu	Ala
		100						105					110		
His	Thr	Asp	Lys	Val	Asn	Pro	Met	Trp	Met	His	Gly	Asn	Asn	Leu	Asn
		115					120					125			
Ser	Tyr	Val	Ala	Trp	Phe	Val	Gly	Thr	Val	Val	Gly	Thr	Ala	Leu	Gly
		130					135				140				
Gly	Leu	Leu	Pro	Asn	Pro	Glu	Ile	Phe	Gly	Leu	Asp	Phe	Ala	Leu	Val
145					150					155					160
Gly	Met	Phe	Ile	Gly	Ile	Phe	Ala	Ser	Gln	Phe	Gln	Met	Met	Gln	Arg
			165						170					175	
Arg	Ile	Pro	Val	Arg	Asn	Leu	Leu	Ile							
			180					185							

(2) INFORMATION FOR SEQ ID NO:3342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 535 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...535

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3342:

Asn	His	Gln	Gln	Ala	Gln	Met	Leu	Arg	Gly	Thr	Ala	Leu	Leu	Thr	Ala
1				5					10					15	
Ser	Asn	Phe	Ile	Ser	Arg	Leu	Leu	Gly	Ala	Val	Tyr	Ile	Ile	Pro	Trp
		20						25					30		
Tyr	Ile	Trp	Met	Gly	Ala	Tyr	Ala	Ala	Lys	Ala	Asn	Gly	Leu	Phe	Thr
		35					40					45			
Met	Gly	Tyr	Thr	Ile	Tyr	Ala	Trp	Phe	Leu	Leu	Val	Ser	Thr	Ala	Gly
		50				55					60				
Ile	Pro	Val	Ala	Val	Ala	Lys	Gln	Val	Ala	Lys	Tyr	Asn	Thr	Met	Arg
65					70					75					80
Glu	Glu	Glu	His	Ser	Phe	Ala	Leu	Ile	Arg	Ser	Phe	Leu	Gly	Phe	Met
			85						90					95	
Thr	Gly	Leu	Gly	Leu	Val	Phe	Ala	Leu	Val	Leu	Tyr	Val	Phe	Ala	Pro
		100						105					110		
Trp	Leu	Ala	Asp	Leu	Ser	Gly	Val	Gly	Lys	Asp	Leu	Ile	Pro	Ile	Met
		115					120					125			
Gln	Ser	Leu	Ala	Trp	Gly	Val	Leu	Ile	Phe	Pro	Ser	Met	Ser	Val	Ile
		130				135					140				
Arg	Gly	Phe	Phe	Gln	Gly	Met	Asn	Asn	Leu	Lys	Pro	Tyr	Ala	Met	Ser
145					150					155					160
Gln	Ile	Ala	Glu	Gln	Val	Ile	Arg	Val	Ile	Trp	Met	Leu	Leu	Ala	Thr
			165						170					175	

Phe	Ile	Ile	Met	Lys	Leu	Gly	Ser	Gly	Asp	Tyr	Leu	Ala	Ala	Val	Thr	180	185	190
Gln	Ser	Thr	Phe	Ala	Ala	Phe	Val	Gly	Met	Val	Ala	Ser	Phe	Ala	Val	195	200	205
Leu	Ile	Tyr	Phe	Leu	Ala	Gln	Glu	Ser	Ser	Leu	Lys	Arg	Val	Phe	Glu	210	215	220
Thr	Gly	Asp	Lys	Ile	Asn	Ser	Lys	Arg	Leu	Leu	Val	Asp	Thr	Ile	Lys	225	230	235
Glu	Ala	Ile	Pro	Phe	Ile	Leu	Thr	Gly	Ser	Ala	Ile	Gln	Ile	Phe	Gln	245	250	255
Ile	Leu	Asp	Gln	Leu	Thr	Phe	Ile	Asn	Ser	Met	Ser	Trp	Phe	Thr	Asn	260	265	270
Tyr	Ser	Asn	Glu	Asp	Leu	Val	Val	Met	Phe	Ser	Tyr	Phe	Ser	Ala	Asn	275	280	285
Pro	Asn	Lys	Ile	Thr	Met	Ile	Leu	Ile	Ser	Val	Gly	Val	Ser	Ile	Gly	290	295	300
Ser	Val	Gly	Leu	Pro	Leu	Leu	Thr	Glu	Asn	Tyr	Val	Lys	Gly	Asp	Leu	305	310	315
Lys	Ala	Ala	Ser	Arg	Leu	Val	Gln	Asp	Ser	Leu	Thr	Leu	Leu	Phe	Met	325	330	335
Phe	Leu	Leu	Pro	Ala	Thr	Val	Gly	Val	Val	Met	Val	Gly	Glu	Pro	Leu	340	345	350
Tyr	Thr	Val	Phe	Tyr	Gly	Lys	Pro	Asp	Ser	Leu	Ala	Leu	Gly	Leu	Phe	355	360	365
Val	Phe	Ala	Val	Leu	Gln	Ser	Ile	Ile	Leu	Gly	Leu	Tyr	Met	Val	Leu	370	375	380
Ser	Pro	Met	Leu	Gln	Ala	Met	Phe	Arg	Asn	Arg	Lys	Ala	Val	Leu	Tyr	385	390	395
Phe	Ile	Tyr	Gly	Ser	Ile	Ala	Lys	Leu	Val	Leu	Gln	Leu	Pro	Thr	Ile	405	410	415
Ala	Leu	Phe	His	Ser	Tyr	Gly	Pro	Leu	Ile	Ser	Thr	Thr	Ile	Ala	Leu	420	425	430
Ile	Ile	Pro	Asn	Val	Leu	Met	Tyr	Arg	Asp	Ile	Cys	Lys	Val	Thr	Gly	435	440	445
Val	Lys	Arg	Lys	Val	Ile	Leu	Lys	Arg	Thr	Ile	Leu	Ile	Ser	Leu	Leu	450	455	460
Thr	Leu	Val	Met	Phe	Leu	Leu	Ile	Gly	Thr	Ile	Gln	Trp	Leu	Leu	Gly	465	470	475
Phe	Phe	Phe	Gln	Pro	Ser	Gly	Arg	Leu	Trp	Ser	Phe	Phe	Tyr	Val	Ala	485	490	495
Leu	Val	Gly	Ala	Met	Gly	Gly	Gly	Leu	Tyr	Met	Val	Met	Ser	Leu	Arg	500	505	510
Thr	Tyr	Leu	Leu	Asp	Lys	Val	Ile	Gly	Lys	Ala	Gln	Ala	Asp	Arg	Leu	515	520	525
Arg	Ala	Lys	Phe	Lys	Leu	Ser										530	535	

(2) INFORMATION FOR SEQ ID NO:3343:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...111

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3343:

Gln	Met	Gln	Gln	Ile	Thr	Glu	Ile	Ile	Ile	Ala	Phe	Ala	Thr	Ser	Phe
1				5					10					15	
Leu	Thr	Val	Ala	Val	Gly	Gly	Ile	Val	Lys	Ala	Val	Lys	Asp	Tyr	Leu
			20					25					30		
Leu	Arg	Lys	Gly	Gly	Glu	Lys	Ala	Val	Ile	Ile	Ala	Glu	Ile	Leu	Ala
		35					40					45			
Lys	Asn	Ala	Val	Asn	Ala	Val	Glu	Gln	Val	Ala	Ala	Glu	Thr	Gly	Tyr
	50				55					60					
Lys	Gly	Asp	Glu	Lys	Leu	Ala	Gln	Ala	Arg	Ala	Lys	Val	Arg	Ala	Glu
65					70				75						80
Leu	Thr	Lys	Tyr	Asn	Ile	Ser	Met	Thr	Asp	Lys	Asp	Leu	Asp	Thr	Phe
				85					90					95	
Val	Glu	Ser	Ala	Val	Lys	Gln	Met	Asn	Asp	Ala	Trp	Lys	Gly	Arg	
			100					105					110		

(2) INFORMATION FOR SEQ ID NO:3344:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 219 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...219

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3344:

Ala	His	Lys	Gln	Lys	Phe	Ser	Pro	Glu	Met	Met	Val	Asn	Lys	Lys	Gln
1				5					10					15	
Val	Lys	Val	Gly	Ile	Ser	Thr	Ile	Tyr	Tyr	Trp	Phe	His	Asn	Gly	His
			20					25					30		
Leu	Gly	Leu	Thr	Lys	Ala	Asp	Met	Leu	Tyr	Pro	Arg	Lys	Arg	Lys	Gly
		35					40					45			
Val	Lys	Lys	Gln	Ala	Ser	Pro	Asn	Phe	Lys	Pro	Ala	Gly	Lys	Ser	Ile
	50				55					60					
Glu	Glu	Arg	Pro	Asp	Val	Ile	Asn	Phe	Arg	Leu	Glu	Asn	Gly	His	Tyr
65					70				75						80
Glu	Ile	Asp	Thr	Val	Leu	Leu	Thr	Lys	Ile	Lys	Asn	Tyr	Cys	Leu	Leu
				85					90					95	

Val	Leu	Thr	Asp	Arg	Arg	Ser	Arg	His	Gln	Ile	Ile	Arg	Leu	Ile	Pro
			100					105					110		
Asn	Lys	Thr	Ala	Glu	Ser	Val	Asn	Gln	Ala	Leu	Thr	Leu	Leu	Leu	Gly
		115					120					125			
Glu	His	Arg	Ile	Leu	Ser	Ile	Thr	Ala	Asp	Asn	Gly	Ser	Glu	Phe	Lys
		130				135					140				
Arg	Leu	Ser	Glu	Val	Phe	Pro	Glu	Glu	His	Ile	Tyr	Tyr	Ala	His	Ala
145					150					155					160
Tyr	Ser	Ser	Trp	Glu	Arg	Gly	Ser	Asn	Glu	Asn	His	Asn	Arg	Leu	Ile
			165						170					175	
Arg	Arg	Trp	Leu	Pro	Lys	Gly	Thr	Lys	Lys	Thr	Thr	Pro	Lys	Glu	Val
			180					185					190		
Ala	Phe	Ile	Glu	Asn	Trp	Ile	Asn	Asn	Tyr	Pro	Lys	Lys	Cys	Leu	Asp
		195					200					205			
Tyr	Lys	Ser	Pro	Ser	Glu	Phe	Leu	Leu	Gly	Gly					
		210					215								

(2) INFORMATION FOR SEQ ID NO:3345:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 219 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...219

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3345:

Ala	His	Lys	Gln	Lys	Phe	Ser	Pro	Glu	Met	Met	Val	Asn	Lys	Lys	Gln
1				5				10						15	
Val	Lys	Val	Gly	Ile	Ser	Thr	Ile	Tyr	Trp	Phe	His	Asn	Gly	His	
			20					25				30			
Leu	Gly	Leu	Thr	Lys	Ala	Asp	Met	Leu	Tyr	Pro	Arg	Lys	Arg	Lys	Gly
		35				40					45				
Val	Lys	Lys	Gln	Ala	Ser	Pro	Asn	Phe	Lys	Pro	Ala	Gly	Lys	Ser	Ile
	50				55				60						
Glu	Glu	Arg	Pro	Asp	Val	Ile	Asn	Leu	Arg	Leu	Glu	Asn	Gly	His	Tyr
65				70					75					80	
Glu	Ile	Asp	Thr	Val	Leu	Leu	Thr	Lys	Ile	Lys	Asn	Tyr	Cys	Leu	Leu
			85					90					95		
Val	Leu	Thr	Asp	Arg	Arg	Ser	Arg	His	Gln	Ile	Ile	Arg	Leu	Ile	Pro
			100					105					110		
Asn	Lys	Thr	Ala	Glu	Ser	Val	Asn	Gln	Ala	Leu	Thr	Leu	Leu	Leu	Gly
		115					120					125			
Glu	His	Arg	Ile	Leu	Ser	Ile	Thr	Ala	Asp	Asn	Gly	Ser	Glu	Phe	Lys
		130				135					140				
Arg	Leu	Ser	Glu	Val	Phe	Pro	Glu	Glu	His	Ile	Tyr	Tyr	Ala	His	Ala
145					150					155					160

Tyr	Ser	Ser	Trp	Glu	Arg	Gly	Ser	Asn	Glu	Asn	His	Asn	Arg	Leu	Ile
				165					170					175	
Arg	Arg	Trp	Leu	Pro	Lys	Gly	Thr	Lys	Lys	Thr	Thr	Pro	Lys	Glu	Val
			180					185					190		
Ala	Phe	Ile	Glu	Asn	Trp	Ile	Asn	Asn	Tyr	Pro	Lys	Lys	Cys	Leu	Asp
		195					200					205			
Tyr	Lys	Ser	Pro	Ser	Glu	Phe	Leu	Leu	Gly	Gly					
	210						215								

(2) INFORMATION FOR SEQ ID NO:3346:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 130 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...130
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3346:

Cys	His	Lys	His	Asn	Met	Gln	Val	Leu	Asp	Val	Val	Lys	Thr	Leu	Leu
1				5					10					15	
His	Ala	Phe	Ala	Leu	Phe	Gln	Asp	Thr	Val	Lys	Ser	Leu	Leu	Thr	Lys
			20					25					30		
Lys	Arg	Val	Glu	Glu	Tyr	Ile	Pro	His	Ala	Asp	Leu	Arg	Leu	Val	Ile
		35					40					45			
Asn	Gln	Pro	Phe	Ala	Val	Thr	Ser	Thr	Val	Gly	Ser	Tyr	Asp	Val	Phe
	50					55					60				
Val	Asn	Val	Val	Gly	Gly	Gly	Tyr	Ala	Gly	Gln	Ser	Gly	Ala	Ile	Arg
65				70					75					80	
His	Gly	Ile	Ala	Arg	Ala	Leu	Leu	Gln	Val	Asp	Pro	Asp	Phe	Arg	Asp
			85					90					95		
Ser	Leu	Lys	Arg	Ala	Gly	Leu	Leu	Thr	Arg	Asp	Ser	Arg	Lys	Val	Glu
			100					105					110		
Arg	Lys	Lys	Pro	Gly	Leu	Lys	Lys	Ala	Arg	Lys	Ala	Ser	Gln	Phe	Ser
		115					120					125			
Lys	Arg														
	130														

(2) INFORMATION FOR SEQ ID NO:3347:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 79 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...79

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3347:

```
Leu Leu Lys Gln Lys Lys Ala Gly Phe Asn Ile Lys Met Val Asp Ile
 1             5             10             15
Ala Gly Ala Gln Leu Ala Asp Arg Val Ile Ala Glu Lys Asn Asn Ala
      20             25             30
Val Ala Asp Met Val Phe Gly Ile Gly Ala Val Asp Ser Asn Lys Ile
      35             40             45
Arg Asp Gln Lys Leu Leu Val Gln Tyr Lys Pro Lys Trp Leu Asp Lys
      50             55             60
Ile Asp Gln Ser Leu Ser Asp Asn Glu Ile Ile Ile Ile Leu
65             70             75
```

(2) INFORMATION FOR SEQ ID NO:3348:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 291 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...291

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3348:

```
Met Lys Lys Gln Glu Lys Leu Ala Leu Val Glu Ser Ala Leu Glu Asp
 1             5             10             15
Phe Tyr Gly Asp Gln Gln Phe Ala Ser Ser Leu Arg Glu Ser Val Leu
      20             25             30
Tyr Ser Ile His Ala Gly Gly Lys Arg Ile Arg Pro Phe Leu Leu Leu
      35             40             45
Glu Val Leu Glu Ala Leu Gln Val Thr Ile Lys Pro Ala His Ala Gln
      50             55             60
Val Ala Thr Ala Leu Glu Met Ile His Thr Gly Ser Leu Ile His Asp
65             70             75             80
Asp Leu Pro Ala Met Asp Asp Asp Asp Tyr Arg Arg Gly Arg Leu Thr
      85             90             95
Asn His Lys Lys Phe Gly Glu Ala Met Ala Ile Leu Ala Gly Asp Ala
      100            105            110
Leu Phe Leu Asp Ser Tyr Ala Leu Ile Ala Gln Ala Asp Leu Pro Ser
```


(A) NAME/KEY: misc_feature
(B) LOCATION 1...277

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3350:

Arg	Arg	Lys	His	Thr	Met	Thr	Gly	Ser	Asn	Lys	Leu	Thr	Lys	Arg	Asp
1				5					10					15	
Tyr	Leu	Lys	Thr	Ser	Leu	Arg	Ala	Phe	Phe	Cys	Gln	Asn	Gly	Phe	Asn
			20					25					30		
Tyr	Ser	Asn	Tyr	Gln	Gly	Leu	Gly	Tyr	Ala	Asn	Val	Met	Tyr	Pro	Ala
		35					40					45			
Leu	Lys	Lys	His	Tyr	Gly	Glu	Asp	Gln	Glu	Gly	Phe	Tyr	Gln	Ala	Leu
	50					55					60				
Glu	Glu	Asn	Cys	Glu	Phe	Tyr	Asn	Thr	Asn	Pro	His	Phe	Leu	Pro	Phe
65					70					75					80
Ile	Thr	Ser	Leu	His	Leu	Val	Met	Leu	Glu	Asn	Gly	Arg	Pro	Ala	Lys
			85						90					95	
Glu	Thr	Arg	Ser	Ile	Lys	Met	Ala	Leu	Met	Gly	Pro	Leu	Ala	Gly	Ile
			100					105					110		
Gly	Asp	Ser	Leu	Ser	Gln	Phe	Cys	Leu	Ala	Pro	Leu	Phe	Ser	Thr	Ile
		115					120					125			
Ala	Ala	Ser	Phe	Ala	Gln	Lys	Ser	Leu	Val	Val	Gly	Pro	Ile	Leu	Phe
	130					135					140				
Phe	Leu	Ala	Met	Asn	Thr	Ile	Leu	Thr	Ala	Ile	Lys	Leu	Ser	Thr	Gly
145					150					155					160
Leu	Tyr	Gly	Tyr	Lys	Leu	Gly	Thr	Thr	Val	Ile	Asp	Lys	Leu	Ser	Glu
			165						170					175	
Gln	Met	Ala	Thr	Ile	Ser	Arg	Ile	Ala	Asn	Ile	Ile	Gly	Val	Thr	Val
			180					185					190		
Ile	Ala	Gly	Leu	Ala	Gly	Thr	Ser	Val	Lys	Ile	Met	Val	Pro	Ile	Thr
	195						200					205			
Phe	Ala	Ala	Gly	Glu	Val	Lys	Ala	Asp	Ala	Lys	Gln	Ser	Ile	Val	Ser
	210					215					220				
Ile	Gln	Gly	Met	Leu	Asp	Lys	Val	Ala	Pro	Ala	Leu	Leu	Pro	Ala	Leu
225					230					235					240
Phe	Thr	Leu	Leu	Val	Tyr	Tyr	Leu	Ile	Lys	Glu	Lys	Lys	Trp	Thr	Thr
			245						250					255	
Tyr	Lys	Leu	Val	Ile	Leu	Thr	Val	Ile	Ile	Gly	Ile	Ile	Gly	Ser	Trp
		260						265					270		
Leu	Lys	Ile	Ile	Ala											
		275													

(2) INFORMATION FOR SEQ ID NO:3351:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 515 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...515

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3351:

Lys	Glu	Glu	His	Met	Ala	His	Glu	Asn	Val	Ile	Glu	Met	Arg	Asp	Ile	1	5	10	15
Thr	Lys	Val	Phe	Gly	Gly	Phe	Val	Ala	Asn	Asp	Lys	Ile	Asn	Leu	His	20	25	30	
Leu	Arg	Lys	Gly	Glu	Ile	His	Ala	Leu	Leu	Gly	Glu	Asn	Gly	Ala	Gly	35	40	45	
Lys	Ser	Thr	Leu	Met	Asn	Met	Leu	Ala	Gly	Leu	Leu	Glu	Pro	Thr	Ser	50	55	60	
Gly	Glu	Ile	Ala	Val	Asn	Gly	Gln	Val	Val	Asn	Leu	Asp	Ser	Pro	Ser	65	70	75	80
Lys	Ala	Ala	Ser	Leu	Gly	Ile	Gly	Met	Val	His	Gln	His	Phe	Met	Leu	85	90	95	
Val	Glu	Ala	Phe	Thr	Val	Ala	Glu	Asn	Ile	Ile	Leu	Gly	Ser	Glu	Leu	100	105	110	
Thr	Lys	Asn	Gly	Val	Leu	Asp	Ile	Ala	Gly	Ala	Ser	Lys	Glu	Ile	Lys	115	120	125	
Ala	Leu	Ser	Glu	Arg	Tyr	Gly	Leu	Ala	Val	Asp	Pro	Ser	Ala	Lys	Val	130	135	140	
Ala	Asp	Ile	Ser	Val	Gly	Ala	Gln	Gln	Arg	Val	Glu	Ile	Leu	Lys	Thr	145	150	155	160
Leu	Tyr	Arg	Gly	Ala	Asp	Ile	Leu	Ile	Phe	Asp	Glu	Pro	Thr	Ala	Val	165	170	175	
Leu	Thr	Pro	Ser	Glu	Ile	Asp	Glu	Leu	Met	Ala	Ile	Met	Lys	Asn	Leu	180	185	190	
Val	Lys	Glu	Gly	Lys	Ser	Ile	Ile	Leu	Ile	Thr	His	Lys	Leu	Asp	Glu	195	200	205	
Ile	Arg	Ala	Val	Ser	Asp	Arg	Val	Thr	Val	Ile	Arg	Arg	Gly	Lys	Ser	210	215	220	
Ile	Glu	Thr	Val	Glu	Ile	Ala	Gly	Ala	Thr	Asn	Ala	Asp	Leu	Ala	Glu	225	230	235	240
Met	Met	Val	Gly	Arg	Ser	Val	Ser	Phe	Lys	Thr	Glu	Lys	Gln	Ala	Ser	245	250	255	
Lys	Pro	Lys	Glu	Val	Val	Leu	Ser	Ile	Lys	Asp	Leu	Val	Val	Asn	Glu	260	265	270	
Asn	Arg	Gly	Val	Pro	Ala	Val	Lys	Asn	Leu	Ser	Leu	Asp	Val	Arg	Ala	275	280	285	
Gly	Glu	Ile	Val	Gly	Ile	Ala	Gly	Ile	Asp	Gly	Asn	Gly	Gln	Ser	Glu	290	295	300	
Leu	Ile	Gln	Ala	Ile	Thr	Gly	Leu	Arg	Lys	Val	Glu	Ser	Gly	Ser	Ile	305	310	315	320
Glu	Leu	Lys	Gly	Asp	Ser	Ile	Val	Gly	Leu	His	Pro	Arg	Gln	Ile	Thr	325	330	335	
Glu	Leu	Ser	Val	Gly	His	Val	Pro	Glu	Asp	Arg	His	Arg	Asp	Gly	Leu	340	345	350	
Ile	Leu	Glu	Met	Met	Ile	Ser	Glu	Asn	Ile	Ala	Leu	Gln	Thr	Tyr	Tyr	355	360	365	
Lys	Glu	Pro	His	Ser	Lys	Asn	Gly	Ile	Leu	Asn	Tyr	Ser	Asn	Ile	Thr	370	375	380	
Ser	Tyr	Ala	Lys	Lys	Leu	Met	Glu	Glu	Phe	Asp	Val	Arg	Ala	Ala	Ser	385	390	395	400

Glu Leu Val Pro Ala Ala Ala Leu Ser Gly Gly Asn Gln Gln Lys Ala

405 410 415

Ile Ile Ala Arg Glu Ile Asp Arg Asp Pro Asp Leu Leu Ile Val Ser

420 425 430

Gln Pro Thr Arg Gly Leu Asp Val Gly Ala Ile Glu Tyr Ile His Lys

435 440 445

Arg Leu Ile Glu Glu Arg Asp Asn Gly Lys Ala Val Leu Val Val Ser

450 455 460

Phe Glu Leu Asp Glu Ile Leu Asn Val Ser Asp Arg Ile Ala Val Ile

465 470 475 480

His Asp Gly Lys Ile Gln Gly Ile Val Ser Pro Glu Thr Thr Asn Lys

485 490 495

Gln Gly Leu Gly Val Leu Met Ala Gly Gly Asn Leu Gly Lys Glu Lys

500 505 510

Ser Asp Val

515

(2) INFORMATION FOR SEQ ID NO:3352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3352:

Leu Glu Trp His Leu Lys Lys Leu Leu Leu Trp Gly Phe Phe Pro Leu

1 5 10 15

Ser Phe Gln Thr Leu Ala Asn Phe Trp Leu Leu Val Leu Leu Ala Val

20 25 30

Pro Tyr Phe Asn Ala Leu Lys Ile Arg Leu Thr Leu Leu Thr Lys Lys

35 40 45

Gly Tyr Arg Val Ile Met Thr Gln Tyr Pro Phe Phe Tyr Phe Glu Asn

50 55 60

Leu Tyr Ser Met Lys Ile Lys Glu Gln Thr Arg Lys Leu Ala Ala Gly

65 70 75 80

Cys Ser Lys His Cys Phe Glu Val Val Asp Glu Thr Asp Glu Val Ser

85 90 95

Asn His Thr Tyr Gly Lys Ala Lys Leu Met Arg Phe Glu Glu Ile Phe

100 105 110

Glu Glu Tyr

115

(2) INFORMATION FOR SEQ ID NO:3353:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 477 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...477
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3353:

Ser	Gly	Trp	Gln	Ala	Cys	Ser	Gln	Trp	Tyr	Pro	Tyr	Phe	Cys	Asn	Trp
1				5					10					15	
Glu	Leu	Arg	Arg	Phe	Ser	Met	Phe	Arg	Lys	Ile	Leu	Ile	Ala	Asn	Arg
			20					25					30		
Gly	Glu	Ile	Ala	Val	Arg	Ile	Ile	Arg	Ala	Ala	Arg	Glu	Leu	Gly	Ile
		35					40					45			
Ala	Thr	Val	Ala	Val	Tyr	Ser	Thr	Ala	Asp	Lys	Glu	Ala	Leu	His	Thr
	50					55					60				
Leu	Leu	Ala	Asp	Glu	Ala	Val	Cys	Ile	Gly	Pro	Gly	Lys	Ala	Thr	Glu
65					70				75						80
Ser	Tyr	Leu	Asn	Ile	Asn	Ala	Val	Leu	Ser	Ala	Ala	Val	Leu	Thr	Glu
			85						90					95	
Ala	Glu	Ala	Ile	His	Pro	Gly	Phe	Gly	Phe	Leu	Ser	Glu	Asn	Ser	Lys
			100					105					110		
Phe	Ala	Thr	Met	Cys	Glu	Glu	Ile	Gly	Ile	Lys	Phe	Ile	Gly	Pro	Ser
		115					120					125			
Gly	His	Val	Met	Asp	Met	Met	Gly	Asp	Lys	Ile	Asn	Ala	Arg	Ala	Gln
	130					135					140				
Met	Ile	Lys	Ala	Gly	Val	Pro	Val	Ile	Pro	Gly	Ser	Asp	Gly	Glu	Val
145					150					155					160
His	Asn	Ser	Glu	Glu	Ala	Leu	Ile	Val	Ala	Glu	Lys	Ile	Gly	Tyr	Pro
			165						170					175	
Val	Met	Leu	Lys	Ala	Ser	Ala	Gly	Gly	Gly	Lys	Gly	Ile	Arg	Lys	
		180					185					190			
Val	Glu	Lys	Pro	Asp	Asp	Leu	Val	Ser	Ala	Phe	Glu	Thr	Ala	Ser	Ser
	195						200					205			
Glu	Ala	Lys	Ala	Asn	Tyr	Gly	Asn	Gly	Ala	Met	Tyr	Ile	Glu	Arg	Val
	210					215					220				
Ile	Tyr	Pro	Ala	Arg	His	Ile	Glu	Val	Gln	Ile	Leu	Gly	Asp	Glu	His
225					230					235					240
Gly	His	Val	Ile	His	Leu	Gly	Glu	Arg	Asp	Cys	Ser	Leu	Gln	Arg	Asn
			245						250					255	
Asn	Gln	Lys	Val	Leu	Glu	Glu	Ser	Pro	Ser	Ile	Ala	Ile	Gly	Lys	Thr
		260					265						270		
Leu	Arg	His	Glu	Ile	Gly	Ala	Ala	Ala	Val	Arg	Ala	Ala	Glu	Phe	Val
	275					280						285			
Gly	Tyr	Glu	Asn	Ala	Gly	Thr	Ile	Glu	Phe	Leu	Leu	Asp	Glu	Ala	Ser
	290					295					300				
Ser	Asn	Phe	Tyr	Phe	Met	Glu	Met	Asn	Thr	Arg	Val	Gln	Val	Glu	His

305		310		315		320									
Pro	Val	Thr	Glu	Phe	Val	Ser	Gly	Val	Asp	Ile	Val	Lys	Glu	Gln	Ile
		325							330					335	
Cys	Ile	Ala	Ala	Gly	Gln	Pro	Leu	Ser	Val	Lys	Gln	Glu	Asp	Ile	Val
		340						345					350		
Leu	Arg	Gly	His	Ala	Ile	Glu	Cys	Arg	Ile	Asn	Ala	Glu	Asn	Pro	Ala
		355					360					365			
Phe	Asn	Phe	Ala	Pro	Ser	Pro	Gly	Lys	Ile	Thr	Asn	Leu	Tyr	Leu	Pro
		370				375					380				
Ser	Gly	Gly	Val	Gly	Leu	Arg	Val	Asp	Ser	Ala	Val	Tyr	Pro	Gly	Tyr
385					390				395					400	
Thr	Ile	Pro	Pro	Tyr	Tyr	Asp	Ser	Met	Ile	Ala	Lys	Ile	Ile	Val	His
			405					410					415		
Gly	Glu	Asn	Arg	Phe	Asp	Ala	Leu	Met	Lys	Met	Gln	Arg	Ala	Leu	Tyr
		420					425					430			
Glu	Leu	Glu	Ile	Glu	Gly	Val	Gln	Thr	Asn	Ala	Asp	Phe	Gln	Leu	Asp
		435				440					445				
Leu	Ile	Ser	Asp	Arg	Asn	Val	Ile	Ala	Gly	Asp	Tyr	Asp	Thr	Cys	Phe
	450				455				460						
Leu	Met	Glu	Thr	Phe	Leu	Pro	Lys	Tyr	Gln	Glu	Lys	Glu			
465					470				475						

(2) INFORMATION FOR SEQ ID NO:3354:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 487 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...487
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3354:

Leu	Arg	Trp	His	Arg	Glu	Phe	Arg	Pro	His	Ala	Ser	Tyr	Phe	Ala	Trp
1			5					10					15		
Gly	Phe	Phe	Ile	Gln	Ser	Leu	Arg	Thr	Arg	Ile	Arg	Thr	Glu	Arg	Glu
		20					25					30			
Ile	Thr	Met	Glu	Arg	Ile	Ile	His	Gly	Asp	Val	Leu	Ser	Pro	Ile	Leu
		35				40					45				
Ala	Tyr	Met	Arg	Leu	Lys	Gly	Gln	His	Lys	Val	Ile	Leu	Glu	Ser	Ile
	50				55				60						
Pro	Arg	Asp	Lys	Glu	Thr	Ala	Arg	Phe	Ser	Ile	Leu	Ala	Tyr	Asn	Pro
65			70					75				80			
Val	Phe	Glu	Ile	Lys	Phe	Glu	Asn	Gly	Val	Leu	Tyr	Gln	Asn	Gly	Gln
		85					90					95			
Val	Ile	Asp	Arg	Asp	Pro	Leu	Asp	Phe	Leu	Tyr	Glu	Val	Ile	His	Lys
	100				105				110						
Ser	Gln	His	His	Ser	Glu	Leu	Pro	Phe	Gly	Gly	Gly	Ala	Ile	Gly	Phe

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...117

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3355:

Gln	Gly	Trp	Gln	Val	Met	Phe	Leu	Lys	Gln	Ser	Arg	Leu	Lys	Pro	Tyr
1				5					10					15	
Pro	Met	Arg	Arg	Phe	Glu	Lys	Thr	Val	Thr	Glu	Glu	Gly	Val	Ala	Lys
			20					25					30		
Glu	Gly	Tyr	Ala	Lys	Glu	Ala	Glu	Thr	Val	Arg	Leu	Glu	Leu	Trp	Pro
		35					40					45			
Ala	Ser	Ser	Lys	Leu	Gln	Ser	Glu	Leu	Tyr	Gly	Glu	Arg	Val	Asn	Asp
	50					55				60					
Ile	Leu	Asn	Ala	Asn	Ala	Asn	Lys	Ser	Ala	Thr	Ile	Lys	Val	Lys	Asp
65					70					75					80
Gly	Val	Cys	Ile	Asp	Ser	Gln	Thr	Glu	Val	Thr	His	Arg	Val	Ile	Ser
				85					90					95	
Lys	Lys	Val	Tyr	Thr	His	His	Gln	Val	Leu	Glu	Leu	Glu	Arg	Val	Arg
			100					105						110	
Ala	Thr	Arg	Gly	Arg											
			115												

(2) INFORMATION FOR SEQ ID NO:3356:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 237 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...237

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3356:

Lys	Ser	Arg	His	Arg	Ile	Met	Pro	Thr	Phe	Ser	Ser	Asn	Ala	Pro	Phe
1				5					10					15	
Asn	Pro	Asn	Pro	Ile	Ser	Lys	Ile	Leu	Val	Val	Phe	Ile	Thr	Gly	Leu
			20					25					30		
Thr	Val	Met	His	Ser	Ile	Asn	Ile	Arg	Phe	Glu	Leu	Ala	Ile	Val	Cys
		35				40						45			
Leu	Ile	Gly	Ile	Leu	Leu	Tyr	Leu	Asn	Gly	Tyr	Lys	Lys	Thr	Leu	Phe
	50					55				60					
Lys	Trp	Ile	Ile	Leu	Cys	Gly	Ile	Leu	Tyr	Ser	Leu	Pro	Asn	Phe	Met

65					70					75				80
Val	Leu	Ser	Glu	Leu	Asn	Pro	Ile	Val	Lys	Met	Phe	Leu	Ser	Ile
				85					90					95
Ile	Val	Ile	Arg	Met	Phe	Ile	Leu	Pro	Phe	Met	Ala	Ala	Ser	Phe
			100					105					110	
Ile	Lys	Thr	Ser	Asp	Val	Gly	Ala	Ile	Ile	Ser	Ser	Met	Asp	Lys
	115					120						125		Leu
Lys	Ile	Ser	Lys	Asn	Val	Ser	Ile	Pro	Ile	Ala	Val	Met	Phe	Arg
	130					135					140			Phe
Phe	Pro	Ser	Phe	Lys	Glu	Glu	Lys	Lys	Asn	Ile	Lys	Met	Ala	Met
145					150				155					160
Val	Arg	Gly	Ile	Asn	Phe	Lys	Asn	Pro	Val	Lys	Tyr	Leu	Glu	Tyr
			165					170					175	
Ser	Val	Pro	Leu	Leu	Ile	Ile	Ser	Ser	Asn	Ile	Ser	Asp	Asp	Ile
		180					185					190		Ala
Lys	Ala	Ala	Glu	Thr	Lys	Ala	Ile	Glu	Asn	Pro	Ile	Ala	Lys	Thr
	195					200					205			Arg
Tyr	Ile	Arg	Val	Lys	Ile	Gln	Leu	Ile	Asp	Phe	Val	Tyr	Val	Leu
210					215				220					Ala
Val	Ala	Gly	Leu	Ile	Val	Gly	Gly	Leu	Ile	Trp	Leu	Lys		
225				230				235						

(2) INFORMATION FOR SEQ ID NO:3357:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 313 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3357:

Glu	Arg	Arg	Gln	Ile	Met	Ser	Thr	Ile	Asp	Lys	Glu	Lys	Phe	Gln	Phe
1			5					10					15		
Val	Lys	Arg	Asp	Asp	Phe	Ala	Ser	Glu	Thr	Ile	Asp	Ala	Pro	Ala	Tyr
		20					25					30			
Ser	Tyr	Trp	Lys	Ser	Val	Phe	Lys	Gln	Phe	Met	Lys	Lys	Lys	Ser	Thr
	35				40						45				
Val	Val	Met	Leu	Gly	Ile	Leu	Val	Ala	Ile	Ile	Leu	Ile	Ser	Phe	Ile
	50				55				60						
Tyr	Pro	Met	Phe	Ser	Lys	Phe	Asp	Phe	Asn	Asp	Val	Ser	Lys	Val	Asn
65			70				75						80		
Asp	Phe	Ser	Val	Arg	Tyr	Ile	Lys	Pro	Asn	Ala	Glu	His	Trp	Phe	Gly
	85						90						95		
Thr	Asp	Ser	Asn	Gly	Lys	Ser	Leu	Phe	Asp	Gly	Val	Trp	Phe	Gly	Ala
	100						105				110				
Arg	Asn	Ser	Ile	Leu	Ile	Ser	Val	Ile	Ala	Thr	Val	Ile	Asn	Leu	Val

Phe	Glu	Val	Val	Asp	Glu	Thr	Asp	Glu	Val	Ser	Ser	Lys	His	Gly	Phe
				85					90					95	
Glu	Val	Ala	Asp	Glu	Thr	Asp	Glu	Val	Ser	Ser	Lys	His	Gly	Phe	Glu
			100					105					110		
Val	Ala	Asp	Arg	Thr	Asp	Glu	Val	Ser	Asn	Ile	Tyr	Thr	Val	Arg	Arg
		115					120					125			
Arg															

(2) INFORMATION FOR SEQ ID NO:3359:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...321

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3359:

Asn	Lys	Gly	Gln	Ser	Pro	Asn	Lys	Leu	Glu	Asp	Leu	Met	Lys	Lys	Leu
1				5					10					15	
Gly	Thr	Leu	Leu	Val	Leu	Phe	Leu	Ser	Ala	Ile	Ile	Leu	Val	Ala	Cys
			20					25					30		
Ala	Ser	Gly	Lys	Lys	Ala	Thr	Thr	Ser	Gly	Gln	Lys	Leu	Lys	Val	Val
		35				40						45			
Ala	Thr	Asn	Ser	Ile	Ile	Ala	Asp	Ile	Thr	Lys	Asn	Ile	Ala	Gly	Asp
	50					55					60				
Lys	Ile	Asp	Leu	His	Ser	Ile	Val	Pro	Ile	Gly	Gln	Asp	Pro	His	Glu
65				70						75				80	
Tyr	Glu	Pro	Leu	Pro	Glu	Asp	Val	Lys	Lys	Thr	Ser	Glu	Ala	Asp	Leu
			85					90						95	
Ile	Phe	Tyr	Asn	Gly	Ile	Asn	Leu	Glu	Thr	Gly	Gly	Asn	Ala	Trp	Phe
			100					105					110		
Thr	Lys	Leu	Val	Glu	Asn	Ala	Lys	Lys	Thr	Glu	Asn	Lys	Asp	Tyr	Phe
		115					120					125			
Ala	Val	Ser	Asp	Gly	Val	Asp	Val	Ile	Tyr	Leu	Glu	Gly	Gln	Asn	Glu
	130					135					140				
Lys	Gly	Lys	Glu	Asp	Pro	His	Ala	Trp	Leu	Asn	Leu	Glu	Asn	Gly	Ile
145					150					155				160	
Ile	Phe	Ala	Lys	Asn	Ile	Ala	Lys	Gln	Leu	Ser	Ala	Lys	Asp	Pro	Asn
			165					170						175	
Asn	Lys	Glu	Phe	Tyr	Glu	Lys	Asn	Leu	Lys	Glu	Tyr	Thr	Asp	Lys	Leu
		180					185						190		
Asp	Lys	Leu	Asp	Lys	Glu	Ser	Lys	Asp	Lys	Phe	Asn	Lys	Ile	Pro	Ala
		195					200					205			
Glu	Lys	Lys	Leu	Ile	Val	Thr	Ser	Glu	Gly	Ala	Phe	Lys	Tyr	Phe	Ser

210	215	220
Lys Ala Tyr Gly Val Pro Ser Ala Tyr Ile Trp Glu Ile Asn Thr Glu		
225	230	235
Glu Glu Gly Thr Pro Glu Gln Ile Lys Thr Leu Val Glu Lys Leu Arg		
	245	250
Gln Thr Lys Val Pro Ser Leu Phe Val Glu Ser Ser Val Asp Asp Arg		
	260	265
Pro Met Lys Thr Val Ser Gln Asp Thr Asn Ile Pro Ile Tyr Ala Gln		
	275	280
Ile Phe Thr Asp Ser Ile Ala Glu Gln Gly Lys Glu Gly Asp Ser Tyr		
	290	300
Tyr Ser Met Met Lys Tyr Asn Leu Asp Lys Ile Ala Glu Gly Leu Ala		
305	310	315
Lys		320

(2) INFORMATION FOR SEQ ID NO:3360:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...246

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3360:

Met	Ala	Phe	Asn	Pro	Ile	Val	Lys	Tyr	Ser	Leu	Ala	Leu	Val	Tyr	Asp
1			5					10						15	
Leu	Arg	Lys	Asn	Leu	Lys	Gly	Leu	Thr	Val	Leu	Ser	Leu	Leu	Ile	Thr
		20						25					30		
Gly	Leu	Phe	Phe	Leu	Thr	Lys	Tyr	Pro	Leu	Glu	Asn	Glu	Ile	Thr	Met
		35				40					45				
Leu	Asp	Val	Gly	Gln	Gly	Glu	Ser	Ile	Phe	Leu	Arg	Asp	Val	Thr	Gly
	50				55				60						
Lys	Thr	Ile	Leu	Ile	Asp	Val	Gly	Gly	Lys	Ala	Glu	Ser	Tyr	Lys	Lys
65				70				75						80	
Ile	Glu	Lys	Trp	Gln	Glu	Lys	Met	Thr	Thr	Ser	Asn	Ala	Gln	Arg	Thr
		85						90					95		
Leu	Ile	Pro	Tyr	Leu	Lys	Ser	Arg	Gly	Val	Ala	Lys	Ile	Asp	Gln	Leu
		100					105					110			
Ile	Leu	Thr	Asn	Thr	Asp	Lys	Glu	His	Val	Gly	Asp	Leu	Ser	Glu	Val
	115				120					125					
Thr	Lys	Ala	Phe	His	Val	Gly	Glu	Ile	Leu	Val	Ser	Lys	Gly	Ser	Leu
	130				135					140					
Lys	Gln	Lys	Gln	Phe	Val	Val	Glu	Leu	Gln	Ala	Thr	Lys	Thr	Lys	Val
145				150				155						160	
Arg	Ser	Met	Thr	Val	Gly	Glu	Asn	Leu	Pro	Ile	Phe	Gly	Ser	Gln	Leu

				165					170					175			
Glu	Val	Leu	Ser	Pro	Arg	Lys	Met	Gly	Asp	Gly	Gly	His	Asp	Asp	Thr		
			180					185					190				
Leu	Val	Leu	Tyr	Gly	Lys	Phe	Leu	Asp	Lys	Gln	Phe	Leu	Phe	Thr	Gly		
		195					200					205					
Asn	Leu	Glu	Glu	Lys	Gly	Glu	Lys	Asp	Leu	Leu	Lys	His	Tyr	Pro	Asp		
	210					215					220						
Leu	Lys	Val	Tyr	Val	Leu	Lys	Ala	Ser	Gln	His	Gly	Asn	Lys	Lys	Ser		
225					230					235					240		
Ser	Ser	Pro	Ala	Phe	Xaa												
				245													

(2) INFORMATION FOR SEQ ID NO:3361:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 300 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3361:

Asn	Asp	Phe	Lys	Ser	Leu	Asn	Arg	Lys	Gly	Glu	Ser	Met	Ala	Leu	Phe		
1				5					10					15			
Ser	Lys	Lys	Asp	Lys	Tyr	Ile	Arg	Ile	Asn	Pro	Asn	Arg	Ser	Val	Arg		
		20					25					30					
Glu	Lys	Pro	Gln	Ala	Lys	Pro	Glu	Val	Pro	Asp	Glu	Leu	Phe	Ser	Gln		
	35					40					45						
Cys	Pro	Gly	Cys	Lys	His	Thr	Ile	Tyr	Gln	Lys	Asp	Leu	Gly	Ser	Glu		
	50				55					60							
Arg	Ile	Cys	Pro	His	Cys	Ser	Tyr	Thr	Phe	Arg	Ile	Ser	Ala	Gln	Glu		
65				70					75					80			
Arg	Leu	Ala	Leu	Thr	Ile	Asp	Met	Gly	Thr	Phe	Lys	Glu	Leu	Phe	Thr		
			85					90						95			
Gly	Ile	Glu	Ser	Lys	Asp	Pro	Leu	His	Phe	Pro	Gly	Tyr	Gln	Lys	Lys		
	100						105						110				
Leu	Ala	Ser	Met	Arg	Glu	Lys	Thr	Gly	Leu	His	Glu	Ala	Val	Val	Thr		
	115					120					125						
Gly	Thr	Ala	Leu	Ile	Lys	Gly	Gln	Thr	Val	Ala	Leu	Gly	Ile	Met	Asp		
	130				135					140							
Ser	Asn	Phe	Ile	Met	Ala	Ser	Met	Gly	Thr	Val	Val	Gly	Glu	Lys	Ile		
145				150				155						160			
Thr	Arg	Leu	Phe	Glu	Tyr	Ala	Thr	Val	Glu	Lys	Leu	Pro	Val	Val	Leu		
		165					170							175			
Phe	Thr	Ala	Ser	Gly	Gly	Ala	Arg	Met	Gln	Glu	Gly	Ile	Met	Ser	Leu		
	180					185						190					
Met	Gln	Met	Ala	Lys	Ile	Ser	Ala	Ala	Val	Lys	Arg	His	Ser	Asn	Ala		

(2) INFORMATION FOR SEQ ID NO:3362:

(A) LENGTH: 75 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: YES

(A) ORGANISM: *Streptococcus pneumoniae*

```
(A) NAME/KEY: misc_feature
(B) LOCATION 1...75
```

Asp	Gly	Phe	Lys	Phe	Ala	Trp	Lys	Met	Asp	Ile	Leu	Thr	Ser	Leu	Gln
1				5					10					15	
Glu	Ser	Glu	Ser	Leu	Ile	Ser	Ile	Gln	Asn	Trp	His	Asn	Ser	Cys	Met
			20					25					30		
Asn	Gly	Asn	Ile	Asn	Pro	Ser	Gln	Asp	Ala	Leu	Val	Leu	Lys	Ile	Ile
		35					40					45			
Glu	Ala	Leu	Ile	Val	Lys	Glu	Glu	Leu	Ser	Tyr	Glu	Ala	Arg	Thr	Ala
	50					55					60				
Cys	Ile	His	Phe	Leu	Leu	Lys	Ile	Leu	Asn	Ile					
65					70					75					

(A) LENGTH: 205 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3363:

```
Ile Met Phe Lys Arg Ile Arg Arg Val Leu Val Leu Ala Val Phe Leu
1          5          10          15
Phe Ala Gly Tyr Lys Ala Tyr Arg Val His Gln Asp Val Lys Gln Val
          20          25          30
Met Thr Tyr Gln Pro Met Val Arg Glu Ile Leu Ser Glu Lys Asp Thr
          35          40          45
Pro Ala Asn Glu Glu Leu Val Leu Ala Met Ile Tyr Thr Glu Thr Lys
          50          55          60
Gly Lys Glu Gly Asp Val Met Gln Ser Ser Glu Ser Ala Ser Gly Ser
65          70          75          80
Thr Asn Thr Ile Asn Asp Asn Ala Ser Ser Ile Arg Gln Gly Ile Gln
          85          90          95
Thr Leu Thr Gly Asn Leu Tyr Leu Ala Gln Lys Lys Gly Val Asp Ile
          100         105         110
Trp Thr Ala Val Gln Ala Tyr Asn Phe Gly Pro Ala Tyr Ile Asp Phe
          115         120         125
Ile Ala Gln Asn Gly Lys Glu Asn Thr Leu Ala Leu Ala Lys Gln Tyr
          130         135         140
Ser Arg Glu Thr Val Ala Pro Leu Leu Gly Asn Thr Thr Gly Lys Thr
145          150         155         160
Tyr Ser Tyr Ile His Pro Ile Ser Ile Phe His Gly Ala Glu Leu Tyr
          165         170         175
Val Asn Gly Gly Asn Tyr Tyr Tyr Ser Arg Gln Val Arg Leu Asn Leu
          180         185         190
Tyr Ile Ile Lys Cys Phe Thr Leu Phe Ser Thr Ser Gly
          195         200         205
```

(2) INFORMATION FOR SEQ ID NO:3364:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 118 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...118

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3364:

Gln Asn Phe Leu Thr Trp Ser Ile Lys Pro Met Cys Met Ser Ile Leu

1				5				10					15				
Phe	Ala	Trp	Phe	Arg	Lys	Asn	Ala	Leu	Arg	Val	Ser	Gln	Gln	Tyr	Val		
			20					25					30				
Met	Ser	Gln	Thr	Val	Lys	Val	Phe	Asp	Leu	Leu	Leu	Lys	Ser	Ser	Ala		
		35					40					45					
Thr	Pro	Gln	Pro	Met	Leu	Phe	Ser	Tyr	Asn	Leu	Phe	Lys	Met	Thr	Gln		
	50					55					60						
Met	Gln	Thr	Asn	Phe	Gly	Phe	Asn	Met	Leu	Ala	Ile	Gln	Asn	Gly	Ile		
65					70					75					80		
Pro	Lys	Ile	Leu	Ser	Leu	Arg	Gln	Ile	Leu	Asp	Ala	Tyr	Ile	Glu	His		
				85					90					95			
Gln	Lys	Glu	Trp	Leu	Phe	Val	Val	His	Val	Leu	Ile	Arg	Lys	Lys	Arg		
			100					105					110				
Lys	Arg	Ala	Leu	Ile	Ser												
			115														

(2) INFORMATION FOR SEQ ID NO:3365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...202

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3365:

Arg	Asp	Phe	Leu	Ser	Asn	Leu	Leu	Lys	Gly	Phe	Ser	Leu	Gly	Leu	Ala		
1				5				10					15				
Leu	Phe	Leu	Leu	Thr	Leu	Leu	Gly	Leu	Val	Val	Leu	Gly	Gln	Tyr	Arg		
		20					25					30					
Leu	Glu	Ser	Ile	His	Leu	Asn	Pro	Tyr	Ser	Leu	Ala	Phe	Val	Val	Phe		
	35					40					45						
Thr	Ile	Pro	Phe	Trp	Ile	Leu	Gln	Gly	Thr	Ala	Glu	Glu	Val	Val	Ala		
	50				55					60							
Arg	Ala	Trp	Leu	Leu	Pro	Gln	Leu	Ala	Ser	Arg	Thr	Asn	Leu	Lys	Leu		
65				70				75						80			
Ala	Ile	Leu	Ile	Ser	Ser	Leu	Phe	Phe	Thr	Leu	Leu	His	Met	Gly	Asn		
			85					90					95				
Ser	Gly	Leu	Thr	Pro	Leu	Ser	Leu	Val	Asn	Leu	Phe	Leu	Phe	Gly	Val		
		100					105					110					
Ala	Met	Ala	Leu	Tyr	Leu	Leu	Lys	Thr	Asp	Thr	Val	Trp	Gly	Val	Ala		
	115					120					125						
Gly	Ile	His	Gly	Ala	Trp	Asn	Phe	Ala	Gln	Gly	Asn	Leu	Phe	Gly	Ile		
	130				135					140							
Leu	Val	Ser	Gly	Gln	Pro	Ser	Gly	Thr	Ser	Leu	Met	Thr	Phe	Leu	Pro		
145				150				155						160			
Gln	Gly	Asn	Gln	Asp	Trp	Leu	Ser	Gly	Gly	Ser	Phe	Gly	Ile	Glu	Gly		

				165					170					175
Ser	Ile	Met	Thr	Ser	Leu	Val	Leu	Leu	Leu	Ile	Val	Tyr	Leu	Ala
				180					185				190	
Asn	Lys	Leu	Lys	Lys	Glu	Asn	Glu	Arg	Met					
				195					200					

(2) INFORMATION FOR SEQ ID NO:3366:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 79 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...79

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3366:

Met	Asn	Ile	Lys	Ile	Ile	Arg	Arg	Thr	Lys	Val	Val	Lys	Asn	Leu	Lys
1			5					10					15		
Leu	Lys	Leu	Ala	Arg	Val	Glu	Leu	Asp	Leu	Thr	Gln	Gly	Gln	Leu	Ala
			20					25					30		
Asp	Ala	Val	Gly	Val	Thr	Arg	Gln	Thr	Ile	Gly	Leu	Ile	Glu	Ala	Gly
			35					40					45		
Lys	Tyr	Asn	Pro	Ser	Leu	Ser	Leu	Cys	Gln	Ser	Ile	Cys	Arg	Cys	Leu
			50				55				60				
Gly	Lys	Thr	Leu	Asp	Gln	Leu	Phe	Trp	Glu	Glu	Glu	Asp	Glu	Lys	
65					70					75					

(2) INFORMATION FOR SEQ ID NO:3367:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 73 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...73

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3367:

```

Ser Ile Cys Leu His Leu Ile Ser Ile Tyr Tyr Ile Ile Ser Ile Asn
1           5           10           15
Asp Asp Gly Asp Cys Phe Val Cys Ala Cys Arg Phe Leu Asn Pro Asp
20           25           30
Arg Ala Glu Tyr Phe Cys Arg Gly Cys Gln Gly Glu Asn Pro Glu
35           40           45
Asp Ile Glu Phe Tyr Asp Glu Gln Leu Gln Ala Glu Lys Val Glu Val
50           55           60
Leu Asn Ile Arg Leu Glu Val Lys Asn
65           70

```

(2) INFORMATION FOR SEQ ID NO:3368:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 546 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...546

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3368:

```

Arg Ser Ile Lys Met Lys Lys Ile Val Lys Leu Ala Leu Thr Ala Ala
1           5           10           15
Ala Val Leu Ile Ala Val Val Gly Leu Val Ala Cys Ser Ser Gly Ser
20           25           30
Lys Lys Ser Asp Phe Ser Glu Ser Gly Lys Glu Lys Val Phe Tyr Leu
35           40           45
Ser Gly Leu Leu Gln Gly Thr Gly Asp Arg Ile Pro Tyr Val Trp Gln
50           55           60
Asn Gly Asp Gly Leu Val Pro Tyr Leu Leu Tyr Arg Thr Leu Leu Met
65           70           75           80
Ala Asp Ser Lys Tyr Glu Lys Ser Thr Pro Asp Leu Ala Lys Asp Trp
85           90           95
Lys Lys Ser Asp Asp Glu Lys Thr Tyr Glu Phe Thr Leu Lys Asp Gly
100          105          110
Leu Lys Trp Ser Asp Gly Glu Ala Leu Thr Ala Ser Asp Val Glu Phe
115          120          125
Ser Val Lys Leu Ala Leu Lys Ala Ser Val Ile Asn Gly Ile Phe Pro
130          135          140
Ser Thr Phe Thr Lys Ile Glu Gly Ala Lys Asp Phe Lys Asp Asp Lys
145          150          155          160
Ala Asp Lys Ile Ser Gly Leu Thr Val Asp Gly Asn Lys Val Thr Phe
165          170          175
Lys Leu Thr Ala Pro Val Gly Asp Phe Glu Gln Met Met Thr Gln Phe
180          185          190
Phe Ile Leu Pro Lys His Lys Leu Glu Ser Glu Asn Pro Leu Glu Leu
195          200          205

```

Asn	Asn	Ser	Ser	Phe	Trp	Thr	Ala	Pro	Val	Thr	Ser	Gly	Met	Tyr	Lys
210						215					220				
Val	Lys	Glu	Ile	Ser	Ala	Gly	Asn	Phe	Leu	Glu	Tyr	Asp	Lys	Asn	Glu
225					230					235					240
Asn	Tyr	Glu	Asn	Glu	Lys	Pro	Lys	Phe	Asp	Lys	Val	Val	Phe	Asn	Tyr
			245						250					255	
Ile	Ser	Asp	Pro	Val	Leu	Ala	Leu	Gln	Asp	Gly	Lys	Ser	Tyr	Phe	Tyr
		260						265					270		
Ser	Thr	Asn	Lys	Pro	Gln	Glu	Ile	Ser	Gln	Leu	Asp	Ala	Val	Ser	Thr
	275						280					285			
Leu	Thr	Lys	Lys	Pro	Ile	Asp	Ile	Leu	Phe	Tyr	Arg	Tyr	Phe	Ile	Ala
	290					295					300				
Asn	Leu	Ala	Gly	Val	Glu	Gly	Asn	Gly	Asp	Ser	Leu	Ile	Ala	Asn	Pro
305					310					315					320
Lys	Val	Arg	Glu	Ala	Ile	Leu	Tyr	Ala	Ile	Asn	Arg	Asp	Glu	Leu	Ala
			325						330					335	
Lys	Ser	Val	Phe	Ser	Gly	Ile	Ala	Asp	Val	Asn	Asn	Thr	Gly	Val	Pro
		340						345					350		
Ser	Ser	Leu	Glu	Ala	His	Leu	Lys	Ser	Ala	Asn	Lys	Phe	Glu	Tyr	Asn
	355						360					365			
Pro	Glu	Lys	Ala	Lys	Gln	Leu	Leu	Lys	Glu	Ala	Lys	Tyr	Asp	Asn	Ser
	370					375					380				
Arg	Asn	Leu	Ile	Leu	Ala	Tyr	Tyr	Tyr	Lys	Asp	Gln	Ala	Ser	Gln	Asp
385					390					395					400
Phe	Met	Gln	Ala	Val	Ser	Tyr	Gln	Leu	Asn	Glu	Val	Gly	Ile	Lys	Asn
			405						410					415	
Glu	Val	Val	Gln	Ile	Thr	Ser	Asp	Ala	Thr	Thr	Gly	Leu	Phe	Lys	Thr
		420						425					430		
Arg	Lys	Tyr	Asp	Leu	Ala	Tyr	Lys	Gly	Leu	Ser	Ser	Phe	Gly	Tyr	Glu
	435						440					445			
Thr	Trp	Tyr	Gly	Glu	Tyr	Ser	Ser	Thr	Asn	Thr	Asn	Phe	Lys	Asn	Ile
	450					455					460				
Thr	Asn	Gly	Glu	Thr	Ser	Phe	Asp	Glu	Leu	Ser	Lys	Lys	Leu	Ser	Glu
465					470					475					480
Thr	Ser	Asp	Val	Lys	Glu	Arg	Asn	Lys	Ile	Leu	Ala	Ser	Leu	Gln	Lys
			485						490					495	
Leu	Glu	Gln	Glu	Lys	Leu	Leu	Lys	Leu	Asn	Leu	Phe	Thr	Phe	Lys	Asn
		500						505					510		
Phe	Leu	Tyr	Leu	Asn	Thr	Glu	Lys	Val	Leu	Ile	Pro	Asp	Asp	Val	Gln
	515						520					525			
Phe	Gly	Asn	Pro	Phe	Tyr	Lys	Phe	Asp	Tyr	Lys	Phe	Glu	Lys	Trp	Asp
	530					535					540				
Ala	Lys														
545															

(2) INFORMATION FOR SEQ ID NO:3369:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...75

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3369:

```
Ile Pro Ile Lys Asp Ile Asp Phe Ser Ile Val Asn Gln Met Asn Asp
1          5          10          15
Leu Val Ser Leu Thr Ile Val Ala Leu Arg Ser Phe Lys Thr Glu Leu
          20          25          30
Ile Phe Leu Trp Gly Ile Glu Gln Val Leu His Glu Leu Ile Asp Ser
          35          40          45
Ile Asn Pro Cys Arg Pro Ser Val His Arg Ser Gln Asn Leu Asp Ile
          50          55          60
Thr Gly Arg Asn Thr Ile Ser Glu Gly Gly Thr
65          70          75
```

(2) INFORMATION FOR SEQ ID NO:3370:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 295 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...295

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3370:

```
Met Glu Ile Lys Ile Glu Thr Gly Gly Leu Arg Leu Asp Lys Ala Leu
1          5          10          15
Ser Asp Leu Ser Glu Leu Ser Arg Ser Leu Ala Asn Glu Gln Ile Lys
          20          25          30
Ser Gly Gln Val Leu Val Asn Gly Gln Val Lys Lys Ala Lys Tyr Thr
          35          40          45
Val Gln Glu Gly Asp Val Val Thr Tyr His Val Pro Glu Pro Glu Val
          50          55          60
Leu Glu Tyr Val Ala Glu Asp Leu Pro Leu Glu Ile Val Tyr Gln Asp
65          70          75          80
Glu Asp Val Ala Val Val Asn Lys Pro Gln Gly Met Val Val His Pro
          85          90          95
Ser Ala Gly His Thr Ser Gly Thr Leu Val Asn Ala Leu Met Tyr His
          100          105          110
Ile Lys Asp Leu Ser Gly Ile Asn Gly Val Leu Arg Pro Gly Ile Val
          115          120          125
His Arg Ile Asp Lys Asp Thr Ser Gly Leu Leu Met Ile Ala Lys Asn
130          135          140
```

Asp	Asp	Ala	His	Leu	Ala	Leu	Ala	Gln	Glu	Leu	Lys	Asp	Lys	Lys	Ser
145					150					155					160
Leu	Arg	Lys	Tyr	Trp	Ala	Ile	Val	His	Gly	Asn	Leu	Pro	Asn	Asp	Arg
				165					170						175
Gly	Val	Ile	Glu	Ala	Pro	Ile	Gly	Arg	Ser	Glu	Lys	Asp	Arg	Lys	Lys
			180					185					190		
Gln	Ala	Val	Thr	Ala	Lys	Gly	Lys	Pro	Ala	Val	Thr	Arg	Phe	His	Val
		195					200					205			
Leu	Glu	Arg	Phe	Gly	Asp	Tyr	Ser	Leu	Val	Glu	Leu	Gln	Leu	Glu	Thr
	210					215					220				
Gly	Arg	Thr	His	Gln	Ile	Arg	Val	His	Met	Ala	Tyr	Ile	Gly	His	Ser
225					230					235					240
Val	Ala	Gly	Asp	Glu	Val	Tyr	Gly	Pro	Arg	Lys	Thr	Leu	Lys	Gly	His
			245						250					255	
Gly	Gln	Phe	Leu	His	Ala	Lys	Thr	Leu	Gly	Phe	Thr	His	Pro	Arg	Thr
		260					265						270		
Gly	Lys	Thr	Leu	Glu	Phe	Lys	Ala	Asp	Ile	Pro	Glu	Ile	Phe	Lys	Glu
	275						280					285			
Thr	Leu	Glu	Arg	Leu	Arg	Lys									
	290					295									

(2) INFORMATION FOR SEQ ID NO:3371:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 448 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...448
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3371:

Phe	Met	Ile	Lys	Ile	Tyr	Asp	Thr	Met	Ser	Arg	Asp	Leu	Arg	Glu	Phe
1			5					10						15	
Val	Pro	Ile	Glu	Asp	Gly	Lys	Ile	Lys	Met	Tyr	Val	Cys	Gly	Pro	Thr
		20					25					30			
Val	Tyr	Asn	Tyr	Ile	His	Val	Gly	Asn	Ala	Arg	Ser	Thr	Val	Ala	Phe
	35					40					45				
Asp	Thr	Ile	Arg	Arg	Tyr	Phe	Glu	Tyr	Arg	Gly	Tyr	Lys	Val	Ala	Tyr
	50				55					60					
Ile	Ser	Asn	Phe	Thr	Asp	Val	Asp	Asp	Lys	Ile	Ile	Asn	Arg	Ala	Arg
65				70					75					80	
Glu	Glu	Gly	Ile	Thr	Pro	Gln	Glu	Val	Ala	Asp	Lys	Tyr	Ile	Ala	Ala
		85						90					95		
Phe	Arg	Glu	Asp	Val	Thr	Ala	Leu	Gly	Val	Lys	Pro	Ala	Thr	Arg	His
	100						105					110			
Pro	Arg	Val	Val	Glu	Phe	Met	Ala	Asp	Ile	Ile	Arg	Phe	Val	Glu	Asp
	115					120						125			

Leu	Ile	Glu	Lys	Gly	Phe	Ala	Tyr	Glu	Ser	Gln	Gly	Asp	Val	Tyr	Phe	130	135	140
Arg	Val	Glu	Lys	Ser	His	Asn	Tyr	Ala	Lys	Leu	Ala	Asn	Lys	Thr	Leu	145	150	155
Glu	Asp	Leu	Glu	Leu	Gly	Ala	Ser	Gly	Arg	Thr	Asp	Glu	Glu	Thr	Ala	165	170	175
Arg	Lys	Glu	Asn	Pro	Val	Asp	Phe	Ala	Leu	Trp	Lys	Ser	Ser	Lys	Pro	180	185	190
Gly	Glu	Ile	Ser	Trp	Asp	Ser	Pro	Trp	Gly	Pro	Gly	Arg	Pro	Gly	Trp	195	200	205
His	Ile	Glu	Cys	Ser	Val	Met	Ser	Thr	Glu	Ile	Leu	Gly	Asp	Thr	Ile	210	215	220
Asp	Ile	His	Gly	Gly	Gly	Ala	Asp	Leu	Glu	Phe	Pro	His	His	Thr	Asn	225	230	235
Glu	Ile	Ala	Gln	Ser	Glu	Ala	Lys	Thr	Gly	Lys	Ala	Phe	Ala	Asn	Tyr	245	250	255
Trp	Met	His	Asn	Gly	Phe	Val	Asn	Ile	Asp	Asn	Val	Lys	Met	Ser	Lys	260	265	270
Ser	Leu	Gly	Asn	Phe	Ile	Thr	Val	His	Asp	Ala	Leu	Lys	Thr	Leu	Asp	275	280	285
Gly	Gln	Val	Leu	Arg	Phe	Phe	Phe	Ala	Thr	Gln	His	Tyr	Arg	Lys	Pro	290	295	300
Ile	Asn	Phe	Thr	Glu	Lys	Ala	Val	Arg	Asp	Ala	Glu	Thr	Asn	Leu	Lys	305	310	315
Tyr	Leu	Lys	Asn	Thr	Tyr	Glu	Gln	Pro	Phe	Thr	Gly	Asn	Val	Asp	Ala	325	330	335
Gln	Glu	Leu	Gln	Asn	Phe	Lys	Asp	Lys	Phe	Val	Ala	Ala	Met	Asp	Glu	340	345	350
Asp	Phe	Asn	Ala	Ala	Asn	Gly	Ile	Thr	Val	Val	Phe	Glu	Met	Ala	Lys	355	360	365
Trp	Ile	Asn	Ser	Gly	Asn	Tyr	Asp	Ala	Ser	Val	Lys	Gln	Ala	Leu	Ala	370	375	380
Asp	Met	Leu	Glu	Ile	Phe	Gly	Ile	Val	Phe	Val	Glu	Glu	Val	Leu	Asp	385	390	395
Ala	Glu	Ile	Glu	Asp	Leu	Ile	Gln	Lys	Arg	Gln	Glu	Ala	Arg	Ala	Asn	405	410	415
Arg	Asp	Phe	Ala	Thr	Ala	Asp	Gln	Ile	Arg	Asp	Gln	Leu	Val	Thr	Gln	420	425	430
Gly	Ile	Lys	Leu	Leu	Asp	Thr	Lys	Asp	Gly	Val	Arg	Trp	Thr	Arg	Asp	435	440	445

(2) INFORMATION FOR SEQ ID NO:3372:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

(B) LOCATION 1...157

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3372:

Thr	Met	Ile	Asn	Asn	Val	Val	Leu	Val	Gly	Arg	Met	Thr	Arg	Asp	Ala
1				5					10					15	
Glu	Leu	Arg	Tyr	Thr	Pro	Ser	Asn	Val	Ala	Val	Ala	Thr	Phe	Thr	Leu
			20					25					30		
Ala	Val	Asn	Arg	Thr	Phe	Lys	Ser	Gln	Asn	Gly	Glu	Arg	Glu	Ala	Asp
		35				40					45				
Phe	Ile	Asn	Val	Val	Met	Trp	Arg	Gln	Gln	Ala	Glu	Asn	Leu	Ala	Asn
	50					55					60				
Trp	Ala	Lys	Lys	Gly	Ser	Leu	Ile	Gly	Val	Thr	Gly	Arg	Ile	Gln	Thr
65				70					75					80	
Arg	Ser	Tyr	Asp	Asn	Gln	Gln	Gly	Gln	Arg	Val	Tyr	Val	Thr	Glu	Val
			85					90						95	
Val	Ala	Glu	Asn	Phe	Gln	Met	Leu	Glu	Ser	Arg	Ser	Val	Arg	Glu	Gly
		100					105						110		
His	Thr	Gly	Gly	Ala	Tyr	Ser	Ala	Pro	Thr	Ala	Asn	Tyr	Ser	Ala	Pro
	115					120						125			
Thr	Asn	Ser	Val	Pro	Asp	Phe	Ser	Arg	Asn	Glu	Asn	Pro	Phe	Gly	Ala
	130					135				140					
Thr	Asn	Pro	Leu	Asp	Ile	Ser	Asp	Asp	Asp	Leu	Pro	Phe			
145				150						155					

(2) INFORMATION FOR SEQ ID NO:3373:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 523 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...523

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3373:

Leu	Met	Ile	Lys	Lys	Glu	Asn	Ile	Met	Thr	Lys	Arg	Val	Leu	Ile	Ser
1				5					10					15	
Val	Ser	Asp	Lys	Ala	Gly	Ile	Val	Glu	Phe	Ala	Gln	Glu	Leu	Lys	Lys
			20					25					30		
Leu	Gly	Trp	Glu	Ile	Ile	Ser	Thr	Gly	Gly	Thr	Lys	Val	Ala	Leu	Asp
		35				40						45			
Asn	Ala	Gly	Val	Asp	Thr	Ile	Ala	Ile	Asp	Asp	Val	Thr	Gly	Phe	Pro
	50					55					60				
Glu	Met	Met	Asp	Gly	Arg	Val	Lys	Thr	Leu	His	Pro	Asn	Ile	His	Gly
65				70					75					80	
Gly	Leu	Leu	Ala	Arg	Arg	Asp	Leu	Asp	Ser	His	Leu	Glu	Ala	Ala	Lys
			85					90						95	

Asp	Asn	Lys	Ile	Glu	Leu	Ile	Asp	Leu	Val	Val	Val	Asn	Leu	Tyr	Pro
			100					105					110		
Phe	Lys	Glu	Thr	Ile	Leu	Lys	Pro	Asp	Val	Thr	Tyr	Ala	Asp	Ala	Val
		115					120					125			
Glu	Asn	Ile	Asp	Ile	Gly	Gly	Pro	Ser	Met	Leu	Arg	Ser	Ala	Ala	Lys
		130				135					140				
Asn	His	Ala	Ser	Val	Thr	Val	Val	Val	Asp	Pro	Ala	Asp	Tyr	Ala	Val
145					150					155					160
Val	Leu	Asp	Glu	Leu	Ala	Ala	Asn	Gly	Glu	Thr	Ser	Tyr	Glu	Thr	Arg
			165						170					175	
Gln	Arg	Leu	Ala	Ala	Lys	Val	Phe	Arg	His	Thr	Ala	Ala	Tyr	Asp	Ala
		180					185						190		
Leu	Ile	Ala	Glu	Tyr	Phe	Thr	Ala	Gln	Val	Gly	Glu	Ser	Lys	Pro	Glu
		195					200					205			
Lys	Leu	Thr	Leu	Thr	Tyr	Asp	Leu	Lys	Gln	Pro	Met	Arg	Tyr	Gly	Glu
		210				215					220				
Asn	Pro	Gln	Gln	Asp	Ala	Asp	Phe	Tyr	Gln	Lys	Ala	Leu	Pro	Thr	Asp
225				230						235					240
Tyr	Ser	Ile	Ala	Ser	Ala	Lys	Gln	Leu	Asn	Gly	Lys	Glu	Leu	Ser	Phe
			245						250					255	
Asn	Asn	Ile	Arg	Asp	Ala	Asp	Ala	Ala	Ile	Arg	Ile	Ile	Arg	Asp	Phe
		260					265						270		
Lys	Asp	Ser	Pro	Thr	Val	Val	Ala	Leu	Lys	His	Met	Asn	Pro	Cys	Gly
		275					280					285			
Ile	Gly	Gln	Ala	Asp	Asp	Ile	Glu	Thr	Ala	Trp	Asp	Tyr	Ala	Tyr	Glu
	290				295					300					
Ser	Asp	Pro	Val	Ser	Ile	Phe	Gly	Gly	Ile	Val	Val	Leu	Asn	Arg	Glu
305				310					315						320
Val	Asp	Ala	Ala	Thr	Ala	Glu	Lys	Met	His	Gly	Val	Phe	Leu	Glu	Ile
			325						330					335	
Ile	Ile	Ala	Pro	Ser	Tyr	Thr	Asp	Glu	Ala	Leu	Ala	Ile	Leu	Ile	Asn
		340					345						350		
Lys	Lys	Lys	Asn	Leu	Arg	Ile	Leu	Ala	Leu	Pro	Phe	Asn	Ala	Gln	Glu
		355					360					365			
Ala	Ser	Glu	Val	Glu	Ala	Glu	Tyr	Thr	Gly	Val	Val	Gly	Gly	Leu	Leu
	370					375					380				
Val	Gln	Asn	Gln	Asp	Val	Val	Lys	Glu	Ser	Pro	Ala	Asp	Trp	Gln	Val
385				390						395					400
Val	Thr	Lys	Arg	Gln	Pro	Thr	Glu	Thr	Glu	Ala	Thr	Ala	Leu	Glu	Phe
			405						410					415	
Ala	Trp	Lys	Ala	Ile	Lys	Tyr	Val	Lys	Ser	Asn	Gly	Ile	Ile	Val	Thr
		420					425						430		
Asn	Asp	His	Met	Thr	Leu	Gly	Val	Gly	Pro	Gly	Gln	Thr	Asn	Arg	Val
	435					440						445			
Ala	Ser	Val	Arg	Leu	Ala	Ile	Asp	Gln	Ala	Lys	Asp	Arg	Leu	Asp	Gly
	450					455					460				
Ala	Val	Leu	Ala	Ser	Asp	Ala	Phe	Phe	Pro	Phe	Ala	Asp	Asn	Val	Glu
465				470						475					480
Glu	Ile	Ala	Lys	Ala	Gly	Ile	Lys	Ala	Ile	Ile	Gln	Pro	Gly	Gly	Ser
			485						490					495	
Val	Arg	Asp	Gln	Glu	Ser	Ile	Glu	Ala	Ala	Asp	Lys	Tyr	Gly	Leu	Thr
		500					505						510		
Met	Val	Phe	Thr	Gly	Val	Arg	His	Phe	Arg	His					
		515					520								

(2) INFORMATION FOR SEQ ID NO:3374:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 275 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...275

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3374:

Met	Met	Ile	Lys	Val	Ile	Ala	Thr	Asp	Met	Asp	Gly	Thr	Leu	Leu	Asp
1				5					10					15	
Ala	Arg	Gly	Gln	Leu	Asp	Leu	Pro	Arg	Leu	Glu	Lys	Ile	Leu	Asp	Gln
			20					25					30		
Leu	Asp	Gln	Arg	Gly	Ile	Arg	Phe	Val	Ile	Ala	Thr	Gly	Asn	Glu	Ile
		35				40						45			
His	Arg	Met	Arg	Gln	Leu	Leu	Ser	Pro	Leu	Val	Asp	Arg	Val	Val	Leu
		50				55					60				
Val	Val	Ala	Asn	Gly	Ala	Arg	Ile	Phe	Glu	Asn	Asn	Glu	Leu	Ile	Gln
65				70						75					80
Ala	Gln	Thr	Trp	Asp	Asp	Ala	Ile	Val	Asn	Lys	Ala	Leu	Ala	His	Phe
				85					90					95	
Lys	Gly	Arg	Ala	Cys	Gln	Asn	Gln	Phe	Val	Val	Thr	Gly	Met	Lys	Gly
			100					105					110		
Asp	Phe	Val	Lys	Glu	Gly	Thr	Ile	Phe	Thr	Asp	Leu	Glu	Ser	Phe	Met
		115				120					125				
Thr	Pro	Glu	Met	Ile	Glu	Lys	Phe	Tyr	Gln	Arg	Met	Gln	Phe	Val	Asp
	130					135					140				
Glu	Leu	Thr	Ser	Asp	Leu	Phe	Gly	Gly	Val	Leu	Lys	Met	Ser	Met	Val
145					150					155					160
Val	Gly	Glu	Glu	Arg	Leu	Ser	Ser	Val	Leu	Glu	Glu	Ile	Asn	Ala	Leu
				165					170					175	
Phe	Asp	Gly	Arg	Val	Arg	Ala	Val	Ser	Ser	Gly	Tyr	Gly	Cys	Ile	Asp
		180						185					190		
Ile	Leu	Gln	Ala	Gly	Ile	His	Lys	Ala	Trp	Gly	Leu	Glu	Glu	Leu	Leu
		195					200					205			
Lys	Arg	Trp	Asp	Leu	Lys	Ser	Gln	Glu	Ile	Met	Ala	Phe	Gly	Asp	Ser
	210					215					220				
Glu	Asn	Asp	Val	Glu	Met	Leu	Glu	Met	Ala	Gly	Ile	Ala	Tyr	Ala	Met
225					230					235					240
Glu	Asn	Ala	Asp	Glu	Lys	Ala	Lys	Ala	Val	Ala	Thr	Ala	Leu	Ala	Pro
				245					250					255	
Ala	Asn	Ser	Gln	Gly	Gly	Val	Tyr	Gln	Val	Leu	Glu	Asn	Trp	Leu	Glu
			260					265					270		
Lys	Gly	Glu													
		275													

(2) INFORMATION FOR SEQ ID NO:3375:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 751 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...751
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3375:

Ala	Arg	Ile	Lys	Met	Asn	Thr	Leu	Leu	Thr	Leu	Arg	Gly	Lys	Ser	Phe
1				5					10					15	
Thr	Gln	Lys	Ser	Arg	Asn	Asn	Gly	Met	Gly	Pro	Ile	Thr	Ile	Pro	Lys
			20					25					30		
Lys	Thr	Ile	Ile	Thr	Leu	Glu	His	Leu	Lys	Tyr	Leu	His	Phe	Ser	Leu
		35					40					45			
Glu	Glu	Thr	Lys	Thr	Tyr	Trp	Glu	Lys	Asn	Asn	Ile	Ile	Asp	Gly	Ile
	50					55					60				
Leu	Ile	Ser	Ile	Tyr	Tyr	Asn	Arg	Ile	Val	Ala	Lys	Ser	Asn	Arg	Ile
65					70				75					80	
Asn	Gly	Tyr	Phe	Asn	Val	Gly	Gly	Gly	Asn	Pro	Phe	Pro	Asn	Asp	Thr
			85					90					95		
Ile	Val	Gly	Ala	Lys	Phe	Asn	Asp	Glu	Lys	Thr	Lys	His	Ile	Val	Thr
		100						105				110			
His	Tyr	Ile	Ser	Arg	Asp	Ala	Leu	Asn	Lys	Thr	Ile	Thr	Val	Leu	Ser
	115					120					125				
Lys	Ile	Ile	Glu	Val	Phe	Glu	Glu	His	Phe	Asp	Arg	Ala	Ile	Thr	Cys
	130					135				140					
Glu	Met	Phe	Ser	Asp	Ser	Ser	Thr	Phe	Ala	Ser	Ile	Asn	Phe	Ser	Glu
145					150				155					160	
Tyr	Gly	Ile	Ser	Lys	Ser	Lys	Phe	Gln	Gln	Tyr	Leu	Arg	Asp	Ser	Cys
			165					170					175		
Phe	Ile	Glu	Asn	Phe	Gly	Val	Glu	His	Thr	Thr	Val	Ser	Asp	Ile	Gln
		180					185					190			
Asn	Ser	Ile	Val	Thr	Phe	Tyr	Asp	Val	His	Thr	Asp	Ile	Phe	Arg	Leu
	195					200					205				
Leu	Asn	Lys	Leu	Asn	Ile	Asp	Ile	Ser	Glu	Ala	Asn	Ile	Met	Asn	Gln
	210					215				220					
Thr	Thr	Val	Leu	Leu	Asp	Glu	Lys	Asn	Ile	Glu	Leu	Leu	Leu	Ser	Lys
225					230					235				240	
Ala	Pro	Tyr	Leu	Val	Ser	Met	Ile	Val	Glu	Asp	Phe	Ser	Lys	Leu	Ser
			245					250					255		
Val	Asp	Asp	Phe	Ser	Leu	Asp	Asn	Asn	Asp	Leu	Lys	Ile	Asn	Leu	Pro
	260					265						270			
Ser	Pro	Met	Asn	Glu	Pro	Val	Val	Gly	Val	Ile	Asp	Thr	Leu	Phe	Asp
	275					280					285				
Lys	Arg	Val	Tyr	Phe	Asn	Glu	Trp	Val	Glu	Tyr	His	Asp	Phe	Val	Ser
	290				295				300						
Pro	Asp	Ile	Ser	Lys	Asp	Ser	Gln	Asp	Tyr	Lys	His	Gly	Thr	Ala	Val

305					310				315				320
Thr	Ser	Leu	Ile	Val	Asp	Gly	Ala	Asn	Leu	Asn	Pro	Asn	Leu
				325					330				335
Gly	Cys	Gly	Asn	Phe	Arg	Val	Arg	His	Phe	Gly	Val	Ser	Leu
			340					345					350
Gly	Phe	Asn	Ser	Phe	Thr	Ile	Ile	Lys	Gln	Ile	Lys	Glu	Ile
		355					360					365	Val
Gln	Asn	Ala	Asp	Ile	Lys	Val	Trp	Asn	Leu	Ser	Leu	Gly	Ser
		370				375					380		Asn
Glu	Ile	Arg	Glu	Asn	Phe	Ile	Ser	Ala	Glu	Gly	Ala	Leu	Leu
385				390					395				400
Ile	Gln	Phe	Glu	Asn	Asp	Val	Ile	Phe	Ile	Ile	Ala	Gly	Thr
			405					410					415
Ser	Val	Ile	Asn	Gly	Lys	Arg	Lys	Arg	Ile	Gly	Ala	Pro	Ala
			420				425						430
Leu	Asn	Ser	Ile	Ile	Val	Asn	Ser	Val	Asp	Phe	Asn	Asn	Gln
		435					440						445
Ser	Tyr	Ser	Arg	Glu	Gly	Ile	Val	Leu	Ser	Phe	Phe	Val	Lys
450						455				460			Pro
Val	Ser	Tyr	Tyr	Gly	Gly	Asn	Gly	Asp	Phe	Ile	Asn	Val	Cys
465				470					475				480
Pro	Leu	Gly	Leu	Gly	Arg	Val	Ala	Gly	Thr	Ser	Phe	Ala	Ala
			485					490					495
Ile	Ala	Arg	Lys	Met	Ala	Tyr	Leu	Ile	His	Ile	Met	Gly	Leu
			500				505						510
Glu	Glu	Ala	Lys	Ala	Leu	Leu	Ile	Asp	Ala	Ala	Ile	Pro	Trp
		515				520					525		Asn
Lys	Lys	Thr	Phe	Thr	Asp	Leu	Ser	Leu	Ile	Gly	Asn	Gly	Ile
		530			535					540			Val
Ile	Lys	Met	Asp	Asp	Ile	Leu	Ser	Thr	Pro	Asp	Asp	Glu	Ile
545				550					555				560
Ile	Val	Ser	Asp	Ile	Ser	Arg	Ala	Tyr	Asp	Thr	Tyr	Asn	Tyr
			565					570					575
Pro	Val	Pro	Ile	Ser	Ser	Glu	Ser	Tyr	Pro	Tyr	Val	Ala	Lys
			580				585						590
Met	Cys	Tyr	Phe	Pro	Asn	Cys	Ser	Arg	Lys	Gln	Gly	Val	Asp
		595				600					605		Tyr
Asn	Thr	Glu	Met	Gln	Leu	Thr	Phe	Gly	Arg	Leu	Lys	Ser	Asp
		610			615						620		Gly
Lys	Ser	Ile	Asn	Lys	Asp	Asn	Gln	His	Ala	Glu	Asp	Ser	Pro
625				630					635				640
Val	Arg	Glu	Asn	Ala	Ala	Arg	Asn	Ile	Phe	Arg	Lys	Trp	Asp
			645					650					655
Lys	His	Ile	Gly	Glu	Ser	Phe	Thr	Ser	Arg	Lys	Arg	Ala	Lys
		660					665					670	Ala
Leu	Asn	Pro	Ser	Asn	Pro	Gln	Trp	Gly	Met	Ser	Ile	Lys	Thr
		675				680					685		Ile
Arg	Leu	Lys	Ser	Gly	Asp	Gly	Gln	Gly	Val	Arg	Phe	Gly	Val
		690			695					700			Val
Thr	Leu	Lys	Glu	Leu	Asn	Gly	Val	Asn	Arg	Ile	Glu	Asp	Phe
705				710					715				Ile
Gln	Ala	Glu	Leu	Arg	Gly	Trp	Leu	Val	Asn	Arg	Leu	Gln	Val
			725					730					Glu
Gln	Val	Asp	Leu	Phe	Asn	Ser	Leu	Asn	Glu	Glu	Ile	Glu	Phe
		740					745					750	Glu

(2) INFORMATION FOR SEQ ID NO:3376:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 106 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...106
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3376:

```

Asn Val Val Lys Ser Thr Phe Phe Ile Phe Ile Phe Gly Ile Pro Leu
1          5          10          15
His Ser Phe Ala Lys Lys Gly Val Thr Asn Arg Pro Tyr Phe Lys Lys
          20          25          30
Arg Ile Glu Lys Arg Ile Gln His Leu Ser His Pro Lys Asn Asn Leu
          35          40          45
Phe Ser Thr Glu Asp Met Gly Phe Glu Pro Thr His Ala Ile Thr Arg
          50          55          60
Leu Pro Arg Phe Gln His Gly Leu Leu Ser Leu Leu Ser Asn Leu Pro
65          70          75          80
Ile Leu Thr Gln Ile Val Tyr His Lys Gly Ser Tyr Leu Ala Ile Lys
          85          90          95
Ile Leu Glu Ile Arg Lys Asn Asp Arg Phe
          100          105

```

(2) INFORMATION FOR SEQ ID NO:3377:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 789 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...789
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3377:

```

Asn Ser Val Lys Lys Asn Asp Ile Ile Glu Phe Met Asp Lys Asn Lys
1          5          10          15
Ile Met Gly Leu Thr Gln Arg Glu Val Lys Glu Arg Gln Ala Glu Gly

```


Ser	Ser	Ile	Ala	Gln	Lys	Ala	Gly	Phe	Ala	Asp	Tyr	His	Ser	Tyr	Val
				485					490					495	
Asp	Cys	Ser	Lys	Ile	Thr	Asp	Glu	Glu	Leu	Met	Ala	Met	Ala	Glu	Glu
			500					505					510		
Thr	Ala	Ile	Phe	Gly	Arg	Val	Ser	Pro	His	Gln	Lys	Lys	Leu	Ile	Ile
		515					520					525			
Gln	Thr	Leu	Lys	Lys	Ala	Gly	His	Thr	Thr	Ala	Met	Thr	Gly	Asp	Gly
	530					535					540				
Val	Asn	Asp	Ile	Leu	Ala	Leu	Arg	Glu	Ala	Asp	Cys	Ser	Ile	Val	Met
545					550					555					560
Ala	Glu	Gly	Asp	Pro	Ala	Thr	Arg	Gln	Ile	Ala	Asn	Leu	Val	Leu	Leu
				565					570					575	
Asn	Ser	Asp	Phe	Asn	Asp	Val	Pro	Glu	Ile	Leu	Phe	Glu	Gly	Arg	Arg
			580					585					590		
Val	Val	Asn	Asn	Ile	Ala	His	Ile	Ala	Pro	Ile	Phe	Leu	Ile	Lys	Thr
		595					600					605			
Ile	Tyr	Ser	Phe	Leu	Leu	Ala	Val	Ile	Cys	Ile	Ala	Ser	Ala	Leu	Leu
	610					615					620				
Gly	Arg	Ser	Glu	Trp	Ile	Leu	Ile	Phe	Pro	Phe	Ile	Pro	Ile	Gln	Ile
625					630					635					640
Thr	Met	Ile	Asp	Gln	Phe	Val	Glu	Gly	Phe	Pro	Pro	Phe	Val	Leu	Thr
				645					650					655	
Phe	Glu	Arg	Asn	Ile	Lys	Pro	Val	Glu	Gln	Asn	Phe	Leu	Arg	Lys	Ser
			660					665					670		
Met	Leu	Arg	Ala	Leu	Pro	Ser	Ala	Leu	Met	Val	Val	Phe	Ser	Val	Leu
		675					680					685			
Phe	Val	Lys	Met	Phe	Gly	Ala	Ser	Gln	Gly	Trp	Ser	Glu	Leu	Glu	Ile
	690					695					700				
Ser	Thr	Leu	Leu	Tyr	Tyr	Leu	Leu	Gly	Ser	Ile	Gly	Phe	Leu	Ser	Val
705					710					715					720
Phe	Arg	Ala	Cys	Met	Pro	Phe	Thr	Leu	Trp	Arg	Val	Leu	Leu	Ile	Val
				725					730					735	
Trp	Ser	Val	Gly	Gly	Phe	Leu	Ala	Thr	Ala	Leu	Phe	Pro	Arg	Ile	Gln
			740					745					750		
Lys	Leu	Leu	Glu	Ile	Ser	Thr	Leu	Thr	Glu	Gln	Thr	Leu	Pro	Val	Tyr
		755					760					765			
Gly	Val	Met	Met	Leu	Val	Phe	Thr	Val	Ile	Phe	Ile	Leu	Thr	Ser	Arg
	770					775					780				
Tyr	Gln	Ala	Lys	Lys											
785															

(2) INFORMATION FOR SEQ ID NO:3378:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

(B) LOCATION 1...156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3378:

Ser	Leu	Val	Lys	Val	Arg	Arg	Asn	Leu	Ile	Asp	Ser	Leu	Ile	Gln	Tyr
1			5					10						15	
Met	Leu	Ile	Ile	Gly	Val	Asn	Asn	Ser	Gly	Gly	Ser	Cys	Arg	Leu	Arg
			20					25					30		
Glu	Phe	Gly	Glu	Lys	Ile	Lys	Arg	Leu	Arg	Leu	Ala	Lys	Lys	Ile	Ser
		35					40					45			
Arg	Ser	Glu	Phe	Cys	Gly	Asp	Glu	Ser	Glu	Leu	Ser	Ile	Arg	Gln	Leu
	50					55					60				
Ile	Arg	Ile	Glu	Asn	Gly	Glu	Ser	Arg	Pro	Thr	Leu	Thr	Lys	Leu	Lys
65					70					75					80
Tyr	Ile	Ala	Glu	Arg	Leu	Gly	Val	Glu	Asp	Tyr	Lys	Leu	Met	Pro	Ser
			85						90				95		
Tyr	Ile	Glu	Leu	Asp	Lys	Glu	Tyr	Leu	Glu	Leu	Lys	Tyr	Phe	Leu	Met
		100						105					110		
Arg	Thr	Pro	Thr	Tyr	Glu	Asp	Glu	Thr	Ile	Ala	Gln	Lys	Lys	Glu	Ser
		115					120					125			
Val	Leu	Ile	Arg	Phe	Leu	Lys	Ser	Ile	Met	Ile	Gly	Tyr	Leu	Arg	Lys
	130					135					140				
Lys	Asp	Leu	Ser	Ser	Gln	Ile	Ile	His	Ile	Trp	His				
145					150					155					

(2) INFORMATION FOR SEQ ID NO:3379:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 189 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...189

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3379:

Thr	Ile	Val	Lys	Glu	Val	Phe	Pro	Met	Ile	Lys	Gln	Ile	Lys	Ala	His
1			5					10						15	
Leu	Asn	Lys	Ser	Ile	Gln	Ser	Ile	Ile	Gly	Gln	Lys	Val	Glu	Phe	Val
		20						25					30		
Lys	Gln	Asp	Glu	Gln	Ala	Phe	Thr	Arg	Lys	Arg	Arg	Leu	Ser	Leu	Glu
		35					40					45			
Thr	Met	Ile	Arg	Thr	Ile	Leu	Gly	Met	Gly	Gly	Lys	Ser	Leu	Ser	Lys
	50					55					60				
Glu	Leu	Leu	Asp	Ala	Arg	Leu	Thr	Val	Ser	Asn	Ser	Ala	Phe	Val	Gln
65					70					75					80
Arg	Arg	Tyr	Gln	Ile	Lys	Pro	Glu	Ala	Phe	Tyr	Ala	Leu	Phe	Lys	Glu
			85						90					95	

```

Phe Thr Ala Pro Ile Pro Leu Asn Thr Asp Phe Pro Ile Phe Ala Ala
    100                      105                      110
Asp Gly Ser Asp Ile Cys Ile Pro Arg Asn Pro Met Asp Thr Glu Thr
    115                      120                      125
Ser Ile Gln Thr Gln Thr Asp Val Lys Ser Tyr Asn Leu Ile His Ile
    130                      135                      140
Asn Ala Leu Tyr Asp Leu Thr Thr Gly Val Tyr Arg Asp Val Ser Ile
    145                      150                      155                      160
Gln Asp Lys His Ala Gln His Glu Arg Leu Ala Leu Ile Gln Met Met
    165                      170                      175
Glu Ala Ser Pro Phe Arg Glu Ser Ser Cys Tyr His Gly
    180                      185

```

(2) INFORMATION FOR SEQ ID NO:3380:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...189

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3380:

```

Thr Ile Val Lys Glu Val Phe Pro Met Ile Lys Gln Ile Lys Ala His
1      5      10      15
Leu Asn Lys Ser Ile Gln Ser Ile Ile Gly Gln Lys Val Glu Phe Val
    20      25      30
Lys Gln Asp Glu Gln Ala Phe Thr Arg Lys Arg Arg Leu Ser Leu Glu
    35      40      45
Thr Met Ile Arg Thr Ile Leu Gly Met Gly Gly Lys Ser Leu Ser Lys
    50      55      60
Glu Leu Leu Asp Ala Arg Leu Thr Val Ser Asn Ser Ala Phe Val Gln
    65      70      75      80
Arg Arg Tyr Gln Ile Lys Pro Glu Ala Phe Tyr Ala Leu Phe Lys Glu
    85      90      95
Phe Thr Ala Pro Ile Pro Leu Asn Thr Asp Phe Pro Ile Phe Ala Ala
    100     105     110
Asp Gly Ser Asp Ile Cys Ile Pro Arg Asn Pro Met Asp Thr Glu Thr
    115     120     125
Ser Ile Gln Thr Gln Thr Asp Val Lys Ser Tyr Asn Leu Ile His Ile
    130     135     140
Asn Ala Leu Tyr Asp Leu Thr Thr Gly Val Tyr Arg Asp Val Ser Ile
    145     150     155     160
Gln Asp Lys His Ala Gln His Glu Arg Leu Ala Leu Ile Gln Met Met
    165     170     175
Glu Ala Ser Pro Phe Arg Glu Ser Ser Cys Tyr His Gly
    180     185

```

(2) INFORMATION FOR SEQ ID NO:3381:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 189 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...189
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3381:

Thr	Ile	Val	Lys	Glu	Val	Phe	Pro	Met	Ile	Lys	Gln	Ile	Lys	Ala	His
1				5					10					15	
Leu	Asn	Lys	Ser	Ile	Gln	Ser	Ile	Ile	Gly	Gln	Lys	Val	Glu	Phe	Val
			20					25					30		
Lys	Gln	Asp	Glu	Gln	Ala	Phe	Thr	Arg	Lys	Arg	Arg	Leu	Ser	Leu	Glu
		35					40					45			
Thr	Met	Ile	Arg	Thr	Ile	Leu	Gly	Met	Gly	Gly	Lys	Ser	Leu	Ser	Lys
	50					55					60				
Glu	Leu	Leu	Asp	Ala	Arg	Leu	Thr	Val	Ser	Asn	Ser	Ala	Phe	Val	Gln
65					70					75					80
Arg	Arg	Tyr	Gln	Ile	Lys	Pro	Glu	Ala	Phe	Tyr	Ala	Leu	Phe	Lys	Glu
			85						90					95	
Phe	Thr	Ala	Pro	Ile	Pro	Leu	Asn	Thr	Asp	Phe	Pro	Ile	Phe	Ala	Ala
		100						105					110		
Asp	Gly	Ser	Asp	Ile	Cys	Ile	Pro	Arg	Asn	Pro	Met	Asp	Thr	Glu	Thr
	115						120					125			
Ser	Ile	Gln	Thr	Gln	Thr	Asp	Val	Lys	Ser	Tyr	Asn	Leu	Ile	His	Ile
	130					135					140				
Asn	Ala	Leu	Tyr	Asp	Leu	Thr	Thr	Gly	Val	Tyr	Arg	Asp	Val	Ser	Ile
145				150						155					160
Gln	Asp	Lys	His	Ala	Gln	His	Glu	Arg	Leu	Ala	Leu	Ile	Gln	Met	Met
			165						170					175	
Glu	Ala	Ser	Pro	Phe	Arg	Glu	Ser	Ser	Cys	Tyr	His	Gly			
		180						185							

(2) INFORMATION FOR SEQ ID NO:3382:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 687 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...687

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3382:

```
Ser Thr Val Lys Lys Asn Leu Val Ile Val Glu Ser Pro Ala Lys Ala
1      5      10      15
Lys Thr Ile Glu Lys Tyr Leu Gly Arg Asn Tyr Lys Val Leu Ala Ser
20      25      30
Val Gly His Ile Arg Asp Leu Lys Lys Ser Ser Met Ser Val Asp Ile
35      40      45
Glu Asn Asn Tyr Glu Pro Gln Tyr Ile Asn Ile Arg Gly Lys Gly Pro
50      55      60
Leu Ile Asn Asp Leu Lys Lys Glu Ala Lys Lys Ala Asn Lys Val Phe
65      70      75      80
Leu Ala Ser Asp Pro Asp Arg Glu Gly Glu Ala Ile Ser Trp His Leu
85      90      95
Ala His Ile Leu Asn Leu Asp Glu Asn Asp Ala Asn Arg Val Val Phe
100     105     110
Asn Glu Ile Thr Lys Asp Ala Val Lys Asn Ala Phe Lys Glu Pro Arg
115     120     125
Lys Ile Asp Met Asp Leu Val Asp Ala Gln Gln Ala Arg Arg Ile Leu
130     135     140
Asp Arg Leu Val Gly Tyr Ser Ile Ser Pro Ile Leu Trp Lys Lys Val

145     150     155     160
Lys Lys Gly Leu Ser Ala Gly Arg Val Gln Ser Ile Ala Leu Lys Leu
165     170     175
Ile Ile Asp Arg Glu Asn Glu Ile Asn Ala Phe Gln Pro Glu Glu Tyr
180     185     190
Trp Thr Val Asp Ala Val Phe Lys Lys Gly Thr Lys Lys Phe His Ala
195     200     205
Ser Phe Tyr Gly Val Asp Gly Lys Lys Met Lys Leu Thr Ser Asn Asp
210     215     220
Glu Val Lys Glu Val Leu Ser Arg Leu Thr Ser Lys Asp Phe Ser Val
225     230     235     240
Asp Gln Val Asp Lys Lys Glu Arg Lys Arg Asn Ala Pro Leu Pro Tyr
245     250     255
Thr Thr Ser Ser Met Gln Met Asp Ala Ala Asn Lys Ile Asn Phe Arg
260     265     270
Thr Arg Lys Thr Met Met Val Ala Gln Gln Leu Tyr Glu Gly Ile Asn
275     280     285
Ile Gly Ser Gly Val Gln Gly Leu Ile Thr Tyr Met Arg Thr Asp Ser
290     295     300
Thr Arg Ile Ser Pro Val Ala Gln Asn Glu Ala Ala Ser Phe Ile Thr
305     310     315     320
Asp Arg Phe Gly Ser Lys Tyr Ser Lys His Gly Ser Lys Val Lys Asn
325     330     335
Ala Ser Gly Ala Gln Asp Ala His Glu Ala Ile Arg Pro Ser Ser Val
340     345     350
Phe Asn Thr Pro Glu Ser Ile Ala Lys Tyr Leu Asp Lys Asp Gln Leu
355     360     365
Lys Leu Tyr Thr Leu Ile Trp Asn Arg Phe Val Ala Ser Gln Met Thr
```

370	375	380
Ala Ala Val Phe Asp Thr Met Ala Val Lys Leu Ser Gln Thr Gly Val		
385	390	395
Gln Phe Ala Ala Asn Gly Ser Gln Val Lys Phe Asp Gly Tyr Leu Ala		400
	405	410
Ile Tyr Asn Asp Ser Asp Lys Asn Lys Met Leu Pro Thr Trp Cys Trp		415
	420	425
Arg Cys Val Pro Gln Val Asn Ser Lys Pro Glu Gln His Phe Thr Gln		430
	435	440
Pro Pro Ala Arg Tyr Ser Glu Ala Thr Leu Ile Lys Thr Leu Glu Glu		445
	450	455
Asn Gly Val Gly Arg Pro Ser Thr Tyr Ala Pro Thr Ile Glu Thr Ile		460
465	470	475
Gln Lys Arg Tyr Tyr Val Arg Leu Ala Ala Lys Arg Phe Glu Pro Thr		480
	485	490
Glu Leu Gly Glu Ile Val Asn Lys Leu Ile Val Glu Tyr Phe Pro Asp		495
	500	505
Ile Val Asn Val Thr Phe Thr Ala Glu Met Glu Gly Lys Leu Asp Asp		510
	515	520
Val Glu Val Gly Lys Glu Gln Trp Arg Arg Val Ile Asp Ala Phe Tyr		525
	530	535
Lys Pro Phe Ser Lys Glu Val Ala Lys Ala Glu Glu Met Glu Lys		540
545	550	555
Ile Gln Ile Lys Asp Glu Pro Ala Gly Phe Asp Cys Glu Val Cys Gly		560
	565	570
Ser Pro Met Val Ile Lys Leu Gly Arg Phe Gly Lys Phe Tyr Ala Cys		575
	580	585
Ser Asn Phe Pro Asp Cys Arg His Thr Gln Ala Ile Val Lys Glu Ile		590
	595	600
Gly Val Glu Cys Pro Ser Cys His Gln Gly Gln Ile Ile Glu Arg Lys		605
	610	615
Thr Lys Arg Asn Arg Leu Phe Tyr Gly Cys Asn Arg Tyr Pro Glu Cys		620
625	630	635
Glu Phe Thr Ser Trp Asp Lys Pro Val Gly Arg Asp Cys Pro Lys Cys		640
	645	650
Gly Asn Phe Leu Met Glu Lys Lys Val Arg Gly Gly Gly Lys Gln Val		655
	660	665
Val Cys Ser Lys Gly Asp Asp Ser Ser Pro Arg Val Xaa Xaa Thr		670
	675	680
		685

(2) INFORMATION FOR SEQ ID NO:3383:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...214

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3383:

```
Arg Glu Val Asn Met Ile Glu Leu Lys Gln Val Ser Lys Ser Phe Gly
1          5          10          15
Glu Arg Glu Leu Phe Ser Asn Leu Ser Met Thr Phe Glu Ala Gly Lys
20          25          30
Val Tyr Ala Leu Ile Gly Ser Ser Gly Ser Gly Lys Thr Thr Leu Met
35          40          45
Asn Met Ile Gly Lys Leu Glu Pro Tyr Asp Gly Thr Ile Phe Tyr Arg
50          55          60

Gly Lys Asp Leu Ala Asn Tyr Lys Ser Ser Asp Phe Phe Arg His Glu
65          70          75          80
Leu Gly Tyr Leu Phe Gln Asn Phe Gly Leu Ile Glu Asn Gln Ser Ile
85          90          95
Glu Glu Asn Leu Lys Leu Gly Leu Thr Gly Gln Lys Leu Ser Arg Ser
100         105         110
Glu Gln Arg Leu Arg Gln Lys Gln Ala Leu Glu Gln Val Gly Leu Ala
115         120         125
Tyr Leu Asp Leu Asp Lys Arg Ile Phe Glu Leu Ser Gly Gly Glu Ser
130         135         140
Gln Arg Val Ala Leu Ala Lys Val Ile Leu Lys Asn Pro Pro Phe Ile
145         150         155         160
Leu Ala Asp Glu Pro Thr Ala Ser Ile Asp Pro Ala Thr Ser Gln Leu
165         170         175
Ile Met Glu Ile Leu Leu Ser Leu Arg Asp Asp Asn Arg Leu Ile Ile
180         185         190
Ile Ala Thr His Asn Pro Ala Ile Trp Glu Met Ala Asp Glu Val Phe
195         200         205
Thr Met Asp Arg Leu Lys
210
```

(2) INFORMATION FOR SEQ ID NO:3384:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 199 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...199

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3384:

```
Phe Gly Val Lys Tyr Leu Gln Arg Met Ile Ala Leu Thr Asp Thr Gly
1          5          10          15
Leu Thr Phe Thr Lys Asp Pro Phe Asp Cys Glu Arg Tyr Glu Asp Leu
20          25          30
```

Arg	Ser	Leu	Leu	Ser	Glu	Met	Leu	Asn	Gln	Gly	Ser	Asp	Leu	Asp	Ala
		35					40					45			
Glu	Glu	Val	Ala	Glu	Val	Leu	Lys	Pro	Thr	Ser	Ala	Tyr	Ala	Thr	Pro
		50				55					60				
Leu	Met	Asp	Val	Arg	Ala	Trp	Ile	Val	Glu	Asp	Glu	Lys	Ile	Cys	Leu
65					70					75					80
Val	Arg	Gly	Gln	Gly	Glu	Asp	Ser	Trp	Ala	Leu	Pro	Gly	Gly	Phe	Gly
			85						90					95	
Glu	Val	Gly	Tyr	Ser	Pro	Thr	Glu	Asn	Ile	Leu	Lys	Glu	Ile	Glu	Glu
			100					105					110		
Glu	Thr	Gly	Phe	Lys	Ala	Lys	Val	Glu	Arg	Leu	Leu	Ala	Val	Phe	Asp
		115					120					125			
Thr	Asn	Arg	Phe	Gln	Leu	Gln	Ser	Lys	Gln	Tyr	Ala	Lys	Phe	Val	Phe
		130				135					140				
Glu	Cys	Lys	Leu	Leu	Asp	Gly	Gln	Phe	Gln	Glu	Asn	Gln	Glu	Ile	Ala
145					150					155					160
Asp	Leu	Gln	Phe	Phe	Ala	Ile	Asp	Gln	Leu	Pro	Asn	Leu	Ser	Glu	Lys
			165					170						175	
Arg	Ile	Thr	Lys	Glu	Gln	Ile	Glu	Ile	Leu	Trp	Gln	Val	Tyr	Gln	Gly
			180					185					190		
Gln	Arg	Glu	Gln	Tyr	Leu	Asp									
			195												

(2) INFORMATION FOR SEQ ID NO:3385:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 121 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3385:

Ile	Asn	Ser	Lys	Glu	Leu	Ser	Ile	Ser	Met	Leu	Lys	Lys	Tyr	Pro	Cys
1				5					10					15	
Thr	Met	Gln	His	Asp	Gln	Ser	Asp	Cys	Ala	Ala	Ala	Val	Val	Ser	Thr
			20					25					30		
Val	Leu	Leu	Ser	Tyr	Lys	Lys	Glu	Leu	Ser	Ile	Met	Lys	Ile	Arg	Glu
		35					40					45			
Ile	Ile	Gly	Thr	Asp	Met	Tyr	Gly	Thr	Thr	Val	Ser	Gly	Ile	Val	Ser
50						55					60				
Gly	Leu	Asn	Lys	Leu	Asn	Phe	Thr	Val	Lys	Ala	Val	Arg	Val	Ala	Leu
65					70				75						80
Glu	Asp	Leu	Thr	Pro	Lys	Leu	Thr	Phe	Pro	Ala	Ile	Leu	Gln	Val	Lys
			85					90					95		
Asn	Asp	Leu	Gly	Gln	Asn	His	Phe	Val	Val	Leu	His	Ser	Ile	Lys	Glu

	100		105		110
Lys	Ile	Lys	Gly	Thr	Arg
				Ile	Thr
				Lys	
	115		120		

(2) INFORMATION FOR SEQ ID NO:3386:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 76 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...76

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3386:

Ala	Phe	Ser	Lys	Glu	Asn	Leu	Tyr	Ser	Met	Lys	Ile	Lys	Glu	Gln	Thr
1				5					10					15	
Arg	Lys	Leu	Thr	Ala	Gly	Cys	Ser	Lys	His	Cys	Phe	Glu	Val	Val	Asp
			20				25						30		
Glu	Thr	Asp	Glu	Val	Ser	Ser	Lys	His	Gly	Phe	Glu	Val	Val	Asp	Glu
		35				40						45			
Thr	Asp	Glu	Val	Ser	Ser	Lys	His	Arg	Phe	Glu	Val	Ala	Asp	Arg	Thr
	50					55					60				
Asp	Glu	Val	Ser	Asn	Ile	Tyr	Thr	Val	Arg	Arg	Arg				
65					70				75						

(2) INFORMATION FOR SEQ ID NO:3387:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 130 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3387:

Ser	Ser	Ser	Lys	Leu	Val	Phe	Leu	Lys	Leu	Lys	Asp	Asp	Phe	Gly	Gly
1				5				10						15	

Tyr	Lys	Met	Thr	Leu	Thr	Ile	His	Val	Tyr	Tyr	Lys	Gly	Asp	Gly	Asp
			20					25					30		
Ser	Ala	Ile	Lys	Phe	Ala	Arg	Glu	Met	Leu	Asp	Ser	Gly	Leu	Val	Glu
		35					40					45			
Glu	Ile	Arg	Asn	Gln	Lys	Gly	Asn	Leu	Lys	Tyr	Glu	Tyr	Phe	Leu	Pro
	50					55					60				
Ile	Glu	Lys	Glu	Gly	Thr	Ile	Leu	Leu	Ile	Asp	Gln	Trp	Ile	Asn	Gln
65					70					75					80
Glu	Thr	Leu	Asp	Lys	His	Tyr	Gln	Ser	Lys	Thr	Met	Gln	Lys	Ile	Leu
				85					90					95	
Asp	Leu	Arg	Lys	Lys	Tyr	His	Leu	Gln	Met	Gln	Val	Glu	Arg	Tyr	Ile
			100					105					110		
Glu	Asp	Asp	Ser	Gly	Met	Pro	Glu	Ser	Asp	Lys	Ser	Phe	Ile	Asp	Thr
		115					120						125		
Gly	Asn														
	130														

(2) INFORMATION FOR SEQ ID NO:3388:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 495 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...495

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3388:

Met	Ser	Ser	Lys	Val	Ile	Val	Thr	Ile	Phe	Gly	Ala	Ser	Gly	Asp	Leu
1				5					10					15	
Ala	Lys	Arg	Lys	Leu	Tyr	Pro	Ser	Leu	Phe	Arg	Leu	Tyr	Gln	Ser	Gly
			20					25					30		
Asn	Leu	Ser	Lys	His	Phe	Ala	Val	Ile	Gly	Thr	Ala	Arg	Arg	Pro	Trp
	35						40					45			
Ser	Lys	Glu	Tyr	Phe	Glu	Ser	Val	Val	Val	Glu	Ser	Ile	Leu	Asp	Leu
	50					55				60					
Ala	Asp	Ser	Thr	Glu	Gln	Ala	Gln	Glu	Phe	Ala	Ser	His	Phe	Tyr	Tyr
65				70					75					80	
Gln	Ser	His	Asp	Val	Asn	Asp	Ser	Glu	His	Tyr	Ile	Ala	Leu	Arg	Gln
			85					90					95		
Leu	Gln	Ala	Glu	Leu	Asn	Glu	Lys	Tyr	Gln	Ala	Glu	His	Asn	Lys	Leu
		100					105					110			
Phe	Phe	Leu	Ser	Met	Ala	Pro	Gln	Phe	Phe	Gly	Thr	Ile	Ala	Lys	His
		115					120				125				
Leu	Lys	Ser	Glu	Asn	Ile	Val	Asp	Gly	Lys	Gly	Phe	Glu	Arg	Leu	Ile
	130					135				140					
Val	Glu	Lys	Pro	Phe	Gly	Thr	Asp	Tyr	Ala	Thr	Ala	Asn	Lys	Leu	Asn
145					150					155					160

Asp	Glu	Leu	Leu	Ala	Thr	Phe	Asp	Glu	Glu	Gln	Ile	Phe	Arg	Ile	Asp	165	170	175
His	Tyr	Leu	Gly	Lys	Glu	Met	Ile	Gln	Ser	Ile	Phe	Ala	Val	Arg	Phe	180	185	190
Ala	Asn	Leu	Ile	Phe	Glu	Asn	Val	Trp	Asn	Lys	Asp	Phe	Ile	Asp	Asn	195	200	205
Val	Gln	Ile	Thr	Phe	Ala	Glu	Arg	Leu	Gly	Val	Glu	Glu	Arg	Gly	Gly	210	215	220
Tyr	Tyr	Asp	Gln	Ser	Gly	Ala	Leu	Arg	Asp	Met	Val	Gln	Asn	His	Thr	225	230	235
Leu	Gln	Leu	Leu	Ser	Leu	Leu	Ala	Met	Asp	Lys	Pro	Ala	Ser	Phe	Thr	245	250	255
Lys	Asp	Glu	Ile	Arg	Ala	Glu	Lys	Ile	Lys	Val	Phe	Lys	Asn	Leu	Tyr	260	265	270
His	Pro	Thr	Asp	Glu	Glu	Leu	Lys	Glu	His	Phe	Ile	Arg	Gly	Gln	Tyr	275	280	285
Arg	Ser	Gly	Lys	Ile	Asp	Gly	Met	Lys	Tyr	Ile	Ser	Tyr	Arg	Ser	Glu	290	295	300
Pro	Asn	Val	Asn	Pro	Glu	Ser	Thr	Thr	Glu	Thr	Phe	Thr	Ser	Gly	Ala	305	310	315
Phe	Phe	Val	Asp	Ser	Asp	Arg	Phe	Arg	Gly	Val	Pro	Phe	Phe	Phe	Arg	325	330	335
Thr	Gly	Lys	Arg	Leu	Thr	Glu	Lys	Gly	Thr	His	Val	Asn	Ile	Val	Phe	340	345	350
Lys	Gln	Met	Asp	Ser	Ile	Phe	Gly	Glu	Pro	Leu	Ala	Pro	Asn	Ile	Leu	355	360	365
Thr	Ile	Tyr	Ile	Gln	Pro	Thr	Glu	Gly	Phe	Ser	Leu	Ser	Leu	Asn	Gly	370	375	380
Lys	Gln	Val	Gly	Glu	Glu	Phe	Asn	Leu	Ala	Pro	Asn	Ser	Leu	Asp	Tyr	385	390	395
Arg	Thr	Asp	Ala	Thr	Ala	Thr	Gly	Ala	Ser	Pro	Glu	Pro	Tyr	Glu	Lys	405	410	415
Leu	Ile	Tyr	Asp	Val	Leu	Asn	Asn	Asn	Ser	Thr	Asn	Phe	Ser	His	Trp	420	425	430
Asp	Glu	Val	Gly	Ala	Ser	Trp	Lys	Leu	Ile	Asp	Arg	Ile	Glu	Glu	Leu	435	440	445
Trp	Ala	Glu	Asn	Gly	Ala	Pro	Leu	His	Asp	Tyr	Lys	Ala	Gly	Ser	Met	450	455	460
Gly	Pro	Gln	Ala	Ser	Phe	Asp	Leu	Leu	Glu	Lys	Phe	Gly	Ala	Lys	Trp	465	470	475
Thr	Trp	Gln	Pro	Asp	Ile	Ala	Tyr	Arg	Gln	Asp	Gly	Arg	Phe	Glu		485	490	495

(2) INFORMATION FOR SEQ ID NO:3389:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3389:

Phe	Thr	Cys	Phe	Cys	Asp	Ile	Ile	Val	Leu	Ser	Leu	His	Arg	Gly	Ile
1			5					10						15	
Val	Met	Lys	Glu	Thr	Val	Tyr	Phe	Gly	Thr	Tyr	Thr	Arg	Arg	Thr	Ser
			20					25					30		
Gln	Gly	Ile	Tyr	Lys	Ala	Asp	Phe	Asp	Thr	Glu	Thr	Gly	Gln	Leu	Ser
		35					40					45			
Asn	Leu	Glu	Leu	Phe	Ala	Ala	Glu	Pro	Ser	Pro	Thr	Tyr	Leu	Ala	Phe
	50					55					60				
Asp	Gln	His	Gln	His	Leu	Tyr	Thr	Val	Gly	Ser	Gln	Asp	Asp	Lys	Gly
65					70				75					80	
Gly	Ile	Ala	Ala	Tyr	Gln	Thr	Asp	Gly	Thr	Val	Leu	Asn	His	Val	Val
			85					90						95	
Glu	Glu	Gly	Ala	Pro	His	Cys	Tyr	Val	Ala	Val	Asp	Glu	Lys	Arg	Asp
		100						105					110		
Leu	Val	Tyr	Ala	Ala	Asn	Tyr	His	Lys	Gly	Gln	Val	Leu	Val	Tyr	Lys
	115					120						125			
Arg	Gln	Glu	Asp	Gly	Ser	Leu	Leu	Leu	Ser	Asp	Met	Asp	Gln	His	Ser
	130					135					140				
Gly	Gln	Gly	Pro	His	Glu	Asn	Gln	Ala	Ser	Pro	His	Val	His	Tyr	Thr
145					150				155					160	
Asp	Leu	Thr	Pro	Asp	His	Tyr	Leu	Val	Thr	Cys	Asp	Leu	Gly	Thr	Asp
			165					170					175		
Gln	Val	Ile	Thr	Tyr	Asp	Leu	Asp	Gln	Glu	Gly	Lys	Leu	Ser	Lys	Leu
		180						185				190			
Tyr	Thr	Tyr	His	Ser	Lys	Pro	Gly	Ala	Gly	Ser	Arg	His	Ile	Ile	Phe
	195						200					205			
His	Asn	His	Tyr	Lys	Ile	Ala	Tyr	Leu	Ile	Cys	Glu	Leu	Asn	Ser	Thr
	210					215					220				
Ile	Glu	Val	Leu	Ile	Tyr	Asp	Gly	Val	Gly	Glu	Phe	Glu	Arg	Met	Gln
225					230				235					240	
Val	Ile	Ser	Thr	Leu	Pro	Glu	Ala	Tyr	Glu	Gly	Phe	Asn	Gly	Thr	Ala
			245					250					255		
Ala	Ile	His	Leu	Ser	Lys	Asp	Gly	Lys	Tyr	Leu	Tyr	Ala	Ser	Asn	Arg
		260						265					270		
Gly	His	Asp	Ser	Ile	Ala	Val	Tyr	Thr	Ile	Leu	Ala	Asp	Gly	Ser	Leu
	275					280						285			
Glu	Leu	Glu	Ile	Val	Pro	Thr	His	Gly	Gln	Thr	Pro	Arg	Asp	Phe	
	290				295					300					
Asp	Leu	Thr	Pro	Asp	Gln	Lys	Phe	Leu	Ile	Val	Val	His	Gln	Asp	Ser
305					310					315				320	
Asp	Asn	Ala	Thr	Val	Phe	Lys	Arg	Asn	Cys	Asp	Asn	Gly	Arg	Leu	Ala
			325						330				335		
Glu	Leu	Ser	Asn	Asp	Phe	His	Val	Pro	Glu	Ala	Val	Cys	Ile	Arg	Phe
			340					345					350		
Ala	Pro														

(2) INFORMATION FOR SEQ ID NO:3390:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 361 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...361

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3390:

His	Met	Ser	Lys	Leu	Gln	Gln	Ile	Leu	Thr	Tyr	Leu	Glu	Ser	Glu	Lys
1			5					10					15		
Leu	Asp	Val	Ala	Val	Val	Ser	Asp	Pro	Val	Thr	Ile	Asn	Tyr	Leu	Thr
		20						25					30		
Asp	Phe	Tyr	Ser	Asp	Pro	His	Glu	Arg	Gln	Met	Phe	Leu	Phe	Val	Leu
	35						40					45			
Ala	Asp	Gln	Glu	Pro	Leu	Leu	Phe	Val	Pro	Ala	Leu	Glu	Val	Glu	Arg
	50					55					60				
Ala	Ser	Ser	Thr	Val	Ser	Phe	Pro	Val	Val	Gly	Tyr	Val	Asp	Ser	Glu
65					70					75					80
Asn	Pro	Trp	Gln	Lys	Ile	Lys	His	Ala	Leu	Pro	Gln	Leu	Asp	Phe	Lys
			85					90						95	
Arg	Val	Ala	Val	Glu	Phe	Asp	Asn	Leu	Ile	Leu	Thr	Lys	Tyr	His	Gly
		100						105					110		
Leu	Lys	Thr	Val	Phe	Glu	Thr	Ala	Glu	Phe	Asp	Asn	Leu	Thr	Pro	Arg
	115						120					125			
Ile	Gln	Arg	Met	Arg	Leu	Ile	Lys	Ser	Ala	Asp	Glu	Val	Gln	Lys	Met
	130				135					140					
Met	Val	Ala	Gly	Leu	Tyr	Ala	Asp	Lys	Ala	Val	His	Val	Gly	Phe	Asp
145				150					155					160	
Asn	Ile	Ser	Leu	Asp	Lys	Thr	Glu	Thr	Asp	Ile	Ile	Ala	Gln	Ile	Asp
			165					170						175	
Phe	Ala	Met	Lys	Arg	Glu	Gly	Tyr	Glu	Met	Ser	Phe	Asp	Thr	Met	Val
		180						185					190		
Leu	Thr	Gly	Asp	Asn	Ala	Ala	Asn	Pro	His	Gly	Ile	Pro	Ala	Ala	Asn
	195						200					205			
Lys	Val	Glu	Asn	Asp	Ala	Leu	Leu	Leu	Phe	Asp	Leu	Gly	Val	Leu	Val
	210					215					220				
Asn	Gly	Tyr	Ala	Ser	Asp	Met	Thr	Arg	Thr	Val	Ala	Val	Gly	Lys	Pro
225				230						235				240	
Asp	Gln	Phe	Lys	Lys	Asp	Ile	Tyr	Asn	Leu	Thr	Leu	Glu	Ala	Gln	Gln
			245						250					255	
Ala	Ala	Leu	Asp	Phe	Ile	Lys	Pro	Gly	Val	Thr	Ala	His	Glu	Val	Asp
		260						265					270		
Arg	Ala	Ala	Arg	Glu	Val	Ile	Glu	Lys	Ala	Gly	Tyr	Gly	Glu	Tyr	Phe
	275					280						285			
Asn	His	Arg	Leu	Gly	His	Gly	Ile	Gly	Met	Asp	Val	His	Glu	Phe	Pro
	290				295						300				
Ser	Ile	Met	Glu	Gly	Asn	Asp	Met	Val	Ile	Glu	Glu	Gly	Met	Cys	Phe
305				310						315				320	
Ser	Val	Glu	Pro	Gly	Ile	Tyr	Ile	Pro	Gly	Lys	Val	Gly	Val	Arg	Ile

				325					330					335					
Glu	Asp	Cys	Gly	Val	Val	Thr	Lys	Asp	Gly	Phe	Asp	Leu	Phe	Thr	Ser				
			340					345					350						
Thr	Ser	Lys	Asp	Leu	Leu	Tyr	Phe	Asp											
		355				360													

(2) INFORMATION FOR SEQ ID NO:3391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3391:

Met	Met	Ser	Asn	Lys	Asn	Lys	Gly	Ile	Leu	Ile	Phe	Ala	Ile	Leu	Tyr				
1				5					10					15					
Thr	Val	Leu	Phe	Val	Phe	Asp	Gly	Val	Lys	Leu	Leu	Ala	Ser	Leu	Met				
			20					25					30						
Pro	Ser	Val	Ile	Ala	Asn	Tyr	Leu	Val	Tyr	Val	Val	Leu	Ala	Leu	Tyr				
		35				40						45							
Gly	Ser	Phe	Leu	Phe	Lys	Asp	Arg	Leu	Ile	Gln	Gln	Trp	Lys	Glu	Ile				
	50					55					60								
Arg	Lys	Thr	Lys	Arg	Lys	Phe	Phe	Phe	Gly	Val	Leu	Thr	Gly	Trp	Leu				
65					70				75					80					
Phe	Leu	Ile	Leu	Met	Thr	Val	Val	Phe	Glu	Phe	Val	Ser	Glu	Met	Leu				
			85					90					95						
Lys	Gln	Phe	Val	Arg	Leu	Asp	Gly	Gln	Gly	Leu	Asn	Gln	Ser	Asn	Ile				
		100					105					110							
Gln	Ser	Thr	Phe	Gln	Glu	Gln	Pro	Leu	Leu	Ile	Ala	Val	Phe	Ala	Cys				
		115					120					125							
Val	Ile	Gly	Pro	Leu	Val	Glu	Glu	Leu	Phe	Phe	Arg	Gln	Val	Leu	Leu				
	130					135					140								
His	Tyr	Leu	Gln	Glu	Arg	Leu	Pro	Gly	Leu	Leu	Ser	Ile	Ile	Leu	Val				
145					150				155					160					
Gly	Leu	Val	Phe	Ala	Leu	Thr	His	Met	His	Ser	Leu	Ala	Leu	Ser	Glu				
			165					170					175						
Trp	Ile	Gly	Ala	Val	Gly	Tyr	Leu	Gly	Gly	Gly	Leu	Ala	Phe	Ser	Ile				
		180					185					190							
Ile	Tyr	Val	Lys	Glu	Lys	Glu	Asn	Ile	Tyr	Tyr	Pro	Leu	Leu	Val	His				
		195				200					205								
Met	Leu	Ser	Asn	Ser	Leu	Ser	Leu	Ile	Ile	Leu	Ala	Ile	Ser	Ile	Val				
	210					215					220								
Lys																			
225																			

(2) INFORMATION FOR SEQ ID NO:3392:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...114

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3392:

Ala	Trp	Ser	Asn	Lys	Ala	Met	Ala	Tyr	Asn	Thr	Asp	Phe	Lys	Gln	Gly
1			5					10					15		
Ala	Leu	Asp	Ser	Ile	Lys	Gly	Gly	His	Arg	His	Val	Glu	Ala	Ala	Lys
		20					25				30				
Val	Phe	Trp	Cys	Trp	Arg	Gln	Asn	Ser	Leu	His	Val	Gly	Lys	Glu	Arg
	35				40					45					
Arg	Glu	Gln	Arg	Asn	Leu	Glu	Arg	Lys	Lys	Arg	Val	Val	Lys	Lys	Arg
	50				55					60					
Lys	Ile	Pro	Leu	Glu	Glu	Leu	Lys	Ala	Phe	Val	Glu	Ala	His	Pro	Asp
65				70					75					80	
Ala	Phe	Leu	Arg	Glu	Ile	Ala	Ala	His	Phe	Asp	Cys	Ala	Val	Pro	Ser
		85						90					95		
Val	Trp	Ala	Ala	Leu	Lys	Gln	Ile	Lys	Val	Thr	Leu	Lys	Lys	Asp	Asp
		100					105						110		
Asp	Leu														

(2) INFORMATION FOR SEQ ID NO:3393:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...274

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3393:

Pro	Leu	Pro	Lys	Gly	Glu	Ala	Met	Ser	Thr	Tyr	Asn	Trp	Asp	Glu	Lys
1			5						10					15	
His	Ile	Leu	Thr	Phe	Pro	Glu	Glu	Lys	Val	Ala	Leu	Ser	Thr	Lys	Asp
		20						25					30		
Val	His	Val	Tyr	Tyr	Gly	Lys	Asn	Glu	Ser	Ile	Lys	Gly	Ile	Asp	Met
		35					40					45			
Gln	Phe	Glu	Arg	Asn	Lys	Ile	Thr	Ala	Leu	Ile	Gly	Pro	Ser	Gly	Ser
	50					55					60				
Gly	Lys	Ser	Thr	Tyr	Leu	Arg	Ser	Leu	Asn	Arg	Met	Asn	Asp	Thr	Ile
65					70					75					80
Asp	Ile	Ala	Lys	Val	Thr	Gly	Gln	Ile	Leu	Tyr	Arg	Gly	Ile	Asp	Val
			85						90					95	
Asn	Arg	Pro	Glu	Ile	Asn	Val	Tyr	Glu	Met	Arg	Lys	His	Ile	Gly	Met
		100						105					110		
Val	Phe	Gln	Arg	Pro	Asn	Pro	Phe	Ala	Lys	Ser	Ile	Tyr	Arg	Asn	Ile
	115						120					125			
Thr	Phe	Ala	His	Glu	Arg	Ala	Gly	Val	Lys	Asp	Lys	Gln	Val	Leu	Asp
	130					135					140				
Glu	Ile	Val	Glu	Thr	Ser	Leu	Arg	Gln	Ala	Ala	Leu	Trp	Asp	Gln	Val
145					150					155					160
Lys	Asp	Asp	Leu	His	Lys	Ser	Ala	Leu	Thr	Leu	Ser	Gly	Gly	Gln	Gln
			165						170					175	
Gln	Arg	Leu	Cys	Ile	Ala	Arg	Ala	Ile	Ser	Val	Lys	Pro	Asp	Ile	Leu
		180						185					190		
Leu	Met	Asp	Glu	Pro	Ala	Ser	Ala	Leu	Asp	Pro	Ile	Ala	Thr	Met	Gln
	195					200						205			
Leu	Glu	Glu	Thr	Met	Phe	Glu	Leu	Lys	Lys	Asn	Phe	Thr	Ile	Ile	Ile
	210					215					220				
Val	Thr	His	Asn	Met	Gln	Gln	Ala	Ala	Arg	Ala	Ser	Asp	Tyr	Thr	Gly
225					230					235					240
Phe	Phe	Tyr	Leu	Gly	Asp	Leu	Ile	Glu	Tyr	Asp	Lys	Thr	Ala	Thr	Ile
			245						250					255	
Phe	Gln	Asn	Ala	Lys	Leu	Gln	Ser	Thr	Asn	Asp	Tyr	Val	Ser	Gly	His
			260					265					270		
Phe	Gly														

(2) INFORMATION FOR SEQ ID NO:3394:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 321 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...321
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3394:

Ile	Met	Pro	Lys	Lys	Ile	Leu	Val	Leu	His	Thr	Gly	Gly	Thr	Ile	Ser
1			5						10					15	
Met	Gln	Ala	Asp	Ala	Ser	Gly	Ala	Val	Val	Thr	Ser	Ser	Asp	Asn	Pro
			20					25					30		
Met	Asn	His	Val	Ser	Asn	Pro	Leu	Glu	Gly	Ile	Gln	Val	His	Ala	Leu
		35					40					45			
Asp	Phe	Asn	Leu	Pro	Ser	Pro	His	Ile	Lys	Pro	Lys	His	Met	Leu	
	50				55					60					
Val	Leu	Tyr	Gln	Lys	Ile	Lys	Glu	Glu	Ala	Asp	Asn	Tyr	Asp	Gly	Val
65					70					75					80
Val	Ile	Thr	His	Gly	Thr	Asp	Thr	Leu	Glu	Glu	Thr	Ala	Tyr	Phe	Leu
				85					90					95	
Asp	Thr	Met	Glu	Val	Pro	His	Met	Pro	Ile	Val	Leu	Thr	Gly	Ala	Met
			100					105					110		
Arg	Ser	Ser	Asn	Glu	Leu	Gly	Ser	Asp	Gly	Val	Tyr	Asn	Tyr	Leu	Ser
			115				120					125			
Ala	Leu	Arg	Val	Ala	Ser	Asp	Asp	Arg	Ala	Ala	Asp	Lys	Gly	Val	Leu
	130					135					140				
Val	Val	Met	Asn	Asp	Glu	Ile	His	Ala	Ala	Lys	Tyr	Val	Thr	Lys	Thr
145					150					155					160
His	Thr	Thr	Asn	Val	Asn	Thr	Phe	Gln	Thr	Pro	Thr	His	Gly	Pro	Leu
			165					170						175	
Gly	Leu	Ile	Met	Lys	Gln	Glu	Ile	Leu	Tyr	Phe	Lys	Thr	Ala	Glu	Pro
		180						185					190		
Arg	Val	Arg	Phe	Asp	Leu	Asp	His	Ile	Gln	Gly	Leu	Val	Pro	Ile	Ile
		195					200					205			
Ser	Ala	Tyr	Ala	Gly	Met	Thr	Asp	Glu	Leu	Ile	Asp	Met	Leu	Asp	Leu
	210					215					220				
Glu	His	Leu	Asp	Gly	Leu	Ile	Ile	Gln	Ala	Phe	Gly	Ala	Gly	Asn	Ile
225					230					235					240
Pro	Lys	Glu	Thr	Ala	Gln	Lys	Leu	Glu	Ser	Leu	Leu	Gln	Lys	Gly	Ile
				245					250					255	
Pro	Val	Ala	Leu	Val	Ser	Arg	Cys	Phe	Asn	Gly	Ile	Ala	Glu	Pro	Val
		260						265					270		
Tyr	Ala	Tyr	Gln	Gly	Gly	Gly	Val	Gln	Leu	Gln	Lys	Ala	Gly	Val	Phe
		275					280					285			
Phe	Val	Lys	Glu	Leu	Asn	Ala	Gln	Lys	Ala	Arg	Leu	Lys	Leu	Leu	Ile
	290					295					300				
Ala	Leu	Asn	Ala	Gly	Leu	Thr	Gly	Gln	Ala	Leu	Lys	Asp	Tyr	Met	Glu
305					310					315					320

Gly

(2) INFORMATION FOR SEQ ID NO:3395:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...431

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3395:

```
Lys Ala Pro Lys Gln Leu Ile Arg Lys Tyr Leu Met Glu His Ile Asn
1      5      10      15
His Thr Thr Leu Leu Ile Gly Ile Lys Asp Lys Asn Ile Thr Leu Asn
      20      25      30
Lys Ala Ile Gln His Asp Thr His Ile Glu Val Phe Ala Thr Leu Asp
      35      40      45
Tyr His Pro Pro Lys Cys Lys His Cys Lys Gly Lys Gln Ile Lys Tyr
      50      55      60
Asp Phe Gln Lys Pro Ser Lys Ile Pro Phe Ile Glu Ile Gly Gly Phe
      65      70      75      80
Pro Ser Leu Ile His Leu Lys Lys Arg Arg Phe Gln Cys Lys Ser Cys
      85      90      95
Arg Lys Val Thr Val Ala Glu Thr Thr Leu Val Gln Lys Asn Cys Gln
      100     105     110
Ile Ser Glu Met Val Arg Gln Lys Ile Ala Gln Leu Leu Leu Asn Arg
      115     120     125
Glu Ala Leu Thr His Ile Ala Ser Lys Leu Ala Ile Ser Thr Ser Thr
      130     135     140
Ser Thr Val Tyr Arg Lys Leu Lys Gln Phe His Phe Gln Glu Asp Tyr
      145     150     155     160
Thr Thr Leu Pro Glu Ile Leu Ser Trp Asp Glu Phe Ser Tyr Gln Lys
      165     170     175
Gly Lys Leu Ala Phe Ile Ala Gln Asp Phe Asn Thr Lys Lys Ile Met
      180     185     190
Thr Ile Leu Asp Asn Arg Arg Gln Thr Thr Ile Arg Asn His Phe Phe
      195     200     205
Lys Tyr Ser Lys Glu Ala Arg Lys Lys Val Lys Val Val Thr Val Asp
      210     215     220
Met Ser Gly Ser Tyr Ile Pro Leu Ile Lys Lys Leu Phe Pro Asn Ala
      225     230     235     240
Lys Ile Val Leu Asp Arg Phe His Ile Val Gln His Met Ser Arg Ala
      245     250     255
Leu Asn Gln Thr Arg Ile Asn Ile Met Lys Gln Phe Asp Asp Lys Ser
      260     265     270
Leu Glu Tyr Arg Ala Leu Lys Tyr Tyr Trp Lys Phe Ile Leu Lys Asp
      275     280     285
Ser Arg Lys Leu Ser Leu Lys Pro Phe Tyr Ala Arg Thr Phe Arg Glu
      290     295     300
Thr Leu Thr Pro Arg Glu Cys Leu Lys Lys Ile Phe Thr Leu Val Pro
      305     310     315     320
Glu Leu Lys Asp Tyr Tyr Asp Leu Tyr Gln Leu Leu Leu Phe His Leu
      325     330     335
Gln Glu Lys Asn Thr Asp Gln Phe Trp Gly Leu Ile Gln Asp Thr Leu
      340     345     350
Pro His Leu Asn Arg Thr Phe Lys Thr Thr Leu Ser Thr Phe Ile Cys
      355     360     365
Tyr Lys Asn Tyr Ile Thr Asn Ala Ile Glu Leu Pro Tyr Ser Asn Ala
      370     375     380
Lys Leu Glu Ala Thr Asn Lys Leu Ile Lys Asp Ile Lys Arg Asn Ala
```

385				390				395				400			
Phe	Gly	Phe	Arg	Asn	Phe	Glu	Asn	Phe	Lys	Lys	Arg	Ile	Phe	Ile	Ala
				405				410						415	
Leu	Asn	Ile	Lys	Lys	Glu	Arg	Thr	Lys	Phe	Val	Leu	Ser	Arg	Ala	
			420					425					430		

(2) INFORMATION FOR SEQ ID NO:3396:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...169

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3396:

Thr	Tyr	Thr	Lys	Thr	Tyr	Lys	Gly	Gly	Lys	Leu	Met	Thr	Ile	Val	Gly
1				5					10					15	
Cys	Arg	Ile	Asp	Gly	Arg	Leu	Ile	His	Gly	Gln	Val	Ala	Asn	Leu	Trp
			20					25					30		
Ala	Gly	Lys	Leu	Asn	Val	Ser	Arg	Ile	Met	Val	Val	Asp	Asp	Glu	Val
		35					40					45			
Val	Asn	Asn	Asp	Ile	Glu	Lys	Ser	Gly	Leu	Lys	Leu	Ala	Thr	Pro	Pro
	50					55				60					
Gly	Val	Lys	Leu	Ser	Ile	Leu	Pro	Val	Glu	Lys	Ala	Ala	Ala	Asn	Ile
65					70					75				80	
Leu	Ala	Gly	Lys	Tyr	Asp	Ser	Gln	Arg	Leu	Phe	Ile	Val	Ala	Arg	Lys
				85				90					95		
Pro	Asp	Arg	Phe	Leu	Gly	Leu	Val	Glu	Ala	Gly	Val	Pro	Leu	Glu	Thr
			100					105					110		
Leu	Asn	Val	Gly	Asn	Met	Ser	Gln	Thr	Pro	Glu	Thr	Arg	Ser	Ile	Thr
		115					120					125			
Arg	Ser	Ile	Asn	Val	Val	Asp	Lys	Asp	Val	Glu	Asp	Phe	His	Lys	Leu
	130					135				140					
Ala	Glu	Lys	Gly	Val	Lys	Leu	Thr	Ala	Gln	Met	Val	Pro	Asn	Asp	Pro
145					150					155					160
Ile	Ser	Asp	Phe	Leu	Ser	Leu	Leu	Lys							
				165											

(2) INFORMATION FOR SEQ ID NO:3397:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...307

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3397:

Glu	Met	Thr	Lys	Thr	Ala	Phe	Leu	Phe	Ala	Gly	Gln	Gly	Ala	Gln	Tyr
1				5					10					15	
Leu	Gly	Met	Gly	Arg	Asp	Phe	Tyr	Asp	Gln	Tyr	Pro	Ile	Val	Lys	Glu
			20					25					30		
Thr	Ile	Asp	Arg	Ala	Ser	Gln	Val	Leu	Gly	Tyr	Asp	Leu	Arg	Tyr	Leu
		35					40					45			
Ile	Asp	Thr	Glu	Glu	Asp	Lys	Leu	Asn	Gln	Thr	Arg	Tyr	Thr	Gln	Pro
	50					55					60				
Ala	Ile	Leu	Ala	Thr	Ser	Val	Ala	Ile	Tyr	Arg	Leu	Leu	Gln	Glu	Lys
65					70					75					80
Gly	Tyr	Gln	Pro	Asp	Met	Val	Ala	Gly	Leu	Ser	Leu	Gly	Glu	Tyr	Ser
				85					90					95	
Ala	Leu	Val	Ala	Ser	Gly	Ala	Leu	Asp	Phe	Glu	Asp	Ala	Val	Ala	Leu
			100					105					110		
Val	Ala	Lys	Arg	Gly	Ala	Tyr	Met	Glu	Glu	Ala	Ala	Pro	Ala	Asp	Ser
		115					120					125			
Gly	Lys	Met	Val	Ala	Val	Leu	Asn	Thr	Pro	Val	Glu	Val	Ile	Glu	Glu
	130					135					140				
Ala	Cys	Gln	Lys	Ala	Ser	Glu	Leu	Gly	Val	Val	Thr	Pro	Ala	Asn	Tyr
145					150					155					160
Asn	Thr	Pro	Ala	Gln	Ile	Val	Ile	Ala	Gly	Glu	Val	Val	Ala	Val	Asp
				165					170					175	
Arg	Ala	Val	Glu	Leu	Leu	Gln	Glu	Ala	Gly	Ala	Lys	Arg	Leu	Ile	Pro
			180					185					190		
Leu	Lys	Val	Ser	Gly	Pro	Phe	His	Thr	Ala	Leu	Leu	Glu	Pro	Ala	Ser
		195					200					205			
Gln	Lys	Leu	Ala	Glu	Thr	Leu	Ala	Gln	Val	Ser	Phe	Ser	Asp	Phe	Thr
	210					215					220				
Cys	Pro	Leu	Val	Gly	Asn	Thr	Glu	Ala	Ala	Val	Met	Gln	Lys	Glu	Asp
225					230					235					240
Ile	Ala	Gln	Leu	Leu	Thr	Arg	Gln	Val	Lys	Glu	Pro	Val	Arg	Phe	Tyr
				245				250					255		
Glu	Ser	Ile	Gly	Val	Met	Gln	Glu	Ala	Gly	Ile	Ser	Asn	Phe	Ile	Glu
			260					265					270		
Ile	Gly	Pro	Gly	Lys	Val	Leu	Ser	Gly	Phe	Val	Lys	Lys	Ile	Asp	Gln
		275					280					285			
Thr	Ala	His	Leu	Ala	His	Val	Glu	Asp	Gln	Ala	Ser	Leu	Val	Ala	Leu
	290					295					300				
Leu	Glu	Lys													
305															

(2) INFORMATION FOR SEQ ID NO:3398:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...159

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3398:

Phe	Met	Ala	Lys	Val	Leu	Leu	Gly	Phe	Met	Gly	Ala	Gly	Lys	Ser	Thr
1				5					10					15	
Ile	Ala	Arg	Gly	Leu	Asp	Thr	Asn	Tyr	Leu	Asp	Met	Asp	Ala	Leu	Ile
			20					25					30		
Glu	Lys	Arg	Leu	Gly	Met	Ser	Ile	Ala	Asn	Phe	Phe	Ala	Glu	Lys	Gly
		35					40					45			
Glu	Glu	Thr	Phe	Arg	Gln	Val	Glu	Ser	Glu	Val	Leu	Ala	Asp	Leu	Leu
	50					55					60				
Gln	Thr	Asp	Gln	Val	Val	Ser	Thr	Gly	Gly	Gly	Val	Val	Ile	Ser	Gln
65				70					75					80	
Arg	Asn	Arg	Asp	Leu	Leu	Lys	Thr	Asn	Thr	Asp	Asn	Ile	Tyr	Leu	Lys
				85					90					95	
Ala	Asp	Phe	Glu	Thr	Leu	Tyr	Gln	Arg	Ile	Ala	Ala	Asp	Lys	Asp	Asn
			100					105					110		
Gln	Arg	Pro	Leu	Phe	Leu	Asn	Asn	Ser	Lys	Glu	Glu	Leu	Val	Ala	Ile
		115					120					125			
Phe	Gln	Glu	Arg	Gln	Ala	Trp	Tyr	Glu	Glu	Val	Ala	Ser	Arg	Val	Leu
	130					135				140					
Asp	Val	Thr	Lys	Leu	Ser	Pro	Glu	Glu	Ile	Ile	Glu	Glu	Leu	Arg	
145				150					155						

(2) INFORMATION FOR SEQ ID NO:3399:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 158 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...158

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3399:

Ala	Arg	Ala	Lys	Ser	Val	His	Trp	Thr	Asp	Leu	Leu	His	Gln	Asp	Ser
1				5					10					15	
Phe	Lys	Leu	Cys	Gln	Lys	Arg	Phe	Tyr	Gln	Pro	Thr	Phe	Arg	Met	His
			20					25					30		
Leu	Thr	His	Arg	Glu	Val	Arg	Asp	Lys	Leu	Leu	Ser	Tyr	Ser	Glu	Gly
		35					40					45			
Leu	Gln	Val	His	Tyr	Glu	Leu	Tyr	Gln	Leu	Leu	Leu	Phe	His	Phe	Gln
	50					55					60				
Glu	Lys	Asn	Ala	Asp	His	Phe	Phe	Gly	Leu	Ile	Glu	Gln	Glu	Leu	Pro
65					70					75					80
Thr	Val	His	Pro	Leu	Phe	Gln	Thr	Val	Phe	Trp	Thr	Phe	Leu	Arg	Asp
				85					90					95	
Arg	Asp	Lys	Ile	Ile	Asn	Ala	Leu	Lys	Leu	Pro	Tyr	Ser	Asn	Ala	Lys
			100					105					110		
Leu	Glu	Ala	Thr	Asn	Asn	Leu	Ile	Lys	Val	Ile	Lys	Cys	Lys	Ala	Phe
		115					120					125			
Gly	Phe	Arg	Asn	Phe	Asn	Asn	Phe	Lys	Lys	Arg	Ile	Leu	Met	Thr	Leu
	130					135					140				
Asn	Ile	Lys	Lys	Glu	Ser	Thr	Asn	Phe	Val	Leu	Ser	Arg	Leu		
145					150					155					

(2) INFORMATION FOR SEQ ID NO:3400:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 305 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...305

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3400:

Ile	Tyr	Tyr	Asn	Lys	Gly	Met	Arg	Asn	Met	Lys	Ala	Lys	Tyr	Ala	Val
1				5					10					15	
Trp	Val	Ala	Phe	Phe	Leu	Asn	Leu	Thr	Tyr	Ala	Ile	Val	Glu	Phe	Ile
			20					25					30		
Ala	Gly	Gly	Ile	Phe	Gly	Ser	Ser	Ala	Val	Leu	Ala	Asp	Ser	Val	His
		35				40						45			
Asp	Leu	Val	Asp	Ala	Ile	Ala	Ile	Gly	Ile	Ser	Ala	Phe	Leu	Glu	Thr
	50				55					60					
Ile	Ser	Asn	Arg	Glu	Glu	Asp	Asn	Gln	Tyr	Thr	Leu	Gly	Tyr	Lys	Arg
65				70					75					80	
Phe	Ser	Leu	Leu	Gly	Ala	Leu	Val	Thr	Ala	Val	Ile	Leu	Val	Thr	Gly
			85					90						95	
Ser	Val	Leu	Val	Ile	Leu	Glu	Asn	Val	Thr	Lys	Ile	Leu	His	Pro	Gln
		100					105					110			
Pro	Val	Asn	Asp	Glu	Gly	Ile	Leu	Trp	Leu	Gly	Ile	Ile	Ala	Ile	Thr

				85					90					95			
Ile	Met	Ser	Trp	Asp	Val	Glu	Thr	Val	Arg	Gly	Val	Thr	Val	Ser	Ile		
			100					105					110				
Gly	Arg	Trp	Arg														
		115															

(2) INFORMATION FOR SEQ ID NO:3402:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 679 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...679

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3402:

Lys	Tyr	Tyr	Lys	Tyr	Ala	Lys	Ile	Gly	Ile	Ala	His	Gly	Glu	Arg	Ile		
1				5				10						15			
Leu	Met	Ile	Asn	His	Ile	Thr	Asp	Asn	Gln	Phe	Lys	Leu	Val	Ser	Lys		
			20					25					30				
Tyr	Gln	Pro	Ser	Gly	Asp	Gln	Pro	Gln	Ala	Ile	Glu	Gln	Leu	Val	Asp		
		35				40					45						
Asn	Ile	Glu	Gly	Gly	Glu	Lys	Ala	Gln	Ile	Leu	Met	Gly	Ala	Thr	Gly		
	50					55				60							
Thr	Gly	Lys	Thr	Tyr	Thr	Met	Ser	Gln	Val	Ile	Ser	Lys	Val	Asn	Lys		
65					70				75					80			
Pro	Thr	Leu	Val	Ile	Ala	His	Asn	Lys	Thr	Leu	Ala	Gly	Gln	Leu	Tyr		
			85					90					95				
Gly	Glu	Phe	Lys	Glu	Phe	Phe	Pro	Glu	Asn	Ala	Val	Glu	Tyr	Phe	Val		
		100					105					110					
Ser	Tyr	Tyr	Asp	Tyr	Tyr	Gln	Pro	Glu	Ala	Tyr	Val	Pro	Ser	Ser	Asp		
	115					120					125						
Thr	Tyr	Ile	Glu	Lys	Asp	Ser	Ser	Val	Asn	Asp	Glu	Ile	Asp	Lys	Leu		
	130				135				140								
Arg	His	Ser	Ala	Thr	Ser	Ala	Leu	Leu	Glu	Arg	Asn	Asp	Val	Ile	Val		
145				150					155					160			
Val	Ala	Ser	Val	Ser	Cys	Ile	Tyr	Gly	Leu	Gly	Ser	Pro	Lys	Glu	Tyr		
			165					170					175				
Ala	Asp	Ser	Val	Val	Ser	Leu	Arg	Pro	Gly	Leu	Glu	Ile	Ser	Arg	Asp		
		180				185						190					
Lys	Leu	Leu	Asn	Asp	Leu	Val	Asp	Ile	Gln	Phe	Glu	Arg	Asn	Asp	Ile		
	195				200						205						
Asp	Phe	Gln	Arg	Gly	Arg	Phe	Arg	Val	Arg	Gly	Asp	Val	Val	Glu	Ile		
	210			215				220									
Phe	Pro	Ala	Ser	Arg	Asp	Glu	His	Ala	Phe	Arg	Val	Glu	Phe	Phe	Gly		
225				230				235						240			
Asp	Glu	Ile	Asp	Arg	Ile	Arg	Glu	Val	Glu	Ala	Leu	Thr	Gly	Gln	Val		

				245					250				255				
Leu	Gly	Glu	Val	Asp	His	Leu	Ala	Ile	Phe	Pro	Ala	Thr	His	Phe	Val		
			260					265					270				
Thr	Asn	Asp	Asp	His	Met	Glu	Val	Ala	Ile	Ala	Lys	Ile	Gln	Ala	Glu		
		275					280					285					
Leu	Glu	Glu	Gln	Leu	Ala	Val	Phe	Glu	Lys	Glu	Gly	Lys	Leu	Leu	Glu		
	290					295					300						
Ala	Gln	Arg	Leu	Lys	Gln	Arg	Thr	Glu	Tyr	Asp	Ile	Glu	Met	Leu	Arg		
305					310					315					320		
Glu	Met	Gly	Tyr	Thr	Asn	Gly	Val	Glu	Asn	Tyr	Ser	Arg	His	Met	Asp		
				325					330					335			
Gly	Arg	Ser	Glu	Gly	Glu	Pro	Pro	Tyr	Thr	Leu	Leu	Asp	Phe	Phe	Pro		
			340					345					350				
Asp	Asp	Phe	Leu	Ile	Met	Ile	Asp	Glu	Ser	His	Met	Thr	Ile	Gly	Gln		
		355					360					365					
Ile	Lys	Gly	Met	Tyr	Asn	Gly	Asp	Arg	Ser	Arg	Lys	Glu	Met	Leu	Val		
	370					375					380						
Asn	Tyr	Gly	Phe	Arg	Leu	Pro	Ser	Ala	Leu	Asp	Asn	Arg	Pro	Leu	Arg		
385					390					395					400		
Arg	Glu	Glu	Phe	Glu	Ser	His	Val	His	Gln	Ile	Val	Tyr	Val	Ser	Ala		
			405						410					415			
Thr	Pro	Gly	Asp	Tyr	Glu	Asn	Glu	Gln	Thr	Glu	Thr	Val	Ile	Glu	Gln		
		420						425					430				
Ile	Ile	Arg	Pro	Thr	Gly	Leu	Leu	Asp	Pro	Glu	Val	Glu	Val	Arg	Pro		
	435						440					445					
Thr	Met	Gly	Gln	Ile	Asp	Asp	Leu	Leu	Gly	Glu	Ile	Asn	Ala	Arg	Val		
	450					455					460						
Glu	Lys	Asn	Glu	Arg	Thr	Phe	Ile	Thr	Thr	Leu	Thr	Lys	Lys	Met	Ala		
465					470					475					480		
Glu	Asp	Leu	Thr	Asp	Tyr	Phe	Lys	Glu	Met	Gly	Ile	Lys	Val	Lys	Tyr		
			485					490						495			
Met	His	Ser	Asp	Ile	Lys	Thr	Leu	Glu	Arg	Thr	Glu	Ile	Ile	Arg	Asp		
		500						505					510				
Leu	Arg	Leu	Gly	Val	Phe	Asp	Val	Leu	Val	Gly	Ile	Asn	Leu	Leu	Arg		
	515						520					525					
Glu	Gly	Ile	Asp	Val	Pro	Glu	Val	Ser	Leu	Val	Ala	Ile	Leu	Asp	Ala		
	530					535					540						
Asp	Lys	Glu	Gly	Phe	Leu	Arg	Asn	Glu	Arg	Gly	Leu	Ile	Gln	Thr	Ile		
545					550					555					560		
Gly	Arg	Ala	Ala	Arg	Asn	Ser	Glu	Gly	His	Val	Ile	Met	Tyr	Ala	Asp		
			565					570						575			
Thr	Val	Thr	Gln	Ser	Met	Gln	Arg	Ala	Ile	Asp	Glu	Thr	Ala	Arg	Arg		
		580						585					590				
Arg	Lys	Ile	Gln	Met	Ala	Tyr	Asn	Glu	Glu	His	Gly	Ile	Val	Pro	Gln		
	595						600					605					
Thr	Ile	Lys	Lys	Glu	Ile	Arg	Asp	Leu	Ile	Ala	Val	Thr	Lys	Ala	Val		
	610					615					620						
Ala	Lys	Glu	Glu	Asp	Lys	Glu	Val	Asp	Ile	Asn	Ser	Leu	Asn	Lys	Gln		
625					630					635					640		
Glu	Arg	Lys	Glu	Leu	Val	Lys	Lys	Leu	Glu	Lys	Gln	Met	Gln	Glu	Ala		
			645					650						655			
Val	Glu	Val	Leu	Asp	Phe	Glu	Leu	Ala	Ala	Gln	Ile	Arg	Asp	Met	Met		
		660					665						670				
Leu	Glu	Val	Lys	Ala	Leu	Asp											
		675															

(2) INFORMATION FOR SEQ ID NO:3403:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 92 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...92
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3403:

```

Ile Cys Tyr Asn Arg Thr Met Glu Glu Glu Gln Leu Leu Lys Ser Gly
1          5          10          15
Glu Arg Ile Asn Gln Leu Phe Ser Thr Asp Ile Lys Ile Ile Gln Asn
          20          25          30
Arg Glu Val Phe Ser Tyr Ser Val Asp Ser Val Leu Leu Ser Arg Phe
          35          40          45
Pro Arg Phe Pro Lys Lys Gly Leu Ile Val Asp Phe Cys Ala Gly Asn
          50          55          60
Gly Ala Val Gly Leu Phe Ala Ser Thr Arg Thr Gln Ala Gln Ile Leu
65          70          75          80
Ser Val Glu Ile Ser Gly Ala Phe Gly Gly Tyr Gly
          85          90

```

(2) INFORMATION FOR SEQ ID NO:3404:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 532 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...532
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3404:

```

Ile Cys Tyr Asn Asn Val Leu Ala Ile Leu Thr His Ser Pro Leu Ile
1          5          10          15
Asn Leu Ala Phe Leu Ala Leu Ile Val Ile Asn Leu Leu Val Ala Tyr
          20          25          30
Phe Gln Ile Gly Leu Leu Phe Ile Gly Ala Arg His Leu Leu Tyr Asn

```

	35					40				45					
Glu	Lys	Arg	Arg	Leu	Ile	Glu	Tyr	Ile	Arg	Lys	Val	Phe	His	Glu	Ser
50						55					60				
Phe	Gly	Phe	Met	Lys	Lys	Leu	Thr	Cys	Ala	Lys	Ala	Leu	Phe	Ile	Phe
65					70					75					80
Phe	Tyr	Ile	Ala	Met	Leu	Phe	Pro	Phe	Ile	Arg	Lys	Met	Leu	Lys	Ile
				85					90					95	
Tyr	Tyr	Leu	Asn	Lys	Ile	Val	Ile	Pro	Glu	Phe	Ile	Gln	Ala	Tyr	Leu
			100					105				110			
Glu	Asp	Arg	Tyr	Trp	Met	Trp	Trp	Leu	Ser	Ile	Leu	Leu	Leu	Ser	Leu
			115					120				125			
Ile	Phe	Leu	Tyr	Val	Ser	Val	Arg	Leu	Met	Phe	Ala	Leu	Pro	Lys	Ile
	130					135					140				
Val	Tyr	Asp	Gln	Leu	Thr	Val	Arg	Glu	Ala	Val	Met	Phe	Ser	Leu	Glu
145					150					155					160
Lys	Thr	Lys	Lys	Arg	Val	Thr	Phe	Tyr	Ala	Trp	Asn	Leu	Phe	Tyr	Ile
				165					170					175	
Leu	Leu	Lys	Ala	His	Leu	Leu	Phe	Tyr	Leu	Pro	Leu	Ile	Pro	Leu	Leu
			180					185				190			
Leu	Ala	Gln	Thr	Leu	Val	Asp	Asp	Ile	Thr	Gln	Arg	Glu	Ser	Leu	Ile
		195					200					205			
Leu	Gly	Ile	Leu	Asn	Phe	Val	Val	Ile	Lys	Asn	Leu	Tyr	Tyr	Met	Ala
	210					215					220				
Leu	Thr	Tyr	Ser	Pro	Val	Lys	Phe	Val	Ser	Phe	Leu	Thr	Gly	Lys	Glu
225					230					235					240
Leu	Asp	Met	Leu	Pro	Arg	Arg	Glu	Lys	Asp	His	Ile	Val	Arg	Trp	Gly
				245					250					255	
Val	Met	Thr	Cys	Ala	Ser	Leu	Phe	Phe	Ala	Leu	Glu	Gly	Tyr	Ile	Tyr
			260					265					270		
Leu	Glu	Ala	Pro	Met	Val	His	Leu	Pro	Gln	Leu	Ile	Ser	His	Arg	Gly
		275					280					285			
Val	Ser	Asn	Ala	Asn	Gly	Ile	Gln	Asn	Thr	Val	Glu	Ser	Leu	Glu	Thr
	290					295					300				
Thr	Ala	Gln	Leu	Lys	Pro	Asp	Leu	Val	Glu	Thr	Asp	Val	Gln	Glu	Thr
305					310					315					320
Lys	Asp	Gly	Gln	Phe	Val	Met	Met	His	Asp	Ala	Asn	Leu	Lys	Asn	Leu
				325					330					335	
Ala	Gly	Ile	Asn	Lys	Ser	Pro	Gln	Asp	Leu	Asn	Leu	Glu	Glu	Leu	Lys
			340					345				350			
Gly	Ile	Asp	Ile	Phe	Glu	Asn	Gly	Tyr	Gln	Thr	Lys	Ile	Ser	Ser	Phe
		355					360					365			
Glu	Asp	Tyr	Leu	Ser	Arg	Ala	Asn	Glu	Leu	Gly	Gln	Lys	Leu	Leu	Ile
	370					375					380				
Glu	Ile	Lys	Thr	Ser	Lys	Lys	Asp	Ser	Pro	Asp	Met	Met	Asn	Arg	Phe
385					390					395					400
Leu	Ala	Arg	Tyr	Ala	Ala	Met	Leu	Lys	Ile	Tyr	Gly	His	Gln	Ile	Gln
				405					410					415	
Ser	Leu	Asp	Tyr	His	Val	Val	Glu	Lys	Val	Arg	Gln	Tyr	Asp	Ala	Glu
			420					425				430			
Leu	Pro	Val	Tyr	Phe	Ile	Met	Pro	Tyr	Asn	Ser	Val	Phe	Pro	Lys	Thr
		435					440					445			
Arg	Ala	Thr	Gly	Tyr	Thr	Met	Glu	Tyr	Ser	Thr	Leu	Asp	Glu	Tyr	Phe
	450					455					460				
Val	Ser	Lys	Leu	Trp	Thr	Thr	Asp	Gln	Lys	Leu	Tyr	Val	Trp	Thr	Val
465					470					475					480
Asn	Asp	Ser	Glu	Ala	Ile	Ser	Lys	Ser	Leu	His	Leu	Gly	Val	Asp	Gly
				485					490					495	

Val	Ile	Thr	Asp	Asp	Leu	Glu	Lys	Val	Gln	Arg	Glu	Ile	Glu	Val	Ala
			500					505					510		
Gln	Glu	Asp	Pro	Glu	Tyr	Thr	Asp	Leu	Leu	Leu	Lys	Lys	Ala	Leu	Glu
		515					520					525			
Phe	Phe	Glu	Phe												
	530														

(2) INFORMATION FOR SEQ ID NO:3405:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 241 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...241

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3405:

His	Ser	Tyr	Asn	Ile	Lys	Lys	Gly	Gly	Thr	Val	Met	Asp	Ala	Ile	Phe
1				5					10					15	
Asp	Leu	Ile	Gly	Lys	Val	Phe	Asn	Pro	Ile	Leu	Glu	Met	Gly	Gly	Pro
			20					25					30		
Val	Ile	Met	Leu	Ile	Ile	Leu	Thr	Val	Leu	Ala	Leu	Leu	Phe	Gly	Val
		35					40					45			
Lys	Phe	Ser	Lys	Ala	Leu	Glu	Gly	Gly	Ile	Lys	Leu	Ala	Ile	Ala	Leu
	50					55				60					
Thr	Gly	Ile	Gly	Ala	Ile	Ile	Gly	Met	Leu	Asn	Gly	Ala	Phe	Ser	Ala
65					70				75						80
Ser	Leu	Ala	Lys	Phe	Val	Glu	Asn	Thr	Gly	Ile	Gln	Leu	Ser	Ile	Thr
			85					90						95	
Asp	Val	Gly	Trp	Ala	Pro	Leu	Ala	Thr	Ile	Thr	Trp	Gly	Ser	Ala	Trp
		100						105					110		
Thr	Leu	Tyr	Phe	Leu	Leu	Ile	Met	Leu	Ile	Val	Asn	Val	Val	Met	Leu
		115					120					125			
Ala	Met	Lys	Lys	Thr	Asp	Thr	Leu	Asp	Val	Asp	Ile	Phe	Asp	Ile	Trp
	130					135					140				
His	Leu	Ser	Ile	Thr	Gly	Leu	Leu	Ile	Lys	Trp	Tyr	Ala	Asp	Asn	Asn
145					150					155					160
Gly	Val	Ser	Gln	Gly	Val	Ser	Leu	Phe	Ile	Ala	Thr	Ala	Ala	Ile	Val
			165						170					175	
Leu	Val	Gly	Val	Leu	Lys	Ile	Ile	Asn	Ser	Asp	Leu	Met	Lys	Pro	Thr
		180					185						190		
Phe	Asp	Asp	Leu	Leu	Asn	Ala	Pro	Ser	Ser	Ser	Pro	Met	Thr	Ser	Thr
	195					200						205			
His	Met	Asn	Tyr	Met	Met	Asn	Pro	Val	Ile	Met	Val	Leu	Asp	Lys	Ile
	210					215					220				
Phe	Glu	Lys	Ser	Ser	Gln	Ala	Leu	Ile	Xaa	Met	Thr	Leu	Met	Leu	Leu
225					230					235					240

Asn

(2) INFORMATION FOR SEQ ID NO:3406:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...145

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3406:

Val	Lys	Tyr	Asn	Asn	Lys	Gly	Val	Lys	Thr	Met	Thr	Val	Ile	Asn	Lys
1				5					10					15	
Phe	Val	Leu	Met	Glu	Gln	Ala	Lys	Lys	Val	Leu	Lys	Asn	Ala	Tyr	Cys
			20					25					30		
Pro	Tyr	Ser	Lys	Phe	Pro	Val	Gly	Ala	Ala	Ile	Leu	Phe	Lys	Asp	Gly
		35					40					45			
Lys	Val	Ile	Thr	Gly	Ala	Asn	Ile	Glu	Asn	Val	Ser	Phe	Gly	Val	Thr
		50				55				60					
Asn	Cys	Ala	Glu	Arg	Ser	Ala	Ile	Phe	Tyr	Gly	Ala	Ser	Gln	Gly	Tyr
65				70					75					80	
Arg	Lys	Gly	Asp	Ile	Leu	Ala	Ile	Ala	Val	Ala	Gly	Glu	Thr	Glu	Asp
			85						90					95	
Tyr	Leu	Pro	Pro	Cys	Asn	Ile	Cys	Arg	Gln	Val	Met	Val	Glu	Phe	Cys
			100					105					110		
Glu	Pro	Asp	Thr	Leu	Val	Phe	Leu	Leu	Asn	Gly	Lys	Gly	Asn	Ile	Leu
		115					120					125			
Glu	Leu	Arg	Leu	Glu	Glu	Leu	Val	Pro	Tyr	Ser	Phe	Ser	Ser	Leu	Glu
		130				135					140				
Met															
145															

(2) INFORMATION FOR SEQ ID NO:3407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 760 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...760

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3407:

Lys	Met	Tyr	Asn	Tyr	Pro	Met	Arg	Ile	His	Tyr	His	Arg	Lys	Asn	Gly
1				5					10					15	
Glu	Tyr	Asp	Thr	Cys	Ser	Phe	Val	Lys	Ser	Gln	Asp	Gln	Arg	Ile	Asp
			20					25					30		
Leu	Leu	Thr	Tyr	Lys	Glu	Asp	Tyr	Phe	Gly	Ala	Leu	Phe	Ser	Phe	Glu
		35					40					45			
His	Pro	Ser	Ser	His	Val	Ile	Glu	Ser	Leu	Asn	Phe	Val	Val	His	Thr
	50					55					60				
Gly	Gln	Thr	Ser	Lys	Glu	Tyr	Ser	Ile	Arg	Phe	Asn	His	Tyr	Pro	Leu
65					70					75					80
Leu	Thr	Glu	Val	Trp	Ile	Leu	Glu	Gly	Asp	Asp	Arg	Ile	Tyr	Tyr	Ser
				85					90					95	
Glu	Asn	Pro	Ala	Ile	Ala	Ser	Pro	Phe	Tyr	Lys	Asn	Gln	Asn	Pro	Phe
			100					105					110		
Ala	Phe	Asp	Lys	Ala	Ile	Asn	Ser	Ala	Ser	Phe	Asp	His	His	Trp	Gly
	115						120					125			
Tyr	Gln	Gly	Glu	Leu	Gly	Cys	Arg	Val	Glu	Asp	Asn	Gln	Ala	His	Phe
	130					135					140				
Ser	Leu	Trp	Ser	Pro	Thr	Ala	Thr	Lys	Val	Gln	Val	Val	Val	Tyr	Glu
145					150					155					160
Ser	Ala	Ala	Asn	Asp	Ala	Pro	Val	Trp	Lys	Thr	Phe	Glu	Met	Lys	Arg
				165					170					175	
Gly	Asn	Ser	Tyr	Ser	Tyr	Asn	His	Lys	Asp	Asn	Thr	Ile	Gly	Val	Trp
			180					185					190		
Ser	Leu	Asp	Val	Glu	Glu	Asp	Leu	Val	Gly	Lys	Thr	Tyr	Gln	Tyr	Gln
		195					200						205		
Val	Gln	Phe	Pro	His	His	Gln	Thr	Leu	Thr	Arg	Asp	Pro	Tyr	Thr	Ile
	210					215					220				
Ala	Thr	Ser	Pro	Asp	Gly	Lys	Arg	Ser	Ala	Ile	Leu	Ser	His	Val	Glu
225					230					235					240
Lys	Gln	Val	Glu	Asn	Phe	Glu	Val	Lys	His	Gly	Ser	Glu	Ala	Thr	Trp
				245					250					255	
Arg	Leu	Glu	Asn	Pro	Cys	Lys	Ala	Val	Ile	Cys	Glu	Met	His	Ile	Arg
			260					265					270		
Asp	Leu	Thr	Lys	Ser	Pro	Thr	Ser	Gly	Val	Asp	Glu	His	Leu	Arg	Gly
	275						280					285			
Thr	Phe	Leu	Gly	Ala	Ala	Gln	Ala	Gly	Thr	Val	Asn	Gln	Tyr	Gly	Gln
	290					295					300				
Ser	Thr	Ala	Phe	Asp	Tyr	Ile	Lys	Lys	Leu	Gly	Tyr	Asn	Tyr	Val	Gln
305					310					315					320
Leu	Gln	Pro	Ile	Ala	Asp	Arg	His	Lys	Glu	Tyr	Asp	Glu	Asp	Gly	Asn
				325					330					335	
Val	Thr	Tyr	Asn	Trp	Gly	Tyr	Asp	Pro	Gln	Asn	Tyr	Asn	Ala	Pro	Glu
			340					345					350		
Thr	Ser	Phe	Ser	Thr	Asn	Pro	Asp	Asp	Pro	Ala	Gln	Val	Ile	Arg	Asp
		355					360					365			
Leu	Lys	Val	Met	Val	Gln	Ala	Tyr	His	Asp	Ala	Gly	Ile	Gly	Val	Ile
	370					375					380				
Met	Asp	Val	Val	Tyr	Asn	His	Thr	Phe	Ser	Val	Val	Asp	Ala	Pro	Phe

385	Gln	Thr	Thr	Val	Pro	Asp	Tyr	Tyr	Tyr	Arg	Met	Asn	Pro	Asp	Gly	Thr	400
					405					410							415
	Phe	Gln	Asn	Gly	Thr	Gly	Val	Gly	Asn	Glu	Thr	Ala	Ser	Glu	His	Glu	
				420					425					430			
	Met	Phe	Arg	Lys	Tyr	Met	Ile	Asp	Ser	Leu	Leu	Tyr	Trp	Val	Gln	Glu	
				435				440					445				
	Tyr	Asn	Ile	Asp	Gly	Phe	Arg	Phe	Asp	Leu	Met	Gly	Ile	His	Asp	Val	
				450			455					460					
	Lys	Thr	Met	Gln	Met	Ile	Arg	Gln	Ser	Leu	Asp	Glu	Ile	Asp	Ser	Asn	
465						470					475					480	
	Ile	Ile	Leu	Tyr	Gly	Glu	Gly	Trp	Asp	Met	Gly	Thr	Gly	Leu	Ala	Pro	
					485				490						495		
	Tyr	Asp	Lys	Ala	Lys	Lys	Asp	Asn	Ala	Tyr	Gln	Met	Pro	Asn	Ile	Gly	
				500				505					510				
	Phe	Phe	Asn	Asp	Asn	Gln	Arg	Asp	Ala	Val	Lys	Gly	Gly	Glu	Val	Tyr	
				515				520					525				
	Gly	Ala	Ile	Lys	Ser	Gly	Phe	Val	Ser	Gly	Ala	Ala	Thr	Glu	Pro	Ile	
				530			535				540						
	Leu	Ala	Lys	Ala	Ile	Leu	Gly	Ser	Arg	Glu	Leu	Gly	Ser	Tyr	Thr	His	
545						550				555						560	
	Pro	Asn	Gln	Val	Leu	Asn	Tyr	Val	Glu	Ala	His	Asp	Asn	Tyr	Asn	Leu	
					565					570					575		
	His	Asp	Leu	Leu	Ala	Thr	Leu	His	Pro	Asp	Gln	Ser	Ser	Glu	Gln	Ile	
				580					585					590			
	Met	Arg	Lys	Val	Glu	Thr	Ala	Thr	Ala	Met	Asn	Leu	Leu	Met	Gln	Gly	
				595			600					605					
	Met	Ala	Phe	Met	Glu	Ile	Gly	Gln	Glu	Phe	Gly	Arg	Thr	Lys	Leu	Val	
				610			615				620						
	Ala	Thr	Gly	Glu	Asn	Gly	Glu	Leu	Thr	His	Asp	Asp	Arg	Glu	Arg	Ala	
625					630					635					640		
	Met	Asn	Ser	Tyr	Asn	Ala	Pro	Asp	Ser	Val	Asn	Gln	Val	Asn	Trp	Asn	
				645					650					655			
	Leu	Ile	Asn	Glu	Arg	Gln	Asp	Ser	Ile	Glu	Phe	Ile	Arg	Gln	Val	Ile	
				660				665					670				
	Arg	Leu	Lys	Thr	Lys	Thr	Gly	Ala	Phe	Ser	Tyr	Ser	Ser	Tyr	Asp	Glu	
				675			680					685					
	Ile	Tyr	His	His	Val	Phe	Val	His	Ser	Ala	Ile	Glu	His	Ser	Gly	Cys	
				690			695				700						
	Leu	Ile	Tyr	Glu	Val	His	Gly	Lys	Glu	His	Leu	Leu	Val	Val	Val	Asn	
705					710					715					720		
	Ala	Lys	Ser	Glu	Pro	Tyr	Gln	Phe	Glu	Asn	Ala	Gly	Asn	Leu	Ala	Met	
				725					730				735				
	Leu	Val	Thr	Asn	Ser	Arg	Ser	Lys	Glu	Asp	Asn	Val	Leu	Asn	Asp	Ile	
				740				745					750				
	Ser	Leu	Ala	Val	Leu	Ser	Val	Leu									
				755			760										

(2) INFORMATION FOR SEQ ID NO:3408:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3408:

```
Lys Trp Tyr Asn Ile Val Arg Arg Ile Glu Glu Lys Cys Lys Leu Ile
1          5          10          15
Ala Gln Ile Asp Thr Lys Thr Val Tyr Ser Phe Met Glu Ser Val Ile
          20          25          30
Ser Ile Glu Lys Tyr Val Arg Ala Ala Lys Glu Tyr Gly Tyr Thr His
          35          40          45
Leu Ala Met Met Asp Ile Asp Asn Leu Tyr Gly Ala Phe Asp Phe Leu
          50          55          60
Glu Ile Thr Lys Lys Tyr Gly Ile His Pro Leu Leu Gly Leu Glu Met
65          70          75          80
Thr Val Phe Val Asp Asp Gln Gly Val Asn Leu Arg Phe Leu Ala Leu
          85          90          95
Ser Ser Val Gly Tyr Gln Gln Leu Met Lys Leu Ser Thr Ala Lys Met
          100          105          110
Gln Gly Glu Lys Thr Trp Ser Val Leu Ser Gln Tyr Leu Glu Asp Ile
          115          120          125
Ala Val Ile Val Pro Tyr Phe Asp Arg Val Asp Ser Leu Glu Val Gly
          130          135          140
Leu Asn Lys Pro Tyr Thr Ser Asn
145          150
```

(2) INFORMATION FOR SEQ ID NO:3409:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 204 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3409:

```
Val Ile His Lys Asn Phe Ser Ile Lys Tyr His Asn Ala Ser Phe Lys
1          5          10          15
Glu Met Val Thr Met Gln Tyr Ser Cys Gly Lys Ile Asn Ile Asn Ile
          20          25          30
```


Pro	Asp	Gly	Tyr	Gly	Asp	Ile	Lys	Asp	Ile	Val	Phe	Ser	Ala	His	Ile
	35						40				45				
Ile	Val	Arg	Tyr	Asn	Asn	Gly	His	Cys	Gly	Gly	Ile	Asp	Pro	His	Ile
	50					55					60				
Ile	Gly	Leu	Cys	Lys	Lys	Gln	Ile	Arg	Arg	Met	Ser	Leu	Tyr	Pro	Ile
65					70					75					80
Leu	Ile	Ile	Val	Ser	Arg	Asp	Ser	Lys	Val	Ile	Asp	Asp	Tyr	Lys	Asn
			85						90					95	
Leu	Asp	Ile	Ala	Tyr	Val	Asp	Cys	Thr	Gln	Cys	Ser	Asn	Asn	Phe	Glu
			100					105						110	
Thr	Ala	Leu	His	Val	Lys	Asn	Ile	Leu	Lys	Leu	Leu	Lys	Ile	Arg	Leu
		115					120						125		
Ile	His	Cys	His	Gly	Tyr	Ser	Thr	Asn	Tyr	Phe	Leu	Tyr	Met	Leu	Lys
	130						135				140				
Lys	Leu	Asp	Lys	Asn	Gly	Phe	Gly	Lys	Val	Lys	Thr	Val	Ile	Thr	Cys
145					150					155					160
His	Gly	Trp	Val	Glu	Tyr	Asn	Leu	Lys	Lys	Lys	Phe	Leu	Thr	Tyr	Phe
			165						170					175	
Asp	Phe	Trp	Thr	Tyr	Ser	Met	Gly	Asp	Ala	Phe	Ile	Cys	Val	Ser	Glu
			180					185					190		
Thr	Met	Lys	Lys	Arg	Leu	Glu	Ser	Ile	Ile	Lys	Lys				
		195						200							

(2) INFORMATION FOR SEQ ID NO:3410:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 323 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...323

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3410:

Ala	Asn	His	Lys	Lys	Phe	His	Phe	Asp	Phe	Lys	Thr	Val	Gln	Glu	Ser
1			5					10					15		
Gln	Lys	Ile	Ile	Leu	Phe	Glu	Arg	Glu	Val	Pro	Thr	Val	Lys	Val	Asn
		20					25					30			
Lys	Ile	Arg	Met	Arg	Glu	Thr	Val	Ile	Ser	Tyr	Ala	Phe	Leu	Ala	Pro
		35				40					45				
Val	Leu	Phe	Phe	Phe	Val	Ile	Phe	Val	Leu	Ala	Pro	Met	Val	Met	Gly
	50				55				60						
Phe	Ile	Thr	Ser	Phe	Phe	Asn	Tyr	Ser	Met	Thr	Arg	Phe	Glu	Phe	Val
65				70				75					80		
Gly	Leu	Asp	Asn	Tyr	Ile	Arg	Met	Phe	Lys	Asp	Pro	Val	Phe	Thr	Lys
			85					90					95		
Ser	Leu	Ile	Asn	Thr	Val	Ile	Leu	Val	Ile	Gly	Ser	Val	Pro	Val	Val
			100					105					110		

Val	Leu	Phe	Ser	Leu	Phe	Val	Ala	Ser	Gln	Thr	Tyr	His	Gln	Asn	Val
	115						120					125			
Ile	Ala	Arg	Ser	Phe	Tyr	Arg	Phe	Val	Phe	Phe	Leu	Pro	Val	Val	Thr
	130					135					140				
Gly	Ser	Val	Ala	Val	Thr	Val	Val	Trp	Lys	Trp	Ile	Tyr	Asp	Pro	Leu
145					150					155					160
Ser	Gly	Ile	Leu	Asn	Phe	Val	Leu	Lys	Ser	Ser	His	Ile	Ile	Ser	Gln
			165					170						175	
Asn	Ile	Ser	Trp	Leu	Gly	Asp	Lys	Asn	Trp	Ala	Leu	Met	Ala	Ile	Met
		180					185						190		
Ile	Ile	Leu	Leu	Thr	Thr	Ser	Val	Gly	Gln	Pro	Ile	Ile	Leu	Tyr	Ile
	195						200					205			
Ala	Ala	Met	Gly	Asn	Ile	Asp	Asn	Ser	Leu	Val	Glu	Ala	Ala	Arg	Val
	210					215					220				
Asp	Gly	Ala	Thr	Glu	Phe	Gln	Val	Phe	Trp	Lys	Ile	Lys	Trp	Pro	Ser
225					230					235					240
Leu	Leu	Pro	Thr	Thr	Leu	Tyr	Ile	Ala	Ile	Ile	Thr	Thr	Ile	Asn	Ser
				245					250					255	
Phe	Gln	Cys	Phe	Ala	Leu	Ile	Gln	Leu	Leu	Thr	Ser	Gly	Gly	Pro	Asn
		260					265						270		
Tyr	Ser	Thr	Ser	Thr	Leu	Met	Tyr	Tyr	Leu	Tyr	Glu	Lys	Ala	Phe	Gln
	275					280						285			
Leu	Thr	Glu	Tyr	Gly	Tyr	Ala	Asn	Thr	Ile	Gly	Val	Phe	Leu	Ala	Val
	290					295					300				
Met	Ile	Ala	Ile	Val	Ser	Phe	Val	Gln	Phe	Lys	Val	Leu	Gly	Asn	Asp
305				310						315					320
Val	Glu	Tyr													

(2) INFORMATION FOR SEQ ID NO:3411:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...77

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3411:

Ser	Ser	His	Lys	Lys	Met	Ser	Thr	Asp	Lys	Arg	Ser	Lys	Ser	Met	Pro
1				5					10					15	
Asn	Tyr	Asn	Ile	Pro	Phe	Ser	Pro	Pro	Asp	Ile	Thr	Glu	Ala	Glu	Ile
			20					25					30		
Ala	Glu	Val	Ala	Asp	Thr	Leu	Arg	Ser	Gly	Trp	Ile	Thr	Thr	Gly	Pro
		35				40						45			
Lys	Thr	Lys	Glu	Leu	Glu	Arg	Arg	Leu	Ser	Leu	Tyr	Thr	Gln	Thr	Pro
50						55					60				

Lys Thr Val Cys Leu Asn Ser Ala Thr Ala Leu Trp Ser
65 70 75

(2) INFORMATION FOR SEQ ID NO:3412:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...241

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3412:

Asp	Trp	His	Lys	Met	Val	Glu	Ser	Tyr	Ser	Lys	Asn	Ala	Asn	His	Asn	
1				5					10					15		
Met	Arg	Arg	Pro	Val	Val	Lys	Glu	Glu	Ile	Val	Asp	Leu	Met	Arg	Gln	
			20					25					30			
Arg	Gln	Lys	Gln	Val	Thr	Gly	Phe	Leu	Lys	Glu	Leu	Glu	Asp	Phe	Ala	
		35					40					45				
Arg	Lys	Glu	Asn	Ile	Pro	Ile	Ile	Pro	His	Glu	Thr	Val	Ala	Tyr	Phe	
	50					55				60						
Arg	Phe	Leu	Met	Glu	Thr	Met	Gln	Pro	Lys	Asn	Ile	Leu	Glu	Ile	Gly	
65					70					75					80	
Thr	Ala	Ile	Gly	Phe	Ser	Ala	Leu	Leu	Met	Ala	Glu	His	Ala	Pro	Asn	
				85					90					95		
Ala	Lys	Ile	Thr	Thr	Ile	Asp	Arg	Asn	Pro	Glu	Met	Ile	Gly	Phe	Ala	
			100					105					110			
Lys	Glu	Asn	Phe	Ala	Gln	Phe	Asp	Ser	Arg	Lys	Gln	Ile	Thr	Leu	Leu	
		115					120					125				
Glu	Gly	Asp	Ala	Val	Asp	Val	Leu	Ser	Thr	Leu	Thr	Glu	Ser	Tyr	Asp	
	130					135					140					
Phe	Val	Phe	Met	Asp	Ser	Ala	Lys	Ser	Lys	Tyr	Ile	Val	Phe	Leu	Pro	
145					150					155					160	
Glu	Ile	Leu	Lys	His	Leu	Glu	Val	Gly	Gly	Val	Val	Val	Leu	Asp	Asp	
			165						170					175		
Ile	Phe	Gln	Gly	Gly	Asp	Val	Ala	Lys	Asp	Ile	Met	Glu	Val	Arg	Arg	
		180						185					190			
Gly	Gln	Arg	Thr	Ile	Tyr	Arg	Gly	Leu	Gln	Lys	Leu	Phe	Asp	Ala	Thr	
		195					200					205				
Leu	Asp	Asn	Pro	Glu	Leu	Thr	Ala	Thr	Leu	Val	Pro	Leu	Gly	Asp	Gly	
	210					215					220					
Ile	Leu	Met	Leu	Arg	Lys	Asn	Val	Ala	Asp	Val	Gln	Leu	Ser	Glu	Ser	
225					230					235					240	
Glu																

(2) INFORMATION FOR SEQ ID NO:3413:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 90 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...90
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3413:

```

Met Lys Asn Lys Arg Tyr Phe Phe Asp Thr Ile Leu Ile Ile Leu Leu
1      5      10      15
Leu Ile Ser Thr Ile Phe Cys Val Ser Pro Val Phe Ile Lys Leu Asp
      20      25      30
Ile Leu Gly Thr Pro Ser His Ala Ile Leu Thr Phe Val Leu Ala Ile
      35      40      45
Pro Leu Phe Tyr Ile Leu Ser Gln Cys Leu His Thr Leu Leu Leu Leu
      50      55      60
Val Ser Ser Ile Phe Cys Lys Leu Arg Pro Ile Tyr Phe Tyr Phe Ile
65      70      75      80
Phe Val Ile Ile Ile Gly Ala Asp Glu Leu
      85      90

```

(2) INFORMATION FOR SEQ ID NO:3414:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 217 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...217
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3414:

```

Lys Glu Asn Lys Met Ile Asp Ile Gln Gly Leu Glu Lys Lys Phe Asn
1      5      10      15
Asp Arg Ala Ile Phe Ser Gly Leu Asn Leu Lys Leu Glu Lys Gly Lys
      20      25      30
Val Tyr Ala Leu Ile Gly Lys Ser Gly Ser Gly Lys Thr Thr Leu Leu

```


Glu	Lys	Ile	Phe	Ile	Ile	Phe	Gly	Trp	Cys	Arg	Ile	Gly	Thr	Leu	Gly
			20					25					30		
Leu	Lys	Ile	Leu	Ala	Ser	Lys	Glu	Ala	Lys	Lys	Gly	Tyr	Ser	Lys	Ala
		35					40					45			
Leu	Ala	Lys	Ala	Tyr	Asn	Leu	Lys	Asn	Lys	Leu	Asn	Ala	Ser	Val	Ser
	50					55					60				
Val	Val	Lys	Gln	His	Gly	Asn	Asn	Val	Leu	Gln	Asn	Ala	Lys	Tyr	Leu
65					70					75					80
Tyr	Glu	Gln	Glu	Lys	Lys	Glu	Lys	Gln	Leu	Asp	Ser	Leu	Ile	Gly	Glu
				85					90					95	

(2) INFORMATION FOR SEQ ID NO:3417:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 143 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...143

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3417:

Thr	Met	Asn	Asn	Leu	Ser	Leu	Val	Leu	Met	Asp	Ile	Ser	Val	Gln	Asn
1				5					10					15	
Arg	Gln	Glu	Ala	Tyr	Lys	Glu	Leu	Ala	Asn	Gln	Ile	Ser	Leu	Leu	Val
			20					25					30		
Ser	Glu	Asp	Thr	Glu	Lys	Ile	Glu	Glu	Leu	Leu	Tyr	Tyr	Arg	Glu	Arg
		35				40						45			
Gln	Gly	Ser	Ile	Glu	Val	Ala	Lys	Gly	Val	Leu	Leu	Pro	His	Cys	Glu
	50					55				60					
Gly	Asn	Phe	Gln	His	His	Val	Leu	Val	Ile	Thr	Arg	Leu	Lys	Ser	Pro
65					70					75					80
Ile	Arg	Glu	Trp	Ser	Lys	Asp	Ile	Gln	Cys	Val	Asp	Leu	Ile	Ile	Gly
				85					90					95	
Leu	Ala	Ile	Ala	Val	Ser	Gln	Asp	Lys	Ser	Cys	Ile	Lys	Thr	Leu	Met
			100					105					110		
Arg	Arg	Leu	Ala	Asp	Glu	Ser	Phe	Ile	Asn	Gln	Leu	Lys	Gln	Leu	Thr
		115					120					125			
Lys	Glu	Glu	Leu	Arg	Glu	Ile	Ile	Tyr	Gly	Asn	Gln	Arg	Tyr	Ser	
	130					135					140				

(2) INFORMATION FOR SEQ ID NO:3418:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 480 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...480

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3418:

```

Lys Met Asn Lys Ser Met Ile Arg Tyr Leu Leu Ser Lys Leu Leu Leu
1      5      10      15
Ile Glu Ala Val Leu Leu Leu Val Pro Val Ala Ile Ala Val Tyr Tyr
20      25      30
Arg Glu Ser Ser Gln Val Phe Thr Ala Leu Phe Ser Thr Ile Gly Ile
35      40      45
Leu Val Leu Leu Gly Gly Ser Gly Ser Leu Gln Lys Pro Lys Asn Gln
50      55      60
Arg Ile Tyr Ala Lys Glu Gly Val Leu Ile Val Ala Leu Cys Trp Ile
65      70      75      80
Leu Trp Ser Phe Phe Gly Gly Leu Pro Phe Val Phe Ser Gly Gln Ile
85      90      95
Pro Ser Val Ile Asp Ala Phe Phe Glu Ile Ser Ser Gly Phe Thr Thr
100     105     110
Thr Gly Ala Ser Ile Leu Asn Asp Val Ser Val Leu Ser Arg Ser Leu
115     120     125
Leu Phe Trp Arg Ser Phe Thr His Leu Ile Gly Gly Met Gly Val Leu
130     135     140
Val Phe Ala Leu Ala Ile Met Asp Asn Ala Lys Asn Ser His Leu Glu
145     150     155     160
Val Met Lys Ala Glu Val Pro Gly Pro Val Phe Gly Lys Val Val Ser
165     170     175
Lys Leu Lys Asn Thr Ala Gln Ile Leu Tyr Leu Leu Tyr Leu Ala Leu
180     185     190
Phe Ser Leu Phe Val Ile Ile Tyr Tyr Leu Ala Gly Met Pro Leu Tyr
195     200     205
Asp Ser Phe Val Ile Ala Met Gly Thr Ala Gly Thr Gly Gly Phe Thr
210     215     220
Val Tyr Asn Asp Gly Ile Ala His Tyr Gly Ser Ser Leu Ile Thr Tyr
225     230     235     240
Leu Val Ser Ile Gly Val Leu Ile Phe Gly Val Asn Phe Asn Leu Tyr
245     250     255
Tyr Tyr Leu Met Leu Arg Arg Ile Lys Ala Phe Phe Gly Asp Glu Glu
260     265     270
Leu Arg Ala Tyr Leu Val Ile Val Leu Val Ser Thr Gly Leu Ile Ser
275     280     285
Leu Asn Thr Leu Tyr Leu Tyr Pro Gly Phe Ser Lys Ser Phe Glu Met
290     295     300
Thr Phe Phe Gln Val Ser Asn Ile Ile Thr Thr Thr Gly Phe Gly Tyr
305     310     315     320
Gly Asp Ile Thr Asn Trp Pro Leu Phe Ser Gln Phe Ile Leu Leu Phe
325     330     335
Leu Met Thr Ile Gly Gly Ser Ala Gly Ser Thr Ala Gly Gly Leu Lys
340     345     350

```


Ile	Ile	Arg	Gly	Leu	Ile	Leu	Ser	Lys	Ile	Ala	Lys	Asn	Gln	Ile	Leu
		355					360					365			
Ser	Ile	Leu	Ser	Pro	His	Arg	Val	Leu	Thr	Leu	His	Val	Asn	Lys	Thr
		370				375					380				
Val	Ile	Asp	Lys	Asp	Thr	Gln	His	Lys	Ile	Leu	Lys	Tyr	Phe	Val	Ile
385					390					395					400
Tyr	Ala	Met	Ile	Leu	Leu	Ser	Leu	Ile	Phe	Ile	Val	Ser	Leu	Asp	Ser
				405					410					415	
Asn	Asp	Phe	Leu	Ile	Val	Thr	Ser	Ala	Val	Phe	Ser	Cys	Phe	Asn	Asn
			420					425					430		
Ile	Gly	Pro	Ile	Leu	Gly	Thr	Thr	Ser	Ser	Phe	Ser	Ile	Phe	Ser	Pro
		435				440						445			
Ile	Ser	Lys	Ile	Leu	Leu	Ser	Phe	Ala	Met	Ile	Ala	Gly	Arg	Leu	Glu
	450					455				460					
Ile	Tyr	Pro	Ile	Leu	Leu	Leu	Phe	Met	Lys	Arg	Thr	Trp	Ser	Lys	Arg
465				470					475						480

(2) INFORMATION FOR SEQ ID NO:3419:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 138 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...138

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3419:

Arg	Met	Asn	Asn	Pro	Lys	Pro	Gln	Glu	Trp	Lys	Ser	Glu	Glu	Leu	Ser
1				5				10						15	
Gln	Gly	Arg	Ile	Ile	Asp	Tyr	Lys	Ala	Phe	Asn	Phe	Val	Asp	Gly	Glu
		20						25				30			
Gly	Val	Arg	Asn	Ser	Leu	Tyr	Val	Ser	Gly	Cys	Met	Phe	His	Cys	Glu
		35				40						45			
Gly	Cys	Tyr	Asn	Val	Ala	Thr	Trp	Ser	Phe	Asn	Ala	Gly	Ile	Pro	Tyr
	50					55				60					
Thr	Ala	Glu	Leu	Glu	Glu	Gln	Ile	Met	Ala	Asp	Leu	Ala	Gln	Pro	Tyr
65				70					75					80	
Val	Gln	Gly	Leu	Thr	Leu	Leu	Gly	Gly	Glu	Pro	Phe	Leu	Asn	Thr	Gly
			85				90							95	
Ile	Leu	Leu	Pro	Leu	Val	Lys	Arg	Ile	Arg	Lys	Glu	Leu	Pro	Asp	Lys
			100				105						110		
Asp	Ile	Trp	Ser	Trp	Thr	Gly	Tyr	Thr	Trp	Glu	Glu	Met	Met	Leu	Glu
	115					120						125			
Thr	Pro	Asp	Lys	Leu	Glu	Phe	Leu	Ser	Leu						
	130					135									

(2) INFORMATION FOR SEQ ID NO:3420:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 256 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...256
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3420:

```

Phe Leu Asp Lys Ile Glu Val Met Thr Arg Tyr Lys Ala Thr Ile Ser
1           5           10           15
Tyr Asp Gly Tyr Ala Phe Asp Gly Phe Gln Arg Gln Pro His Ala Arg
          20           25           30
Ser Val Gln Glu Glu Ile Glu Lys Thr Leu Thr Arg Leu Asn Lys Gly
          35           40           45
Gln Thr Ile Thr Val His Gly Ala Gly Arg Thr Asp Ser Gly Val His
          50           55           60
Ala Leu Gly Gln Val Ile His Phe Asp Leu Pro Tyr Gln Met Asp Glu
65           70           75           80
Glu Lys Leu Arg Phe Ala Leu Asp Thr Gln Ser Pro Glu Asp Ile Asp
          85           90           95
Val Ile Ser Ile Glu Leu Val Ala Asp Asp Phe His Cys Arg Tyr Ala
          100          105          110
Lys His Ser Lys Thr Tyr Glu Phe Ile Val Asp Arg Gly Arg Pro Lys
          115          120          125
Asn Pro Met Arg Arg His Tyr Ala Thr His Phe Pro Tyr Pro Leu Asp
          130          135          140
Val Glu Arg Met Gln Ile Ala Ile Lys Lys Leu Glu Gly Thr His Asp
145          150          155          160
Phe Thr Gly Phe Thr Ala Ser Gly Thr Ser Val Glu Asp Lys Val Arg
          165          170          175
Thr Ile Thr Glu Ala Ser Leu Ile Val Asp Glu Thr Gly Gln Phe Leu
          180          185          190
Thr Phe Thr Phe Ser Gly Asn Gly Phe Leu Tyr Lys Gln Ile Arg Asn
          195          200          205
Met Val Gly Thr Leu Leu Lys Ile Gly Asn Asn Arg Met Pro Val Glu
210          215          220
Gln Ile Ala Leu Ile Leu Glu Lys Lys Asp Arg Gln Leu Ala Gly Pro
225          230          235          240
Thr Ala Ala Pro Asn Gly Leu Tyr Leu Lys Glu Ile Arg Tyr Glu Glu
          245          250          255

```

(2) INFORMATION FOR SEQ ID NO:3421:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 amino acids
 - (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3421:

Ala	Leu	Asp	Asn	His	Cys	Gln	Pro	Ser	Phe	His	Lys	Leu	Ile	Gln	Met
1				5					10					15	
Ile	Ile	Phe	Tyr	Ser	Leu	Trp	Thr	Met	Leu	Met	Asp	Asn	Ala	Ile	Trp
			20					25					30		
His	Lys	Ser	Ser	Ala	Leu	Lys	Ile	Pro	Thr	Asn	Ile	Gly	Phe	Ala	Phe
		35				40						45			
Ile	Pro	Pro	Tyr	Thr	Pro	Glu	Met	Asn	Pro	Ile	Glu				
	50					55					60				

(2) INFORMATION FOR SEQ ID NO:3422:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 666 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...666

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3422:

Ser	Ala	Asp	Lys	Lys	Ser	Met	Leu	Arg	Asn	Tyr	Glu	Ile	Ile	Lys	Lys
1				5					10					15	
Glu	Asn	Ile	Met	Ile	Asn	Ile	Thr	Phe	Ser	Asp	Gly	Ala	Val	Arg	Glu
			20					25					30		
Phe	Glu	Ser	Gly	Val	Thr	Thr	Phe	Glu	Ile	Ala	Gln	Ser	Ile	Ser	Asn
		35				40					45				
Ser	Leu	Ala	Lys	Lys	Ala	Leu	Ala	Gly	Lys	Phe	Asn	Gly	Lys	Leu	Ile
	50				55					60					
Asp	Thr	Thr	Arg	Ala	Ile	Thr	Glu	Asp	Gly	Ser	Ile	Glu	Ile	Val	Thr
65				70				75						80	
Pro	Asp	His	Glu	Asp	Ala	Leu	Pro	Ile	Leu	Arg	His	Ser	Ala	Ala	His
			85			90						95			
Leu	Phe	Ala	Gln	Ala	Ala	Arg	Arg	Leu	Phe	Pro	Asp	Ile	His	Leu	Gly

Trp	Leu	Ala	Pro	His	Gln	Val	Thr	Leu	Ile	Pro	Val	Ser	Asn	Glu	Lys
				565					570					575	
His	Val	Asp	Tyr	Ala	Trp	Glu	Val	Ala	Lys	Lys	Leu	Arg	Asp	Arg	Gly
			580					585					590		
Val	Arg	Ala	Asp	Val	Asp	Glu	Arg	Asn	Glu	Lys	Met	Gln	Phe	Lys	Ile
		595				600						605			
Arg	Ala	Ser	Gln	Thr	Ser	Lys	Ile	Pro	Tyr	Gln	Leu	Ile	Val	Gly	Asp
	610					615					620				
Lys	Glu	Met	Glu	Asp	Glu	Thr	Val	Asn	Val	Arg	Arg	Tyr	Gly	Gln	Lys
625					630					635					640
Glu	Thr	Gln	Thr	Val	Ser	Val	Asp	Asn	Phe	Val	Gln	Ala	Ile	Leu	Ala
				645					650					655	
Asp	Ile	Ala	Asn	Lys	Ser	Arg	Val	Glu	Lys						
			660					665							

(2) INFORMATION FOR SEQ ID NO:3423:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 239 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...239
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3423:

Thr	Ala	Asp	Lys	Lys	Ser	Glu	Ala	Leu	Tyr	Leu	Val	Gln	Asp	Ser	Val
1				5					10					15	
Ala	Gly	Leu	Asp	Asp	Tyr	Ile	Thr	Gly	Lys	Thr	Ser	Asp	Phe	Ser	Thr
		20						25					30		
Val	Gly	Val	Lys	Ala	Leu	Asp	Asp	Gln	Thr	Val	Gln	Tyr	Thr	Leu	Val
		35				40					45				
Lys	Pro	Glu	Leu	Tyr	Trp	Asn	Ser	Lys	Thr	Leu	Ala	Thr	Ile	Leu	Phe
	50				55					60					
Pro	Val	Asn	Ala	Asp	Phe	Leu	Lys	Ser	Lys	Gly	Asp	Asp	Phe	Gly	Lys
65				70						75				80	
Ala	Asp	Pro	Ser	Ser	Ile	Leu	Tyr	Asn	Gly	Pro	Phe	Leu	Met	Lys	Ala
				85				90						95	
Leu	Val	Ser	Lys	Ser	Ala	Ile	Glu	Tyr	Lys	Lys	Asn	Pro	Asn	Tyr	Trp
			100					105					110		
Asp	Ala	Lys	Asn	Val	Phe	Val	Asp	Asp	Val	Lys	Leu	Thr	Tyr	Tyr	Asp
		115					120					125			
Gly	Ser	Asp	Gln	Glu	Ser	Leu	Glu	Arg	Asn	Phe	Thr	Ala	Gly	Ala	Tyr
	130					135					140				
Thr	Thr	Ala	Arg	Leu	Phe	Pro	Asn	Ser	Ser	Ser	Tyr	Glu	Gly	Ile	Lys
145				150						155				160	
Glu	Lys	Tyr	Lys	Asn	Asn	Ile	Ile	Tyr	Ser	Met	Gln	Asn	Ser	Thr	Ser
				165				170						175	

Tyr	Phe	Phe	Asn	Phe	Asn	Leu	Asp	Arg	Lys	Ser	Tyr	Asn	Tyr	Thr	Ser
			180					185					190		
Lys	Thr	Ser	Asp	Ile	Glu	Lys	Lys	Ser	Thr	Gln	Glu	Ala	Val	Leu	Asn
		195					200					205			
Lys	Asn	Phe	Arg	Gln	Ala	Ile	Asn	Phe	Ala	Phe	Asp	Arg	Thr	Ser	Tyr
	210					215					220				
Gly	Ala	Gln	Ser	Glu	Gly	Lys	Arg	Arg	Cys	Asn	Lys	Asp	Phe	Ala	
225					230					235					

(2) INFORMATION FOR SEQ ID NO:3424:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 577 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...577

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3424:

Asn	Cys	Asp	Lys	Ile	Val	Glu	Lys	Ser	Lys	Lys	Glu	Leu	Leu	Met	Asn
1				5					10					15	
Thr	Lys	Glu	Leu	Ile	Ala	Ser	Lys	Leu	Ser	Ser	Ile	Ile	Asp	Ser	Leu
			20					25					30		
Asp	Gln	Glu	Ala	Ile	Leu	Lys	Leu	Leu	Glu	Thr	Pro	Lys	Asn	Ser	Glu
		35				40						45			
Met	Gly	Asp	Ile	Ala	Phe	Pro	Ala	Phe	Ser	Leu	Ala	Lys	Val	Glu	Arg
	50					55					60				
Lys	Ala	Pro	Gln	Met	Ile	Ala	Ala	Glu	Leu	Ala	Glu	Lys	Met	Asn	Ser
65				70					75					80	
Gln	Ala	Phe	Glu	Lys	Val	Val	Ala	Thr	Gly	Pro	Tyr	Val	Asn	Phe	Phe
			85						90				95		
Leu	Asp	Lys	Ser	Ala	Ile	Ser	Ala	Gln	Val	Leu	Gln	Ala	Val	Thr	Thr
				100				105					110		
Glu	Lys	Glu	His	Tyr	Ala	Asp	Gln	Asn	Ile	Gly	Lys	Gln	Glu	Asn	Val
		115					120					125			
Val	Ile	Asp	Met	Ser	Ser	Pro	Asn	Ile	Ala	Lys	Pro	Phe	Ser	Ile	Gly
	130					135					140				
His	Leu	Arg	Ser	Thr	Val	Ile	Gly	Asp	Ser	Leu	Ser	His	Ile	Phe	Gln
145				150					155					160	
Lys	Ile	Gly	Tyr	Gln	Thr	Val	Lys	Val	Asn	His	Leu	Gly	Asp	Trp	Gly
			165						170				175		
Lys	Gln	Phe	Gly	Met	Leu	Ile	Val	Ala	Tyr	Lys	Lys	Trp	Gly	Asp	Glu
		180						185				190			
Glu	Ala	Val	Lys	Ala	His	Pro	Ile	Asp	Glu	Leu	Leu	Lys	Leu	Tyr	Val
	195					200						205			
Arg	Ile	Asn	Ala	Glu	Ala	Glu	Asn	Asp	Pro	Ser	Leu	Asp	Glu	Glu	Ala

210	215	220
Arg Glu Trp Phe Arg Lys Leu Glu Asn Gly Asp Glu Glu Ala Leu Ala		
225	230	235
Leu Trp Gln Trp Phe Arg Asp Glu Ser Leu Val Glu Phe Asn Arg Leu		
	245	250
Tyr Asn Glu Leu Lys Val Glu Phe Asp Ser Tyr Asn Gly Glu Ala Phe		
	260	265
Tyr Asn Asp Lys Met Asp Ala Val Val Asp Ile Leu Ser Glu Lys Gly		
	275	280
Leu Leu Leu Glu Ser Glu Gly Ala Gln Val Val Asn Leu Glu Lys Tyr		
	290	295
Gly Ile Glu His Pro Ala Leu Ile Lys Lys Ser Asp Gly Ala Thr Leu		
305	310	315
Tyr Ile Thr Arg Asp Leu Ala Ala Ala Leu Tyr Arg Lys Asn Glu Tyr		
	325	330
Gln Phe Ala Lys Ser Ile Tyr Val Val Gly Gln Glu Gln Ser Ala His		
	340	345
Phe Lys Gln Leu Lys Ala Val Leu Gln Glu Met Gly Tyr Asp Trp Ser		
	355	360
Asp Asp Ile Thr His Val Pro Phe Gly Leu Val Thr Lys Glu Gly Lys		
	370	375
Lys Leu Ser Thr Arg Lys Gly Asn Val Ile Leu Leu Glu Pro Thr Ile		
385	390	395
Ala Glu Ala Val Ser Arg Ala Lys Val Gln Ile Glu Ala Lys Asn Pro		
	405	410
Glu Leu Glu Asn Lys Asp Gln Val Ala His Ala Val Gly Val Gly Ala		
	420	425
Ile Lys Phe Tyr Asp Leu Lys Thr Asp Arg Thr Asn Gly Tyr Asp Phe		
	435	440
Asp Leu Glu Ala Met Val Ser Phe Glu Gly Glu Thr Gly Pro Tyr Val		
	450	455
Gln Tyr Ala Tyr Ala Arg Ile Gln Ser Ile Leu Arg Lys Ala Asp Phe		
465	470	475
Lys Pro Glu Thr Ser Gly Asn Tyr Ser Leu Asn Asp Thr Glu Ser Trp		
	485	490
Glu Ile Ile Lys Leu Ile Gln Asp Phe Pro Arg Ile Ile Asn Arg Ala		
	500	505
Ala Asp Asn Phe Glu Pro Ser Ile Ile Ala Lys Phe Ala Ile Ser Leu		
	515	520
Ala Gln Ser Phe Asn Lys Tyr Tyr Ala His Thr Arg Ile Leu Asp Glu		
	530	535
Ser Pro Glu Arg Asp Ser Arg Leu Ala Leu Ser Tyr Ala Thr Ala Val		
545	550	555
Val Leu Lys Glu Ala Leu Arg Leu Leu Gly Val Glu Ala Pro Glu Lys		
	565	570
		575
Met		

(2) INFORMATION FOR SEQ ID NO:3425:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...93

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3425:

Lys	Arg	Asp	Lys	Gly	Glu	Ile	Lys	Met	Ala	Glu	Ile	Tyr	Leu	Ala	Gly
1				5					10					15	
Gly	Cys	Phe	Trp	Gly	Leu	Glu	Glu	Tyr	Phe	Ser	Arg	Ile	Ser	Gly	Val
			20					25					30		
Leu	Glu	Thr	Ser	Val	Gly	Tyr	Ala	Asn	Gly	Gln	Val	Glu	Thr	Thr	Asn
		35					40					45			
Tyr	Gln	Leu	Ile	Lys	Glu	Thr	Asp	His	Ala	Glu	Thr	Val	Gln	Val	Ile
	50					55					60				
Tyr	Asp	Glu	Lys	Glu	Val	Ser	Leu	Arg	Glu	Ile	Leu	Leu	Tyr	Tyr	Phe
65					70					75					80
Arg	Val	Ile	Asp	Pro	Leu	Ile	Tyr	Gln	Ser	Thr	Arg	Glu			
				85					90						

(2) INFORMATION FOR SEQ ID NO:3426:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 198 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...198

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3426:

Met	Ser	Asp	Asn	Phe	Phe	Gly	Lys	Thr	Leu	Ala	Val	Arg	Lys	Ile	Asp
1				5					10					15	
Ala	Ile	Pro	Gly	Leu	Leu	Glu	Phe	Asp	Ile	Pro	Val	His	Gly	Asp	Asn
			20					25					30		
Arg	Gly	Trp	Phe	Lys	Glu	Asn	Phe	Gln	Lys	Glu	Lys	Met	Glu	Pro	Leu
		35					40					45			
Gly	Phe	Pro	Glu	Ser	Phe	Phe	Ala	Ala	Gly	Lys	Leu	Gln	Asn	Asn	Val
	50					55					60				
Ser	Phe	Ser	Arg	Lys	Asn	Val	Leu	Arg	Gly	Leu	His	Ala	Glu	Pro	Trp
65					70					75					80
Asp	Lys	Tyr	Ile	Ser	Val	Ala	Asp	Asp	Gly	Lys	Val	Leu	Gly	Ser	Trp
				85					90				95		
Val	Asp	Leu	Arg	Glu	Gly	Glu	Thr	Phe	Gly	Asn	Thr	Tyr	Gln	Thr	Val

		100						105					110				
Ile	Asp	Ala	Ser	Lys	Gly	Ile	Phe	Val	Pro	Arg	Gly	Val	Ala	Asn	Gly		
		115						120					125				
Phe	Gln	Val	Leu	Ser	Asp	Thr	Val	Ser	Tyr	Ser	Tyr	Leu	Val	Asn	Asp		
		130						135				140					
Tyr	Trp	Ala	Leu	Glu	Leu	Lys	Pro	Lys	Tyr	Ala	Phe	Val	Asn	Tyr	Ala		
		145				150				155					160		
Asp	Pro	Ser	Leu	Gly	Ile	Glu	Trp	Glu	Asn	Ile	Ala	Glu	Ala	Glu	Val		
			165						170					175			
Ser	Glu	Ala	Asp	Lys	Asn	His	Pro	Leu	Leu	Lys	Asp	Val	Lys	Pro	Leu		
			180					185						190			
Lys	Lys	Glu	Asp	Leu	Glu												
			195														

(2) INFORMATION FOR SEQ ID NO:3427:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 62 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...62
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3427:

Asp	Lys	Asp	Lys	Thr	Leu	Phe	Ser	Ala	Asn	Leu	Leu	Val	Thr	Asn	Gly		
1				5				10						15			
Thr	Lys	Arg	Leu	Ala	Thr	Lys	Glu	Asp	Ile	Pro	Ile	Lys	Ile	Gly	Thr		
		20					25					30					
Ser	Asp	Val	Ala	Ile	Thr	Asp	Phe	Glu	Ile	Met	Tyr	Met	Leu	Ala	Met		
		35				40				45							
Ile	Val	Thr	Leu	Lys	Lys	Ile	Ser	Ala	Lys	Phe	Ala	Asn	Asn				
	50				55				60								

(2) INFORMATION FOR SEQ ID NO:3428:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 191 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...191

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3428:

```
Ala Glu Asp Asn Leu Met Ala Arg Leu Phe Thr Leu Ser Glu Ser Lys
1      5      10      15
Tyr Tyr Leu Met Ala Leu Asp Ala Gly Thr Gly Ser Ile Arg Ala Val
      20      25      30
Ile Phe Asp Leu Glu Gly Asn Gln Ile Ala Val Gly Gln Ala Glu Trp
      35      40      45
Arg His Leu Ala Val Pro Asp Val Pro Gly Ser Met Glu Phe Asp Leu
      50      55      60
Asn Lys Asn Trp Gln Leu Ala Cys Glu Cys Met Arg Gln Ala Leu His
      65      70      75      80
Asn Ala Gly Ile Ala Pro Glu Tyr Ile Ala Ala Val Ser Ala Cys Ser
      85      90      95
Met Arg Glu Gly Ile Val Leu Tyr Asn Asn Glu Gly Ala Pro Ile Trp
      100     105     110
Ala Cys Ala Asn Val Asp Ala Arg Ala Ala Arg Glu Val Ser Glu Leu
      115     120     125
Lys Glu Leu His Asn Asn Thr Phe Glu Asn Glu Val Tyr Arg Ala Thr
      130     135     140
Gly Gln Thr Leu Ala Leu Ser Ala Ile Pro Arg Leu Leu Trp Leu Ala
      145     150     155     160
His His Arg Ser Asp Ile Tyr Arg Gln Ala Ser Thr Ile Thr Met Ile
      165     170     175
Ser Asp Trp Leu Ala Tyr Met Leu Ser Gly Glu Leu Ala Val Asp
      180     185     190
```

(2) INFORMATION FOR SEQ ID NO:3429:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 239 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...239

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3429:

```
Asn Phe Cys Asn Arg Lys Gly Ile Glu Met Lys Ile Gly Ile Ile Ala
1      5      10      15
Ala Met Pro Glu Glu Leu Ala Tyr Leu Val Gln His Leu Asp Asn Thr
      20      25      30
Gln Glu Gln Val Val Leu Arg Asn Thr Tyr His Thr Gly Thr Ile Ala
      35      40      45
```

```

Ser His Glu Val Val Leu Val Glu Ser Gly Ile Gly Lys Val Met Ser
50          55          60
Ala Met Ser Val Ala Ile Leu Ala Asp His Phe Gln Val Asp Ala Leu
65          70          75          80
Ile Asn Thr Gly Ser Ala Gly Ala Val Ala Glu Gly Ile Ala Val Gly
85          90          95
Asp Val Val Ile Ala Asp Lys Leu Ala Tyr His Asp Val Asp Val Thr
100        105        110
Ala Phe Gly Tyr Ala Tyr Gly Gln Met Ala Gln Gln Pro Leu Tyr Phe
115        120        125
Glu Ser Asp Lys Thr Phe Val Ala Gln Ile Gln Glu Ser Leu Ser Gln
130        135        140
Leu Asp Gln Asn Trp His Leu Gly Leu Ile Ala Thr Gly Asp Ser Phe

145          150          155          160
Val Ala Gly Asn Asp Lys Ile Glu Ala Ile Lys Ser His Phe Pro Glu
165          170          175
Val Leu Ala Val Glu Met Glu Gly Ala Ala Ile Ala Gln Ala Ala His
180          185          190
Ala Leu Asn Leu Pro Val Leu Val Ile Arg Ala Met Ser Asp Asn Ala
195          200          205
Asn His Glu Ala Asn Ile Phe Phe Asp Glu Phe Ile Ile Glu Ala Gly
210          215          220
Arg Arg Ser Ala Gln Val Leu Leu Thr Phe Leu Lys Ala Leu Asp
225          230          235

```

(2) INFORMATION FOR SEQ ID NO:3430:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...83

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3430:

```

Gln Asp Cys Lys Arg Lys Gly Ser Leu Met Ala Glu Val Glu Glu Leu
1          5          10          15
Arg Val Gln Pro Gln Asp Ile Leu Ala Glu Gln Ser Val Leu Gly Ala
20          25          30
Ile Phe Ile Asp Glu Ser Lys Leu Val Phe Val Arg Glu Tyr Ile Glu
35          40          45
Ser Arg Asp Phe Phe Lys Tyr Ala His Arg Leu Ile Phe Gln Ala Met
50          55          60
Val Asp Leu Ser Asp Arg Gly Asp Ala Ile Asp Ala Thr Thr Val Pro
65          70          75          80
Tyr Tyr Pro

```

(2) INFORMATION FOR SEQ ID NO:3431:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 467 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...467

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3431:

Asp	Tyr	Cys	Asn	Gly	Ile	Lys	Tyr	Gly	Ile	Ile	Asp	Lys	Ile	Asp	Arg
1			5					10					15		
Ile	Glu	Asp	Val	Met	Ser	Phe	Thr	Lys	Phe	Gln	Phe	Lys	Asn	Tyr	Ile
			20					25					30		
Arg	Glu	Ala	Leu	Lys	Glu	Leu	Lys	Phe	Thr	Thr	Pro	Thr	Glu	Val	Gln
			35				40					45			
Asp	Lys	Leu	Ile	Pro	Ile	Val	Leu	Ala	Gly	Arg	Asp	Leu	Val	Gly	Glu
			50			55				60					
Ser	Lys	Thr	Gly	Ser	Gly	Lys	Thr	His	Thr	Phe	Leu	Leu	Pro	Ile	Phe
65					70					75					80
Gln	Gln	Leu	Asp	Glu	Ala	Ser	Asp	Ser	Val	Gln	Ala	Val	Ile	Thr	Ala
			85						90					95	
Pro	Ser	Arg	Glu	Leu	Ala	Thr	Gln	Ile	Tyr	Gln	Val	Ala	Arg	Gln	Ile
			100					105					110		
Ser	Ala	His	Ser	Asp	Val	Glu	Val	Arg	Val	Val	Asn	Tyr	Val	Gly	Gly
		115					120					125			
Thr	Asp	Lys	Ala	Arg	Gln	Ile	Glu	Lys	Leu	Ala	Ser	Asn	Gln	Pro	His
	130					135					140				
Ile	Val	Ile	Gly	Thr	Pro	Gly	Arg	Ile	Tyr	Asp	Leu	Val	Lys	Ser	Gly
145					150					155					160
Asp	Leu	Ala	Ile	His	Lys	Ala	Lys	Thr	Phe	Val	Val	Asp	Glu	Ala	Asp
			165						170					175	
Met	Thr	Leu	Asp	Met	Gly	Phe	Leu	Glu	Thr	Val	Asp	Lys	Ile	Ala	Gly
			180					185					190		
Ser	Leu	Pro	Lys	Asp	Leu	Gln	Phe	Met	Val	Phe	Ser	Ala	Thr	Ile	Pro
		195					200					205			
Gln	Lys	Leu	Gln	Pro	Phe	Leu	Lys	Lys	Tyr	Leu	Ser	Asn	Pro	Val	Met
	210					215					220				
Glu	Lys	Ile	Lys	Thr	Lys	Thr	Val	Ile	Ser	Asp	Thr	Ile	Asp	Asn	Trp
225					230					235					240
Leu	Ile	Ser	Thr	Lys	Gly	His	Asp	Lys	Asn	Ala	Gln	Ile	Tyr	Gln	Leu
			245						250					255	
Thr	Gln	Leu	Met	Gln	Pro	Tyr	Leu	Ala	Met	Ile	Phe	Val	Asn	Thr	Lys
			260					265					270		
Thr	Arg	Ala	Asp	Glu	Leu	His	Ser	Tyr	Leu	Thr	Ala	Gln	Gly	Leu	Lys

				85					90					95					
Tyr	Phe	Ser	Phe	His	Arg	Lys	Ser	Leu	Ser	Pro	Asp	Asp	Leu	Arg	Ser				
			100					105					110						
Arg	Ile	Ile	Trp	Ser	Phe	Ile	Leu	Glu	Ile	Ala	Ile	Ile	Leu	Val	Phe				
		115					120						125						
Ile	Leu	Lys	Ile	Pro	Phe	Ala	Ile	Ile	Met	Leu	Thr	Thr	Ile	Phe	Phe				
	130					135					140								
Trp	Thr	Ile	Met	Asp	Ile	Asn	His	Leu	Val	Phe	Asn	Lys	Thr	Glu	Phe				
145				150						155					160				
Leu	Phe	Asn	Gln	Asn	Lys	Trp	Glu	Lys	Glu	Asp	Ser	Phe	Glu	Ser	Asp				
			165						170					175					
Leu	Thr	Lys	Thr	Leu	Lys	Asp	Lys	Ile	Gln	Lys	Ser	Glu	Leu	Ser	Tyr				
		180					185						190						
Ser	Asp	Leu	Met	Ser	Leu	Leu	Leu	Tyr	Asp	Ala	Met	Asn	Gln	Ser	Thr				
	195					200						205							
Phe	Leu	Thr	Asp	Ser	Glu	Leu	Phe	Glu	Asp	Ile	Leu	Lys	Lys	Ile	Glu				
	210					215					220								
Asp	Ser	His	Asn	Thr	Leu	Leu	Cys	Thr	Gly	Phe	Val	Glu	Leu	Leu	Leu				
225				230						235					240				
Tyr	Glu	Met	Ser	Ile	Ser	Asn	Asn	Asn	Asn	Trp	Ser	Asn	Lys	Val	Asp				
			245						250					255					
Lys	Ile	Arg	Ile	His	Leu	Ile	Arg	Ile	Asn	Gln	Leu	Asp	Phe	Phe	Tyr				
		260					265						270						
Tyr	Thr	Ser	Trp	Leu	Arg	Gln	Asn	Phe	Asp	Phe	Cys	Met	Asn	Arg	Glu				
	275					280						285							
Tyr	His	Lys	Met	Lys	Ser	Arg	Lys	Leu	Leu	Leu	Ser	Asn	Lys	Lys	Ile				
	290					295					300								

Val
305

(2) INFORMATION FOR SEQ ID NO:3433:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 685 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...685
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3433:

Arg	Lys	Cys	Lys	Gly	Lys	Asn	Met	Thr	Lys	Asn	Leu	Leu	Val	Glu	Leu				
1				5				10					15						
Gly	Leu	Glu	Glu	Leu	Pro	Ala	Tyr	Val	Val	Thr	Pro	Ser	Glu	Lys	Gln				
		20					25					30							
Leu	Gly	Glu	Lys	Met	Ala	Ala	Phe	Leu	Lys	Glu	Asn	Arg	Leu	Ser	Phe				
	35					40					45								
Glu	Ala	Ile	Gln	Thr	Phe	Ser	Thr	Pro	Arg	Arg	Leu	Ala	Val	Arg	Val				

50		55		60
Thr Gly Leu Ser Asp	Lys Gln Ser Asp Leu Thr Glu Asp Phe Lys Gly			
65	70	75	80	
Pro Ala Lys Lys Ile Ala Leu Asp Ser Asp Gly Asn Phe Thr Lys Ala				
	85	90	95	
Ala Gln Gly Phe Val Arg Gly Lys Gly Leu Thr Val Glu Asp Ile Glu				
	100	105	110	
Phe Arg Glu Ile Lys Gly Glu Glu Tyr Val Tyr Val Thr Lys Glu Glu				
	115	120	125	
Val Gly Gln Ser Val Glu Ala Ile Val Pro Gly Val Val Asp Val Leu				
	130	135	140	
Lys Ser Leu Thr Phe Pro Val Ser Met His Trp Ala Gly Asn Ser Phe				
145	150	155	160	
Glu Tyr Ile Arg Pro Val His Thr Leu Thr Val Leu Leu Asp Glu Gln				
	165	170	175	
Glu Phe Asp Leu Asp Phe Leu Asp Ile Lys Gly Ser Arg Val Ser Arg				
	180	185	190	
Gly His Arg Phe Leu Gly Lys Glu Thr Lys Ile Gln Ser Ala Leu Ser				
	195	200	205	
Tyr Glu Glu Asp Leu Arg Lys Gln Phe Val Ile Ala Asp Pro Cys Glu				
210	215	220		
Arg Glu Gln Met Ile Val Asp Gln Ile Lys Glu Ile Glu Ala Lys His				
225	230	235	240	
Gly Val Arg Ile Glu Ile Asp Ala Asp Leu Leu Asn Glu Val Leu Asn				
	245	250	255	
Leu Val Glu Tyr Pro Thr Ala Phe Met Gly Ser Phe Asp Ala Lys Tyr				
	260	265	270	
Leu Glu Val Pro Glu Glu Val Leu Val Thr Ser Met Lys Glu His Gln				
	275	280	285	
Arg Tyr Phe Val Val Arg Asp Gln Asp Gly Lys Leu Leu Pro Asn Phe				
290	295	300		
Ile Ser Val Arg Asn Gly Asn Ala Glu Arg Leu Lys Asn Val Ile Lys				
305	310	315	320	
Gly Asn Glu Lys Val Leu Val Ala Arg Leu Glu Asp Gly Glu Phe Phe				
	325	330	335	
Trp Arg Glu Asp Gln Lys Leu Val Ile Ser Asp Leu Val Glu Lys Leu				
	340	345	350	
Asn Asn Val Thr Phe His Glu Lys Ile Gly Ser Leu Arg Glu His Met				
	355	360	365	
Ile Arg Thr Gly Gln Ile Thr Val Leu Leu Ala Glu Lys Ala Gly Leu				
370	375	380		
Ser Val Asp Glu Thr Val Asp Leu Ala Arg Ala Ala Ala Ile Tyr Lys				
385	390	395	400	
Phe Asp Leu Leu Thr Gly Met Val Gly Glu Phe Asp Glu Leu Gln Gly				
	405	410	415	
Ile Met Gly Glu Lys Tyr Thr Leu Leu Ala Gly Glu Thr Pro Ala Val				
	420	425	430	
Ala Ala Ala Ile Arg Glu His Tyr Met Pro Thr Ser Ala Glu Gly Glu				
	435	440	445	
Leu Pro Glu Ser Lys Val Gly Ala Val Leu Ala Ile Ala Asp Lys Leu				
450	455	460		
Asp Thr Ile Leu Ser Phe Phe Ser Val Gly Leu Ile Pro Ser Gly Ser				
465	470	475	480	
Asn Asp Pro Tyr Ala Leu Arg Arg Ala Thr Gln Gly Val Val Arg Ile				
	485	490	495	
Leu Asp Ala Phe Gly Trp His Ile Ala Met Asp Glu Leu Ile Asp Ser				
	500	505	510	

Leu	Tyr	Ala	Leu	Lys	Phe	Asp	Ser	Leu	Thr	Tyr	Glu	Asn	Lys	Ala	Glu
		515					520					525			
Val	Met	Asp	Phe	Ile	Lys	Ala	Arg	Val	Asp	Lys	Met	Met	Gly	Ser	Thr
		530				535					540				
Pro	Lys	Asp	Ile	Lys	Glu	Ala	Val	Leu	Ala	Gly	Ser	Asn	Phe	Val	Val
545					550					555					560
Ala	Asp	Met	Leu	Glu	Ala	Ala	Ser	Ala	Leu	Val	Glu	Val	Ser	Lys	Glu
			565						570					575	
Glu	Asp	Phe	Lys	Pro	Ser	Val	Glu	Ser	Leu	Ser	Arg	Ala	Phe	Asn	Leu
			580					585					590		
Ala	Glu	Lys	Ala	Glu	Gly	Val	Ala	Thr	Val	Asp	Ser	Ala	Leu	Phe	Glu
		595				600						605			
Asn	Asp	Gln	Glu	Lys	Ala	Leu	Ala	Glu	Ala	Val	Glu	Thr	Leu	Val	Leu
		610				615					620				
Ser	Gly	Pro	Ala	Ser	Gln	Gln	Leu	Lys	Gln	Leu	Phe	Ala	Leu	Ser	Pro
625					630				635						640
Val	Ile	Asp	Ala	Phe	Phe	Glu	Asn	Thr	Met	Val	Met	Ala	Glu	Asp	Gln
			645					650					655		
Ala	Val	Arg	Gln	Asn	Arg	Leu	Ala	Ile	Leu	Ser	Gln	Leu	Thr	Lys	Lys
			660			665						670			
Ala	Ala	Lys	Phe	Ala	Cys	Phe	Asn	Gln	Ile	Asn	Thr	Lys			
		675				680						685			

(2) INFORMATION FOR SEQ ID NO:3434:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 357 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...357
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3434:

Thr	Tyr	Arg	Asn	Gly	Cys	Phe	Thr	Ser	Pro	Ser	Ser	Asn	Leu	Thr	Ser
1				5				10					15		
Ser	Ser	Leu	Leu	Val	Phe	Met	Arg	Ala	Phe	Ser	Asp	Phe	Gly	Thr	Pro
			20				25					30			
Met	Leu	Ile	Gly	Glu	Gly	Tyr	Arg	Thr	Phe	Pro	Val	Leu	Ile	Tyr	Thr
		35				40					45				
Gln	Phe	Ile	Ser	Glu	Val	Glu	Gly	Asn	Ser	Ala	Phe	Ala	Ile	Met	Ala
		50				55				60					
Ile	Ile	Ile	Ala	Leu	Ala	Ile	Phe	Leu	Ile	Gln	Lys	His	Ile	Ala	Asn
65				70				75					80		
Arg	Tyr	Ser	Phe	Ser	Met	Asn	Leu	Ile	His	Pro	Ile	Glu	Pro	Lys	Lys
			85				90					95			
Thr	Thr	Lys	Gly	Lys	Met	Ala	Ala	Ile	Tyr	Ala	Thr	Val	Tyr	Gly	Ile
		100					105					110			

Ile	Phe	Ile	Ser	Val	Leu	Pro	Gln	Ile	Tyr	Leu	Ile	Tyr	Thr	Ser	Phe
		115					120					125			
Leu	Lys	Thr	Ser	Gly	Met	Val	Phe	Val	Lys	Gly	Tyr	Ser	Pro	Asn	Ser
	130					135					140				
Tyr	Lys	Leu	Ala	Phe	Asn	Arg	Met	Gly	Ser	Ala	Ile	Phe	Asn	Thr	Ile
145					150					155					160
Arg	Ile	Pro	Leu	Ile	Ala	Leu	Val	Leu	Val	Leu	Phe	Ala	Thr	Phe	
			165						170					175	
Ile	Ser	Tyr	Leu	Ala	Val	Arg	Lys	Arg	Asn	Leu	Phe	Thr	Asn	Leu	Ile
			180					185					190		
Asp	Asn	Leu	Ser	Met	Val	Pro	Tyr	Ile	Val	Pro	Gly	Thr	Val	Leu	Gly
		195					200					205			
Ile	Ala	Phe	Ile	Ser	Ser	Phe	Asn	Thr	Gly	Leu	Phe	Gly	Ser	Gly	Phe
	210					215					220				
Leu	Met	Ile	Thr	Gly	Thr	Ala	Phe	Ile	Leu	Ile	Met	Ser	Leu	Ser	Val
225				230						235					240
Arg	Arg	Leu	Pro	Tyr	Thr	Ile	Arg	Ser	Ser	Val	Ala	Ser	Leu	Gln	Gln
			245					250						255	
Ile	Ala	Pro	Ser	Ile	Glu	Glu	Ala	Ala	Glu	Ser	Leu	Gly	Ser	Ser	Arg
		260					265						270		
Leu	Asn	Thr	Phe	Ala	Lys	Ile	Thr	Thr	Pro	Met	Met	Leu	Ser	Gly	Ile
	275					280						285			
Ile	Ser	Gly	Ala	Ile	Leu	Ser	Trp	Val	Thr	Leu	Ile	Ser	Glu	Leu	Ser
	290					295					300				
Thr	Ser	Ile	Leu	Tyr	Pro	Pro	Leu	Gln	Cys	Gln	Asn	Lys	Asn	Asn	Asp
305				310						315					320
Cys	Ser	Tyr	Leu	Tyr	Arg	Gly	Ser	Gln	Arg	Lys	Leu	Arg	Cys	Ser	Arg
			325					330					335		
Ser	Leu	Val	Asn	Tyr	Pro	Asp	Cys	Ser	Asn	Ser	Arg	Phe	Leu	Ala	Leu
		340					345						350		
Val	Tyr	Glu	Asn	Leu											
		355													

(2) INFORMATION FOR SEQ ID NO:3435:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 121 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...121
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3435:

Ala	Thr	Ser	Lys	Ser	Ala	Ser	Ser	Val	Ala	Leu	His	Arg	Ser	Ala	Ser
1			5					10						15	
Arg	Cys	Gly	Thr	Thr	Phe	Lys	Gly	Glu	Asn	Ile	Lys	Met	Gly	Arg	Ser
		20					25						30		

Leu	Lys	Lys	Gly	Pro	Phe	Val	Asp	Glu	His	Leu	Met	Lys	Lys	Val	Glu
	35						40					45			
Ala	Gln	Ala	Asn	Asp	Glu	Lys	Lys	Lys	Val	Ile	Lys	Thr	Trp	Ser	Arg
	50					55					60				
Arg	Ser	Thr	Ile	Phe	Pro	Ser	Phe	Ile	Gly	Tyr	Thr	Ile	Ala	Val	Tyr
65					70					75					80
Asp	Gly	Arg	Lys	His	Val	Pro	Val	Tyr	Ile	Gln	Glu	Asp	Met	Val	Gly
			85					90						95	
His	Lys	Leu	Gly	Glu	Phe	Ala	Pro	Thr	Arg	Thr	Tyr	Lys	Gly	His	Ala
		100						105					110		
Ala	Asp	Asp	Lys	Lys	Thr	Arg	Arg	Lys							
	115						120								

(2) INFORMATION FOR SEQ ID NO:3436:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3436:

Asp	Leu	Ser	Lys	Glu	Lys	Leu	Glu	Asn	Val	Ser	Glu	Asp	Ile	Met	Ser
1			5					10						15	
Ile	Glu	Met	Thr	Val	Ser	Glu	Ile	Ala	Glu	Val	Leu	Gly	Leu	Ser	Arg
		20						25					30		
Gln	Ala	Ile	Asn	Asn	Arg	Val	Lys	Glu	Leu	Pro	Glu	Glu	Asp	Thr	Asp
	35					40					45				
Lys	Asn	Asp	Lys	Gly	Val	Thr	Val	Val	Thr	Arg	Ser	Gly	Leu	Ile	Lys
	50				55					60					
Leu	Glu	Glu	Ile	Tyr	Lys	Lys	Thr	Ile	Phe	Glu	Asp	Glu	Pro	Val	Ser
65				70					75						80
Glu	Asp	Val	Lys	Gln	Arg	Glu	Leu	Met	Glu	Ile	Leu	Val	Asp	Glu	Lys
			85					90					95		
Asn	Ala	Ala	Ile	Leu	Ser	Leu	Glu	Gln	Cys	His	Thr	Arg	Leu	Arg	Ile
		100						105					110		
Cys	Arg	Xaa													
	115														

(2) INFORMATION FOR SEQ ID NO:3437:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...160
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3437:

```

Lys Ala Ser Lys Phe Met Ser Arg Ser Gln Leu Thr Ile Leu Thr Asn
1      5      10      15
Ile Cys Leu Ile Glu Asp Leu Glu Thr Gln Cys Val Val Met Gln Tyr
20      25      30
Arg Ala Pro Glu Thr Asn Arg Trp Ser Gly Tyr Ala Phe Pro Gly Gly
35      40      45
His Val Glu Asn Gly Glu Ala Phe Ala Glu Ser Val Ile Arg Glu Ile
50      55      60
Tyr Glu Glu Thr Gly Leu Thr Ile Gln Asn Pro Gln Leu Val Gly Val
65      70      75      80
Lys Asn Trp Pro Leu Asp Thr Gly Gly Arg Tyr Ile Val Phe Cys Tyr
85      90      95
Lys Ala Thr Glu Phe Thr Gly Thr Leu Gln Ser Ser Asp Glu Gly Glu
100     105     110
Val Ser Trp Val Gln Lys Asp Gln Ile Pro Asn Leu Asn Leu Ala Tyr
115     120     125
Asp Met Leu Pro Leu Met Glu Met Met Glu Ala Pro Asp Lys Ser Glu
130     135     140
Phe Phe Tyr Pro Arg Arg Thr Glu Asp Asp Trp Glu Lys Lys Ile Phe
145     150     155     160

```

(2) INFORMATION FOR SEQ ID NO:3438:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 63 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...63
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3438:

```

Leu Gln Ser Asn Asp Gln Thr Pro Thr Arg Thr Glu Gln Gly Asn Leu
1      5      10      15
Phe Lys Leu Thr Ala Leu Ala Lys Leu Ser Asn Glu Asp Ser Lys Leu

```

		20					25					30					
Ile	Gln	Tyr	Gly	Leu	Gln	Gly	Arg	Val	Thr	Ser	Val	Thr	Thr	Lys	Lys		
		35					40					45					
Thr	Tyr	Phe	Asp	Tyr	Phe	Lys	Asp	Lys	Ile	Leu	Thr	His	Ser	Asp			
	50					55				60							

(2) INFORMATION FOR SEQ ID NO:3439:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 95 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...95
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3439:

Ile	Ile	Gly	Asn	Pro	Lys	Ile	Asn	Gly	Ser	Leu	Ile	Leu	Asn	Lys	Ala		
1				5				10					15				
Gly	Thr	Thr	Asp	Ala	Arg	Pro	Ile	Ala	Leu	Ser	Cys	Ser	Asp	Leu	Glu		
		20					25					30					
Ala	Lys	Ala	Ile	Tyr	Lys	His	Ser	Pro	Lys	Val	Ala	Pro	Glu	Pro	Pro		
	35				40			45									
Ala	Ile	Thr	Asn	Ile	Leu	Glu	Asn	Ser	Pro	Ala	Thr	Ala	Lys	Cys	Pro		
	50				55			60									
Pro	Ala	Ala	Phe	Ser	Ala	Met	Leu	Ala	Arg	Ala	Ile	Gly	Leu	Thr	Asn		
65				70				75							80		
Ala	Lys	Thr	Met	Phe	Ala	Pro	Trp	Ile	Pro	Thr	Ile	Gln	Ser	Ser			
		85					90							95			

(2) INFORMATION FOR SEQ ID NO:3440:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 120 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3440:

```
Lys Arg Gly Asn Leu Met Glu Gln Phe Leu Asp Asn Ile Lys Asp Leu
1      5      10      15
Glu Val Thr Thr Val Val Arg Ala Gln Glu Ala Leu Asp Lys Lys Glu
20      25      30
Thr Ala Thr Phe Phe Ile Gly Arg Lys Thr Cys Pro Tyr Cys Arg Lys
35      40      45
Phe Ala Gly Thr Leu Ser Gly Val Val Ala Glu Thr Lys Ala His Ile
50      55      60
Tyr Phe Ile Asn Ser Glu Glu Pro Ser Gln Leu Asn Asp Leu Gln Ala
65      70      75      80
Phe Arg Ser Arg Tyr Gly Ile Pro Thr Val Pro Gly Phe Val His Ile
85      90      95
Thr Asp Gly Gln Ile Asn Val Arg Cys Asp Ser Ser Met Ser Ala Gln
100     105     110
Glu Ile Lys Asp Phe Ala Gly Leu
115     120
```

(2) INFORMATION FOR SEQ ID NO:3441:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 441 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...441

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3441:

```
Leu Val Gly Lys Lys Arg Arg Phe Ile Met Ser Lys Met Asp Val Gln
1      5      10      15
Lys Ile Ile Ala Pro Met Met Lys Phe Val Asn Met Arg Gly Ile Ile
20      25      30
Ala Leu Lys Asp Gly Met Leu Ala Ile Leu Pro Leu Thr Val Val Gly
35      40      45
Ser Leu Phe Leu Ile Met Gly Gln Leu Pro Phe Val Gly Leu Asn Lys
50      55      60
Asn Ile Ala Ser Val Phe Gly Ala Asn Trp Thr Glu Pro Phe Met Gln
65      70      75      80
Val Tyr Ser Gly Thr Phe Ala Ile Met Gly Leu Ile Ser Cys Phe Ser
85      90      95
Ile Ala Tyr Ser Tyr Ala Lys Asn Ser Gly Val Glu Ala Leu Pro Ala
100     105     110
Gly Val Leu Ser Val Ser Ala Phe Phe Ile Leu Leu Arg Ser Ser Tyr
115     120     125
Ile Pro Lys Gln Gly Glu Ala Ile Gly Asp Ala Ile Ser Lys Val Trp
130     135     140
```

Phe	Gly	Gly	Gln	Gly	Ile	Ile	Gly	Ala	Ile	Ile	Ile	Gly	Leu	Val	Val
145					150				155						160
Gly	Ser	Ile	Tyr	Thr	Phe	Phe	Ile	Lys	Arg	Lys	Ile	Val	Ile	Lys	Met
				165					170						175
Pro	Glu	Gln	Val	Pro	Gln	Ala	Ile	Ala	Lys	Gln	Phe	Glu	Ala	Met	Ile
			180					185						190	
Pro	Ala	Phe	Val	Ile	Phe	Leu	Ser	Ser	Met	Ile	Val	Tyr	Ile	Leu	Ala
		195					200					205			
Lys	Ser	Leu	Thr	Asn	Gly	Gly	Thr	Phe	Ile	Glu	Met	Ile	Tyr	Ser	Ala
	210					215					220				
Ile	Gln	Val	Pro	Leu	Gln	Gly	Leu	Thr	Gly	Ser	Leu	Tyr	Gly	Ala	Ile
225					230					235					240
Gly	Ile	Ala	Phe	Phe	Ile	Ser	Phe	Leu	Trp	Trp	Phe	Gly	Val	His	Gly
			245						250					255	
Gln	Ser	Val	Val	Asn	Gly	Val	Val	Thr	Ala	Leu	Leu	Leu	Ser	Asn	Leu
			260					265						270	
Asp	Ala	Asn	Lys	Ala	Met	Leu	Ala	Ser	Ala	Asn	Leu	Ser	Leu	Glu	Asn
		275					280					285			
Gly	Ala	His	Ile	Val	Thr	Gln	Gln	Phe	Leu	Asp	Ser	Phe	Leu	Ile	Leu
	290					295					300				
Ser	Gly	Ser	Gly	Ile	Thr	Phe	Gly	Leu	Val	Val	Ala	Met	Leu	Phe	Ala
305					310					315					320
Ala	Lys	Ser	Lys	Gln	Tyr	Gln	Ala	Leu	Gly	Lys	Val	Ala	Ala	Phe	Pro
			325						330					335	
Ala	Ile	Phe	Asn	Val	Asn	Glu	Pro	Val	Val	Phe	Gly	Phe	Pro	Ile	Val
		340					345						350		
Met	Asn	Pro	Val	Met	Phe	Val	Pro	Phe	Ile	Leu	Val	Pro	Val	Leu	Ala
	355						360					365			
Ala	Val	Ile	Val	Tyr	Gly	Ala	Ile	Ala	Thr	Gly	Phe	Met	Gln	Pro	Phe
	370					375					380				
Ser	Gly	Val	Thr	Leu	Pro	Trp	Ser	Thr	Pro	Ala	Ile	Leu	Ser	Gly	Phe
385					390					395					400
Leu	Val	Gly	Gly	Trp	Gln	Gly	Val	Ile	Thr	Gln	Leu	Val	Ile	Leu	Ala
			405						410					415	
Met	Ser	Thr	Leu	Val	Tyr	Phe	Pro	Phe	Phe	Lys	Val	Gln	Asp	Arg	Leu
			420				425						430		
Ala	Tyr	Gln	Asn	Glu	Ile	Lys	Gln	Ser							
		435					440								

(2) INFORMATION FOR SEQ ID NO:3442:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

- (B) LOCATION 1...174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3442:

Phe	Trp	Gly	Lys	Thr	Met	Asn	Ser	Arg	Val	Glu	Phe	Arg	Ile	Phe	Thr
1			5						10				15		
Ile	Val	Asp	Leu	Asp	Lys	Glu	Glu	Glu	Tyr	Leu	His	Glu	Met	His	Leu
		20						25				30			
Lys	Gly	Trp	Arg	Tyr	Arg	Thr	Ser	Arg	Phe	Gly	Leu	Phe	Tyr	Phe	Asp
		35					40				45				
Gln	Cys	Gln	Pro	Asp	Asp	Val	Ile	Tyr	Arg	Ile	Tyr	Asp	Ser	Arg	Phe
	50					55				60					
Leu	Lys	Lys	Tyr	Lys	His	Glu	Leu	Gln	Asp	Phe	Arg	Asp	Arg	Gly	Trp
65					70				75					80	
Glu	Leu	Ile	Gly	Ala	Gly	Ser	Cys	Ser	Ile	Leu	Arg	Lys	Ser	Ser	Ser
			85					90				95			
Asp	Leu	Leu	Pro	Glu	Asp	Gln	Val	Tyr	Met	Ser	Lys	Gly	Leu	Lys	Trp
		100						105				110			
Glu	Val	Met	Arg	Ser	Arg	Leu	Arg	Ser	Cys	Thr	Thr	Thr	Phe	Leu	Gly
		115					120					125			
Gly	Leu	Val	Val	Cys	Thr	Ser	Leu	Phe	Arg	Glu	Asp	Leu	Ser	Met	Ser
	130					135				140					
Phe	Phe	Leu	Ile	Phe	Val	Leu	Tyr	Ala	Phe	Leu	Ile	Ser	Tyr	Leu	Ile
145					150				155					160	
His	Gly	Tyr	Phe	Arg	Leu	Lys	Arg	Lys	Tyr	Arg	Val	Asp	Glu		
			165						170						

(2) INFORMATION FOR SEQ ID NO:3443:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...286

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3443:

Phe	Ile	Cys	Leu	Gly	Cys	Asp	Cys	Phe	Gly	Ser	Ile	Phe	Arg	Arg	Lys
1			5						10				15		
Leu	Ser	Ala	Phe	Ser	Gly	Asp	Asp	Arg	Met	Asn	Lys	Gly	Ile	Tyr	Gln
		20						25				30			
His	Phe	Ser	Ile	Glu	Asp	Arg	Pro	Phe	Leu	Asp	Lys	Gly	Met	Glu	Trp
		35					40				45				
Ile	Lys	Lys	Val	Glu	Asp	Ser	Tyr	Ala	Pro	Phe	Leu	Thr	Pro	Phe	Ile
	50					55				60					
Asn	Pro	His	Gln	Glu	Lys	Leu	Leu	Lys	Ile	Leu	Ala	Lys	Thr	Tyr	Gly
65					70				75					80	
Leu	Ala	Cys	Ser	Ser	Ser	Gly	Glu	Phe	Val	Ser	Ser	Glu	Tyr	Val	Arg

				85					90					95					
Val	Leu	Leu	Tyr	Pro	Asp	Tyr	Phe	Gln	Pro	Glu	Phe	Ser	Asp	Phe	Glu				
			100					105					110						
Ile	Ser	Leu	Gln	Glu	Ile	Val	Tyr	Ser	Asn	Lys	Phe	Glu	His	Leu	Thr				
		115					120					125							
His	Ala	Lys	Ile	Leu	Gly	Thr	Val	Ile	Asn	Gln	Leu	Gly	Ile	Glu	Arg				
	130					135					140								
Lys	Leu	Phe	Gly	Asp	Ile	Leu	Val	Asp	Glu	Glu	Arg	Ala	Gln	Ile	Met				
145				150					155						160				
Ile	Asn	Gln	Gln	Phe	Leu	Leu	Leu	Phe	Gln	Asp	Gly	Leu	Lys	Lys	Ile				
		165						170						175					
Gly	Arg	Ile	Pro	Val	Ser	Leu	Glu	Glu	Arg	Pro	Phe	Thr	Glu	Lys	Ile				
		180					185						190						
Asp	Lys	Leu	Glu	Gln	Tyr	Arg	Glu	Leu	Asp	Leu	Ser	Val	Ser	Ser	Phe				
	195					200					205								
Arg	Leu	Asp	Val	Leu	Leu	Ser	Asn	Val	Leu	Lys	Leu	Phe	Arg	Asn	Gln				
	210				215						220								
Ala	Asn	Gln	Leu	Ile	Glu	Lys	Lys	Leu	Val	Gln	Val	Asn	Tyr	His	Val				
225				230					235					240					
Val	Asp	Lys	Ser	Asp	Tyr	Thr	Val	Gln	Val	Gly	Asp	Leu	Ile	Ser	Val				
		245						250					255						
Arg	Lys	Phe	Gly	Arg	Leu	Arg	Leu	Leu	Gln	Asp	Lys	Gly	Gln	Thr	Lys				
		260					265						270						
Lys	Glu	Lys	Lys	Lys	Ile	Thr	Val	Gln	Leu	Leu	Leu	Ser	Lys						
	275					280						285							

(2) INFORMATION FOR SEQ ID NO:3444:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3444:

Phe	Ser	Ile	Leu	Leu	Thr	Asn	Asn	Lys	Val	Arg	Arg	Ile	Phe	Met	Tyr
1			5					10					15		
Ser	Ile	Ser	Phe	Gln	Glu	Asp	Ser	Leu	Leu	Pro	Arg	Glu	Arg	Leu	Ala
		20					25				30				
Lys	Glu	Gly	Val	Glu	Ala	Leu	Ser	Asn	Gln	Glu	Leu	Leu	Ala	Ile	Leu
	35					40					45				
Leu	Arg	Thr	Gly	Thr	Arg	Gln	Val	Ser	Val	Phe	Glu	Ile	Ala	Gln	Lys
	50				55				60						
Val	Leu	Asn	Asn	Leu	Ser	Ser	Leu	Thr	Asp	Leu	Lys	Lys	Met	Thr	Leu
65				70				75					80		

Gln	Glu	Leu	Gln	Ser	Leu	Ser	Gly	Ile	Gly	Arg	Val	Lys	Ala	Ile	Glu
			85						90					95	
Leu	Gln	Ala	Met	Ile	Glu	Leu	Gly	His	Arg	Ile	His	Lys	His	Glu	Thr
		100						105					110		
Leu	Glu	Met	Glu	Ser	Ile	Leu	Ser	Gln	Lys	Leu	Ala	Lys	Lys	Met	
		115					120					125			
Gln	Gln	Glu	Leu	Gly	Asp	Lys	Lys	Gln	Glu	His	Leu	Val	Ala	Leu	Tyr
	130					135					140				
Leu	Asn	Thr	Gln	Asn	Gln	Ile	Ile	His	Gln	Gln	Thr	Ile	Phe	Ile	Gly
145					150					155					160
Ser	Val	Thr	Arg	Ser	Ile	Ala	Glu	Pro	Arg	Glu	Ile	Leu	His	Tyr	Ala
			165						170					175	
Ile	Lys	His	Met	Ala	Thr	Ser	Leu	Ile	Leu	Val	His	Asn	His	Pro	Ser
		180						185					190		
Gly	Ala	Val	Ala	Pro	Ser	Gln	Asn	Asp	Asp	His	Val	Thr	Lys	Leu	Val
	195					200						205			
Lys	Glu	Ala	Cys	Glu	Leu	Met	Gly	Ile	Val	Leu	Leu	Asp	His	Leu	Ile
	210					215					220				
Val	Ser	His	Ser	Asn	Tyr	Phe	Ser	Tyr	Arg	Glu	Lys	Thr	Asp	Leu	Ile
225					230					235					240

(2) INFORMATION FOR SEQ ID NO:3445:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 275 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...275

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3445:

Glu	Thr	Ile	Leu	Lys	Lys	Asn	Leu	Pro	Phe	Thr	Gly	Asn	Ile	Ala	Tyr
1			5						10					15	
Thr	Thr	Arg	Glu	Phe	Thr	Tyr	Asp	Asn	Pro	Leu	Met	Gln	Leu	Val	Arg
		20					25					30			
His	Thr	Ile	Glu	Tyr	Ile	Lys	Asn	Gln	Lys	Ser	Ile	Gly	Gln	Gly	Val
	35					40					45				
Leu	Asp	Asn	Leu	Ser	Thr	Ser	Arg	Glu	Asn	Val	Ser	Glu	Ile	Val	Arg
	50					55				60					
Val	Thr	Pro	Ser	Tyr	Lys	Leu	Ala	Asp	Arg	Ala	Lys	Ile	Ile	Arg	Gly
65				70					75					80	
Asn	Gln	Ser	Lys	Pro	Ile	Arg	His	Ala	Tyr	Phe	His	Glu	Tyr	Arg	Asn
		85						90					95		
Leu	Gln	Glu	Leu	Cys	Leu	Met	Ile	Leu	Asn	Gln	Glu	Lys	His	Gly	Leu
		100					105					110			
Gly	Tyr	Gln	Asp	Gln	Lys	Ile	Tyr	Gly	Ile	Leu	Phe	Asp	Val	Ala	Trp
	115					120						125			

Leu	Trp	Glu	Glu	Tyr	Val	Tyr	Thr	Leu	Leu	Pro	Lys	Gly	Phe	Val	His
130						135					140				
Pro	Arg	Asn	Lys	Asp	Lys	Thr	Asp	Gly	Ile	Ser	Val	Phe	Ser	Val	Gly
145					150					155					160
Lys	Arg	Lys	Val	Tyr	Pro	Asp	Phe	Tyr	Asp	Arg	Glu	Arg	Lys	Ile	Val
			165						170					175	
Leu	Asp	Ala	Lys	Tyr	Lys	Lys	Leu	Glu	Leu	Thr	Glu	Lys	Gly	Ile	Asn
		180						185					190		
Arg	Glu	Asp	Leu	Phe	Gln	Leu	Ile	Ser	Tyr	Ser	Tyr	Ile	Leu	Lys	Ala
		195					200					205			
Glu	Lys	Ala	Gly	Leu	Ile	Phe	Pro	Ser	Met	Glu	Gln	Ser	Val	Asn	Ser
	210					215					220				
Glu	Ile	Gly	Lys	Val	Ala	Gly	Tyr	Gly	Ala	Gln	Leu	Lys	Lys	Trp	Ser
225					230					235					240
Ile	Arg	Ile	Pro	Gln	Asn	Ala	Ser	Ser	Tyr	Ser	Ala	Phe	Cys	Lys	Met
				245					250					255	
Met	Glu	Asn	Ser	Glu	Glu	Asn	Phe	Lys	Ala	Ile	Ile	Asp	Glu	Glu	Val
			260					265					270		
Gly	Arg	Lys													
		275													

(2) INFORMATION FOR SEQ ID NO:3446:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 272 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...272

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3446:

Asn	Val	Phe	Lys	Glu	Gly	Asn	Asp	Met	Ser	Glu	Glu	Thr	Ile	Asp	Tyr
1				5					10					15	
Gly	Gln	Val	Thr	Gly	Met	Val	His	Ser	Thr	Glu	Ser	Phe	Gly	Ser	Val
			20					25					30		
Asp	Gly	Pro	Gly	Ile	Arg	Phe	Ile	Val	Phe	Leu	Gln	Gly	Cys	His	Met
		35					40					45			
Arg	Cys	Gln	Tyr	Cys	His	Asn	Pro	Asp	Thr	Trp	Ala	Met	Glu	Ser	Asn
	50					55				60					
Lys	Ser	Arg	Glu	Arg	Thr	Val	Asp	Asp	Val	Leu	Thr	Glu	Ala	Leu	Arg
65					70					75					80
Tyr	Arg	Gly	Phe	Trp	Gly	Asn	Lys	Gly	Gly	Ile	Thr	Val	Ser	Gly	Gly
			85					90						95	
Glu	Ala	Leu	Leu	Gln	Ile	Asp	Phe	Leu	Ile	Ala	Leu	Phe	Thr	Lys	Ala
		100						105					110		
Lys	Glu	Gln	Gly	Ile	His	Cys	Thr	Leu	Asp	Thr	Cys	Ala	Leu	Pro	Phe
		115					120					125			

Arg	Asn	Lys	Pro	Arg	Tyr	Leu	Glu	Lys	Phe	Asp	Lys	Leu	Met	Ala	Val
130						135					140				
Thr	Asp	Leu	Val	Leu	Leu	Asp	Ile	Lys	Glu	Ile	Asn	Glu	Glu	Gln	His
145					150					155					160
Lys	Ile	Val	Thr	Ser	Gln	Thr	Asn	Lys	Asn	Ile	Leu	Ala	Cys	Ala	Gln
				165					170					175	
Tyr	Leu	Ser	Asp	Ile	Gly	Lys	Pro	Val	Trp	Ile	Arg	His	Val	Leu	Val
			180					185					190		
Pro	Gly	Leu	Thr	Asp	Arg	Asp	Asp	Asp	Leu	Ile	Glu	Leu	Gly	Lys	Phe
		195				200						205			
Val	Lys	Thr	Leu	Lys	Asn	Val	Asp	Lys	Phe	Glu	Ile	Leu	Pro	Tyr	His
	210				215						220				
Thr	Met	Gly	Glu	Phe	Lys	Trp	Arg	Glu	Leu	Gly	Ile	Pro	Tyr	Ser	Leu
225					230					235					240
Glu	Gly	Val	Lys	Pro	Pro	Thr	Ala	Asp	Arg	Val	Lys	Asn	Ala	Lys	Lys
				245					250					255	
Leu	Met	Asp	Thr	Glu	Ser	Tyr	Gln	Asp	Tyr	Met	Lys	Arg	Val	His	Gly
			260					265					270		

(2) INFORMATION FOR SEQ ID NO:3447:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...63

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3447:

Thr	Tyr	Phe	Asn	Pro	Ile	Ile	Tyr	Arg	Arg	Ile	Phe	Thr	Pro	Phe	Tyr
1				5					10					15	
Ile	Leu	Glu	Ala	His	Lys	Lys	His	Tyr	Gly	Lys	Phe	Ala	Asp	Gly	Ser
			20					25					30		
Thr	Gln	Glu	Ile	Asp	Val	Pro	Tyr	Asp	Ile	Pro	Asp	Thr	Trp	Glu	Trp
		35					40					45			
Val	Arg	Phe	Thr	Thr	Leu	Val	Lys	Ile	Val	Lys	Ser	Gly	Ser	Ser	
	50					55					60				

(2) INFORMATION FOR SEQ ID NO:3448:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...67

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3448:

```
Ala His Phe Lys Ile Thr Leu Thr Phe Phe Thr Lys Arg Arg Lys Leu
1          5          10          15
Cys Val Met Ile Met Asp Ser Ala Phe Lys Phe Leu Asn Ser Ile Pro
          20          25          30
Ser Phe Tyr Leu Tyr Tyr Glu Arg Lys Tyr Asn Asn Cys Gln Val Thr
          35          40          45
Lys Val Asn Phe Ile Lys Lys Leu Gln Ala Lys Phe Val Lys Phe Thr
50          55          60
Leu Ser Arg
65
```

(2) INFORMATION FOR SEQ ID NO:3449:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 395 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...395

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3449:

```
Leu Asp Phe Asn Pro Cys Gly Arg Arg Gln Thr Gly Asp Val Val Ser
1          5          10          15
Ala Glu Val Leu Thr Val Asp Ala Thr Gln Ala Asn Val Ala Ile Ser
          20          25          30
Gly Thr Gly Val Glu Gly Val Leu Thr Leu Arg Glu Leu Thr Asn Asp
          35          40          45
Arg Asp Ala Asp Ile Asn Asp Phe Val Lys Val Gly Glu Val Leu Asp
50          55          60
Val Leu Val Leu Arg Gln Val Val Gly Lys Asp Thr Asp Thr Val Thr
65          70          75          80
Tyr Leu Val Ser Lys Lys Arg Leu Glu Ala Arg Lys Ala Trp Asp Lys
          85          90          95
Leu Val Gly Arg Glu Glu Glu Val Val Thr Val Lys Gly Thr Arg Ala
100          105          110
Val Lys Gly Gly Leu Ser Val Glu Phe Glu Gly Val Arg Gly Phe Ile
```

	115					120					125				
Pro	Ala	Ser	Met	Leu	Asp	Thr	Arg	Phe	Val	Arg	Asn	Ala	Glu	Arg	Phe
	130					135					140				
Val	Gly	Gln	Glu	Phe	Asp	Thr	Lys	Ile	Lys	Glu	Val	Asn	Ala	Lys	Glu
145					150					155					160
Asn	Arg	Phe	Ile	Leu	Ser	Arg	Arg	Glu	Val	Val	Glu	Ala	Ala	Thr	Ala
				165				170				175			
Ala	Ala	Arg	Ala	Glu	Val	Phe	Gly	Lys	Leu	Ala	Val	Gly	Asp	Val	Val
			180				185				190				
Thr	Gly	Lys	Val	Ala	Arg	Ile	Thr	Ser	Phe	Gly	Ala	Phe	Ile	Asp	Leu
		195				200				205					
Gly	Gly	Val	Asp	Gly	Leu	Val	His	Leu	Thr	Glu	Leu	Ser	His	Glu	Arg
	210				215				220						
Asn	Val	Ser	Pro	Lys	Ser	Val	Val	Thr	Val	Gly	Glu	Glu	Ile	Glu	Val
225				230				235				240			
Lys	Ile	Leu	Asp	Leu	Asn	Glu	Glu	Glu	Gly	Arg	Val	Ser	Leu	Ser	Leu
			245				250				255				
Lys	Ala	Thr	Val	Pro	Gly	Pro	Trp	Asp	Gly	Val	Glu	Gln	Lys	Leu	Ala
		260				265				270					
Lys	Gly	Asp	Val	Val	Glu	Gly	Thr	Val	Lys	Arg	Leu	Thr	Asp	Phe	Gly
	275				280				285						
Ala	Phe	Val	Glu	Val	Leu	Pro	Gly	Ile	Asp	Gly	Leu	Val	His	Val	Ser
	290				295				300						
Gln	Ile	Ser	His	Lys	Arg	Ile	Glu	Asn	Pro	Lys	Glu	Ala	Leu	Lys	Val
305				310				315				320			
Gly	Gln	Glu	Val	Gln	Val	Lys	Val	Leu	Glu	Val	Asn	Ala	Asp	Ala	Glu
			325				330				335				
Arg	Val	Ser	Leu	Ser	Ile	Lys	Ala	Leu	Glu	Glu	Arg	Pro	Ala	Gln	Glu
	340				345				350						
Glu	Gly	Gln	Lys	Glu	Glu	Lys	Arg	Ala	Ala	Arg	Pro	Arg	Arg	Pro	Arg
	355				360				365						
Arg	Gln	Glu	Lys	Arg	Asp	Phe	Glu	Leu	Pro	Glu	Thr	Gln	Thr	Gly	Phe
	370				375				380						
Ser	Met	Ala	Asp	Leu	Phe	Gly	Asp	Ile	Glu	Leu					
385				390				395							

(2) INFORMATION FOR SEO ID NO:3450:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...176

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3450:

Arg	Ser	Phe	Asn	Met	Glu	Tyr	Glu	Leu	Leu	Ile	Arg	Glu	Ala	Glu	Pro
1			5					10					15		
Lys	Asp	Ala	Ala	Glu	Leu	Val	Ala	Phe	Leu	Asn	Arg	Val	Ser	Leu	Glu
		20					25					30			
Thr	Asp	Phe	Thr	Ser	Leu	Asp	Gly	Asp	Gly	Ile	Leu	Leu	Thr	Ser	Glu
	35					40					45				
Glu	Met	Glu	Ile	Phe	Leu	Asn	Lys	Gln	Ala	Ser	Ser	Asp	Asn	Gln	Ile
	50				55					60					
Thr	Leu	Leu	Ala	Phe	Leu	Asn	Gly	Lys	Ile	Ala	Gly	Ile	Val	Asn	Ile
65					70				75					80	
Thr	Ala	Asp	Gln	Arg	Lys	Arg	Val	Arg	His	Ile	Gly	Asp	Leu	Phe	Ile
			85					90					95		
Val	Ile	Gly	Lys	Arg	Tyr	Trp	Asn	Asn	Gly	Leu	Gly	Ser	Leu	Leu	Leu
		100					105					110			
Glu	Glu	Ala	Ile	Glu	Trp	Ala	Gln	Ala	Ser	Gly	Ile	Leu	Arg	Arg	Leu
		115				120					125				
Gln	Leu	Thr	Val	Gln	Thr	Arg	Asn	Gln	Ala	Ala	Val	His	Leu	Tyr	Gln
	130				135						140				
Lys	His	Gly	Phe	Val	Ile	Glu	Gly	Ser	Gln	Glu	Arg	Gly	Ala	Tyr	Ile
145					150				155					160	
Glu	Glu	Gly	Lys	Phe	Ile	Asp	Val	Tyr	Leu	Met	Gly	Lys	Leu	Ile	Gly
			165					170					175		

(2) INFORMATION FOR SEQ ID NO:3451:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 144 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...144

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3451:

Ser	Ser	Phe	Lys	Ile	Ser	Val	Ser	Lys	Arg	Val	Phe	Pro	Cys	Lys	Ser
1			5					10					15		
His	Arg	Leu	Arg	Lys	Ile	Pro	Arg	Thr	Phe	Ile	Ser	Ile	Pro	Pro	Thr
		20					25				30				
Thr	Tyr	Gly	Ile	Leu	Ser	Val	Ile	Glu	Ile	Val	Phe	Leu	Arg	Leu	Pro
	35				40					45					
Asp	Pro	Glu	Asn	Ser	Leu	Asn	Ser	Ser	Pro	Val	Ser	Tyr	Met	Arg	Asp
	50				55				60						
Cys	Ser	Leu	Ser	Ser	Phe	Met	Met	Leu	Val	Val	Val	Ala	Gly	Val	Ser
65					70				75					80	
Pro	Val	Ser	Leu	Thr	Ile	Ser	Val	Arg	Asp	Val	Ala	Gly	Phe	Arg	Tyr
			85				90						95		
Arg	Asn	Ser	Ser	Ile	Val	Ala	Leu	Phe	Cys	Lys	Lys	Lys	Lys	Lys	Lys
		100					105					110			

Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Arg	Gly	Glu	Lys	Lys	Lys	Lys	Lys
		115					120					125			
Lys	Lys	Lys	Lys	Lys	His	Lys	Gln	Lys	Pro	Pro	Pro	Ser	Phe	Ser	Ser
		130				135					140				

(2) INFORMATION FOR SEQ ID NO:3452:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 275 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...275

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3452:

Ile	Arg	Phe	Lys	Leu	Ser	Arg	Arg	Cys	Ser	Met	Leu	Ala	Ser	Glu	Val
1			5					10						15	
Ile	Gln	Ala	Tyr	Glu	Ala	Phe	Cys	Pro	Gln	Glu	Phe	Ser	Met	Glu	Gly
		20					25					30			
Asp	Ser	Arg	Gly	Leu	Gln	Ile	Gly	Thr	Leu	Asp	Lys	Gly	Ile	Gln	Arg
	35				40						45				
Val	Met	Val	Ala	Leu	Asp	Ile	Arg	Glu	Glu	Thr	Val	Ala	Glu	Ala	Ile
	50				55					60					
Glu	Lys	Gly	Val	Asp	Leu	Ile	Ile	Val	Lys	His	Ala	Pro	Ile	Phe	Arg
65				70					75					80	
Pro	Ile	Lys	Asp	Leu	Leu	Ala	Ser	Arg	Pro	Gln	Asn	Gln	Ile	Tyr	Ile
			85				90						95		
Asp	Leu	Ile	Lys	His	Asp	Ile	Ala	Val	Tyr	Val	Ser	His	Thr	Asn	Ile
	100						105					110			
Asp	Ile	Val	Glu	Asn	Gly	Leu	Asn	Asp	Trp	Phe	Cys	Gln	Met	Leu	Gly
	115					120					125				
Ile	Glu	Glu	Thr	Thr	Tyr	Leu	Gln	Glu	Thr	Gly	Pro	Glu	Arg	Gly	Ile
	130					135				140					
Gly	Arg	Ile	Gly	Asn	Ile	Gln	Pro	Gln	Thr	Phe	Trp	Glu	Leu	Ala	Gln
145				150					155						160
Gln	Val	Lys	Gln	Val	Phe	Asp	Leu	Asp	Ser	Leu	Arg	Met	Val	His	Tyr
			165					170						175	
Gln	Glu	Asn	Asp	Leu	Gln	Lys	Pro	Ile	Ser	Arg	Val	Ala	Ile	Cys	Gly
		180					185					190			
Gly	Ser	Gly	Gln	Ser	Phe	Tyr	Lys	Asp	Ala	Leu	Ala	Lys	Gly	Ala	Asp
	195					200					205				
Val	Tyr	Ile	Thr	Gly	Asp	Ile	Tyr	Tyr	His	Thr	Ala	Gln	Asp	Met	Leu
	210					215				220					
Ser	Asp	Gly	Leu	Leu	Ala	Leu	Asp	Pro	Gly	His	Tyr	Ile	Glu	Val	Leu
225					230				235						240
Phe	Val	Glu	Lys	Ile	Ala	Ala	Leu	Leu	Thr	Gln	Trp	Lys	Glu	Lys	Lys
			245					250					255		

Gly Trp Glu Leu Glu Ile Leu Pro Ser Gln Ala Ser Thr Asn Pro Phe
260 265 270
Arg His Ile
275

(2) INFORMATION FOR SEQ ID NO:3453:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...319

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3453:

Met Asp Ile Lys Ile Lys Arg Glu Glu Ile Met Lys Lys Phe Ser Lys
1 5 10 15
Thr Leu Arg Asp Asn Trp Ile Phe Leu Leu Met Val Leu Pro Gly Ala
20 25 30
Leu Trp Leu Ile Leu Phe Phe Tyr Ile Pro Val Phe Gly Asn Val Val
35 40 45
Ala Phe Lys Asp Tyr His Met Thr Ser Asn Gly Phe Ile Asp Ser Ile
50 55 60
Ile Asn Ser Lys Trp Val Gly Leu Asp Asn Phe Arg Phe Leu Phe Ser
65 70 75 80
Ser Arg Asp Ala Phe Ile Ile Thr Arg Asn Thr Val Leu Tyr Asn Leu
85 90 95
Gly Phe Ile Phe Leu Gly Leu Val Val Ser Val Gly Ile Ala Ile Ile
100 105 110
Leu Ser Glu Leu Arg Ser Lys Arg Met Val Lys Ile Phe Gln Thr Ser
115 120 125
Met Leu Phe Pro Tyr Phe Leu Ser Trp Val Ile Ile Ser Phe Phe Thr
130 135 140
Asp Ala Phe Leu Asn Ile Asp Lys Gly Val Phe Asn His Leu Leu Glu
145 150 155 160
Ser Leu Gly Leu Lys Glu Val Asn Phe Tyr Ala Asp Leu Gly Ile Trp
165 170 175
Pro Tyr Leu Leu Leu Phe Leu Gly Ile Trp Lys Gly Phe Gly Tyr Ser
180 185 190
Ser Val Met Tyr Tyr Ala Thr Ile Met Gly Ile Asp Pro Thr Tyr Tyr
195 200 205
Glu Ala Ala Thr Val Asp Gly Ala Ser Lys Trp Gln Arg Ile Arg Asn
210 215 220
Val Thr Ile Pro Gln Leu Thr Pro Leu Val Thr Val Leu Thr Ile Leu
225 230 235 240
Ala Val Gly Asn Ile Phe Arg Ala Asp Phe Gly Leu Phe Tyr Gln Ile

				245					250					255	
Pro	His	Asn	Ala	Gly	Gln	Leu	Tyr	Asn	Val	Thr	Asn	Val	Leu	Asp	Val
			260					265					270		
Tyr	Val	Phe	Asn	Gly	Leu	Thr	Gln	Thr	Ala	Asp	Ile	Gly	Met	Ala	Ala
		275					280					285			
Ala	Ala	Gly	Leu	Tyr	Gln	Ser	Val	Val	Gly	Leu	Ile	Leu	Val	Ile	Leu
	290					295					300				
Ser	Asn	Leu	Leu	Ala	Arg	Arg	Val	Asp	Pro	Asn	Ser	Ala	Leu	Phe	
305					310					315					

(2) INFORMATION FOR SEQ ID NO:3454:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 102 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...102
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3454:

Arg	Ser	Ile	Asn	Met	Lys	Gln	Thr	Val	Lys	Lys	Leu	Ala	Leu	Val	Ala
1				5					10					15	
Ser	Ile	Ala	Ala	Thr	Leu	Gly	Gly	Ser	Val	Ala	Val	Ala	Ser	Ala	Ala
		20						25					30		
Val	Gln	Tyr	Pro	Glu	Gly	Gly	Val	Trp	Thr	Tyr	Gly	Ser	Gly	Asn	Gly
		35				40					45				
Gly	Ala	Tyr	Ser	Asn	Tyr	Tyr	His	Pro	Ser	Lys	Tyr	His	Ser	Ser	Thr
	50				55					60					
Val	Val	Ser	Arg	Lys	Thr	Gly	Ser	Ser	Asp	Lys	Gly	Tyr	Ala	Gly	Ala
65				70					75					80	
Gly	Gly	Thr	Ser	Arg	Ala	Trp	Ile	Arg	Thr	Ser	Trp	Gly	Glu	Lys	Val
			85					90					95		
Ala	Phe	Tyr	Tyr	Asn	Val										
			100												

(2) INFORMATION FOR SEQ ID NO:3455:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 92 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...92

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3455:

```
Val Ala Ile Lys Ile Val Val Pro Cys Arg Leu Ile Arg Ser Lys Arg
1      5      10      15
Phe Ile Ile Ser His Glu Leu Ser Gly Ser Arg Phe Pro Val Gly Ser
      20      25      30
Ser Ala Ile Asn Thr Leu Gly Leu Phe Thr Ile Ala Arg Ala Ile Ala
      35      40      45
Ile Arg Cys Cys Ser Pro Pro Glu Ser Ser Phe Gly Lys Glu Arg Thr
      50      55      60
Leu Cys Phe Asn Pro Thr Arg Ser Lys Thr Ser Ile Thr Arg Leu Leu
65      70      75      80
Ile Leu Arg Arg Phe Ser Pro Ile Thr Ser Ile Ala
      85      90
```

(2) INFORMATION FOR SEQ ID NO:3456:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 433 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...433

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3456:

```
His Met Ile Asn Arg Tyr Ser Arg Pro Glu Met Ala Asn Ile Trp Ser
1      5      10      15
Glu Glu Asn Lys Tyr Arg Ala Trp Leu Glu Val Glu Ile Leu Ser Asp
      20      25      30
Glu Ala Trp Ala Glu Leu Gly Glu Ile Pro Lys Glu Asp Val Ala Leu
      35      40      45
Ile Arg Lys Lys Ala Asp Phe Asp Ile Asp Arg Ile Leu Glu Ile Glu
      50      55      60
Gln Glu Thr Arg His Asp Val Val Ala Phe Thr Arg Ala Val Ser Glu
65      70      75      80
Thr Leu Gly Glu Glu Arg Lys Trp Val His Tyr Gly Leu Thr Ser Thr
      85      90      95
Asp Val Val Asp Thr Ala Tyr Gly Tyr Leu Tyr Lys Gln Ala Asn Asp
      100      105      110
Ile Ile Arg Arg Asp Leu Glu Asn Phe Thr Asn Ile Ile Ala Asp Lys
```


(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...146

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3457:

```
Ile Phe Val Lys Cys Phe Ile Leu His Phe Tyr Tyr Lys Phe Leu Tyr
1      5      10      15
His Lys Leu Leu Leu Gln Lys Asp Lys Asp Thr Thr Phe Ala Leu Phe
      20      25      30
Asp Ser Leu Phe Lys His Ser Ile Ile Phe Leu His Ser Tyr Lys Asn
      35      40      45
Thr Ser Asp Glu Arg Ala Cys Phe Leu Ile Ser Leu Asn Asn Lys Lys
      50      55      60
Arg Lys Leu Lys Pro Ala Asp Asn Leu Tyr Ser His Phe Ile Ser Phe
      65      70      75      80
Thr Ser Val Leu Arg Thr Leu Ala Tyr Phe Leu Ala Leu Val Lys Cys
      85      90      95
Arg Val Thr Gly Leu Asn Thr Pro Leu Leu Ser Leu Arg Lys Pro Lys
      100     105     110
Thr Ala Asp Leu Leu Phe Leu Ser Ser Lys Asn Met Thr Ser Asn Phe
      115     120     125
Ile Val Phe Leu Asp Lys Ser Leu Ala Thr Met Gln Gln Leu Ile Ile
      130     135     140
Leu Glu
145
```

(2) INFORMATION FOR SEQ ID NO:3458:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 79 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...79

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3458:

```
Gly His Val Lys Asn Thr Leu Met Asp His Pro Val Asn Gly Glu Ile
1      5      10      15
Glu Thr Leu Leu Lys Leu Ser Cys Arg Arg Asp Val Gln His Phe Leu
      20      25      30
Glu Gln Val Glu His Ser Asp Phe Arg Pro Leu Ser Glu Leu Thr Asp
      35      40      45
Gly Ile His Tyr His Leu Val Glu Ala Glu Thr Gln Gln Asp Leu His
      50      55      60
Tyr Ile Glu Glu Ala Leu Asp Gln Leu Gly Tyr Leu Val Lys Asp
      65      70      75
```

(2) INFORMATION FOR SEQ ID NO:3459:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...62

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3459:

Gln	Ser	Val	Lys	Glu	Glu	Thr	Asp	Glu	Leu	Asp	Lys	Lys	Gln	Ala	Tyr
1			5					10					15		
Ile	Val	Ser	Cys	His	Ser	Gly	Leu	Arg	Ser	Tyr	Ile	Ala	Glu	Pro	Ile
		20					25					30			
Leu	Lys	Gln	Ala	Gly	Phe	Thr	Ala	Gln	Asn	Leu	Asp	Gly	Ala	Tyr	Ser
	35					40				45					
Leu	Tyr	Lys	Met	Val	Asn	Pro	Xaa	Arg	Val	Lys	Tyr	Gly	Asn		
	50				55					60					

(2) INFORMATION FOR SEQ ID NO:3460:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...293

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3460:

Ile	Ser	Val	Lys	Leu	Tyr	Gly	Pro	Gly	Thr	Cys	Leu	Tyr	Leu	Gln	Arg
1			5					10					15		
Gly	Glu	Lys	Thr	Met	Pro	Ser	Met	Lys	Glu	Tyr	Ala	Leu	Gln	Tyr	Gln
		20					25				30				
Lys	Leu	Gly	Phe	Ser	Val	Ile	Pro	Ile	Asn	Pro	Lys	Asn	Lys	Met	Pro
	35					40				45					
Leu	Ile	Glu	Phe	Ala	Asp	Lys	Pro	Ala	Met	Thr	Pro	Ser	Glu	Ile	Glu

50	55	60													
Asn	Phe	Trp	Asp	Gly	Tyr	Pro	Asn	Ala	Asn	Ile	Ala	Leu	Lys	Thr	Thr
65					70					75					80
Asn	Phe	Phe	Val	Ile	Asp	Ile	Asp	Lys	His	Gly	Lys	Ser	Asn	Gly	Phe
			85						90					95	
Glu	Ser	Leu	Lys	Lys	Trp	Lys	His	Leu	Asn	Leu	Ile	Glu	Pro	Thr	Leu
		100						105					110		
Gln	Ala	Lys	Thr	Ala	Ser	Gly	Gly	Lys	His	Leu	Phe	Tyr	Phe	Lys	Arg
	115					120					125				
Glu	Asp	Glu	Pro	Ile	Thr	Gln	Met	Ile	Gly	Phe	Leu	Pro	Gly	Val	Asp
130						135				140					
Ile	Lys	Ala	His	Glu	Asn	Asn	Tyr	Val	Leu	Val	Ala	Pro	Ser	Ala	Thr
145					150				155						160
Asp	Lys	Gly	Gln	Tyr	Glu	Trp	Asp	Leu	Glu	Lys	Ser	Lys	Glu	Gly	Gly
			165					170						175	
Thr	Met	Val	Thr	Pro	Ser	Lys	Tyr	Leu	Ile	Gln	Ser	Ile	Lys	Lys	Gln
	180							185				190			
Tyr	Gly	Glu	Thr	His	Gly	Tyr	Lys	Tyr	Asp	Gly	Lys	Asp	Gly	Leu	Arg
	195					200					205				
Asp	Leu	Val	Arg	Arg	Ser	His	Thr	Arg	Asp	Arg	Thr	Gln	Thr	Thr	Asp
210					215						220				
Leu	Phe	Glu	Thr	Ile	Ala	Leu	Gly	Phe	Gly	Asp	Glu	Gly	Gly	Arg	Asn
225					230				235						240
Asp	Lys	Leu	Ala	Lys	Phe	Val	Gly	Gly	Leu	Leu	Tyr	Arg	Ala	Val	Asp
			245					250						255	
Asp	Gly	Val	Val	Gln	Leu	Ala	Arg	Leu	Ala	Asn	Ala	Asn	Ser	Pro	
	260						265					270			
Thr	Pro	Leu	Pro	Glu	Lys	Glu	Met	Met	Arg	Thr	Ile	Glu	Ser	Met	Ile
	275					280						285			
Lys	Lys	Asp	Arg	Arg											
290															

(2) INFORMATION FOR SEQ ID NO:3461:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 77 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...77
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3461:

Thr	Pro	Val	Lys	Pro	Ser	Ala	Ala	Thr	Arg	Ser	Ala	Phe	Leu	Ala	Ala
1			5					10					15		
Leu	Ala	Ile	Pro	Phe	Ser	Arg	Ser	Asn	Ser	Ile	Ala	Phe	Ser	Met	Ser
	20						25				30				
Pro	Ser	Val	Ser	Thr	Ser	Ala	Phe	Leu	Ala	Ser	Ile	Thr	Pro	Ala	Pro

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumòniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...72

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3463:

Arg	Ala	Val	Asn	Ala	Val	Gln	Ala	Gly	Gln	Ala	Asp	Ala	Ile	Met	Ala
1			5					10					15		
Gly	Met	Thr	Lys	Thr	Lys	Glu	Arg	Glu	Lys	Val	Phe	Thr	Met	Ser	Asp
			20					25					30		
Thr	Tyr	Tyr	Asp	Thr	Lys	Val	Val	Ile	Ala	Thr	Thr	Lys	Ser	His	Lys
		35				40						45			
Ile	Ser	Lys	Tyr	Asp	Gln	Leu	Thr	Gly	Lys	Thr	Val	Cys	Val	Lys	Asn
	50				55						60				
Gly	Thr	Gly	Ala	Gln	Arg	Val	Pro								
65					70										

(2) INFORMATION FOR SEQ ID NO:3464:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...77

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3464:

Tyr	Leu	Ser	Lys	His	Cys	Ser	Thr	Ala	Asp	Phe	Cys	Pro	Arg	Thr	Glu
1			5					10					15		
Pro	Pro	Leu	Thr	Thr	Gln	Thr	Pro	Leu	His	Tyr	Ile	Gly	Gln	Pro	His
			20					25					30		
Gly	Lys	Ile	Ile	Ala	Arg	Leu	Ile	Asn	Asn	Ile	Ile	His	Thr	Arg	Ile
		35				40						45			
Gln	Asn	Ile	Phe	Leu	Phe	Ile	Leu	Phe	Leu	Leu	Ser	Leu	Phe	Ser	Thr
	50				55						60				
Tyr	Ile	Val	Pro	Leu	Ile	Lys	Leu	Ile	Ser	Lys	Leu	Arg			
65					70					75					

(2) INFORMATION FOR SEQ ID NO:3465:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...62

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3465:

```
Asp Phe Ser Asn Arg Phe Ile Leu Ile Ile Pro Tyr Leu Lys Gly Gly
1      5      10      15
Glu Glu Met Arg Pro Arg Arg Tyr Pro Tyr Ser Gly Lys Lys Glu Ser
      20      25      30
Thr Phe Val Lys Ala Asp Pro Glu Leu Met Leu Asn Ile Asn Lys Ile
      35      40      45
Asp Val Gly Asn Ile Gln Ala Lys Asn Ile Phe Gly Lys Ile
50      55      60
```

(2) INFORMATION FOR SEQ ID NO:3466:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...332

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3466:

```
Ser Asp Ser Lys Ser Tyr Lys Lys Arg Ile Leu Ser Ile Pro Thr Ser
1      5      10      15
Lys Lys Gly Asn Ile Met Lys Ser Tyr Gln Ala Val Tyr Gln Ile Leu
      20      25      30
Ser Lys Glu Thr Asp Tyr Ile Ser Gly Glu Lys Ile Ala Glu Lys Leu
      35      40      45
Ser Leu Ser Arg Thr Ala Ile Trp Lys Ala Ile Lys Arg Leu Glu Gln
```

50		55		60											
Glu	Gly	Ile	Glu	Ile	Asp	Ser	Ile	Lys	Asn	Arg	Gly	Tyr	Lys	Leu	Met
65					70					75				80	
Asn	Gly	Asp	Leu	Ile	Leu	Pro	Glu	Ile	Leu	Glu	Glu	Asn	Leu	Pro	Ile
			85						90					95	
Lys	Val	Ser	Phe	Lys	Pro	Glu	Thr	Lys	Ser	Thr	Gln	Leu	Asp	Ala	Lys
			100					105					110		
Glu	Ala	Ile	Asp	Leu	Gly	His	Glu	Ala	Asn	Thr	Leu	Tyr	Leu	Ala	Ser
		115					120					125			
Tyr	Gln	Thr	Ala	Gly	Arg	Gly	Arg	Phe	Gln	Arg	Ser	Phe	Tyr	Ser	Pro
	130					135					140				
Gln	Gly	Gly	Ile	Tyr	Met	Thr	Leu	His	Leu	Lys	Pro	Asn	Leu	Pro	Tyr
145					150					155					
Asp	Arg	Leu	Pro	Ser	Tyr	Thr	Leu	Leu	Val	Ala	Gly	Ala	Val	Tyr	Lys
			165						170					175	
Ala	Ile	Lys	Asn	Leu	Thr	Leu	Ile	Asp	Val	Asp	Ile	Lys	Trp	Val	Asn
			180					185					190		
Asp	Ile	Tyr	Leu	Asn	Asn	His	Lys	Ile	Gly	Gly	Ile	Leu	Thr	Glu	Ala
		195					200					205			
Met	Thr	Ser	Val	Glu	Thr	Gly	Leu	Val	Thr	Asp	Ile	Ile	Ile	Gly	Val
	210					215					220				
Gly	Ile	Asn	Phe	Thr	Ile	Lys	Asp	Phe	Pro	Gln	Glu	Leu	Lys	Glu	Lys
225					230					235					
Ala	Ala	Ser	Leu	Phe	Lys	Ala	Thr	Ala	Pro	Ile	Thr	Arg	Asn	Glu	Leu
			245						250					255	
Ile	Ile	Glu	Ile	Trp	Arg	Ala	Phe	Phe	Glu	Thr	Pro	Ala	Glu	Glu	Leu
		260						265					270		
Leu	Tyr	Leu	Tyr	Lys	Lys	Gln	Ser	Phe	Ile	Leu	Gly	Lys	Glu	Val	Thr
	275						280					285			
Phe	Thr	Leu	Glu	Gln	Lys	Asp	Tyr	Lys	Gly	Leu	Ala	Lys	Asp	Ile	Ser
	290					295					300				
Glu	Asn	Gly	Lys	Leu	Leu	Val	Gln	Cys	Asp	Asn	Gly	Lys	Glu	Ile	Trp
305					310					315					
Leu	Asn	Ser	Gly	Glu	Ile	Ser	Leu	Asn	Ser	Trp	Lys				
			325						330						

(2) INFORMATION FOR SEQ ID NO:3467:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...111

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3467:

Gln Leu Ser Asn Leu Gln Tyr Trp Thr Ser Leu Phe Ala Ser Pro Trp

1				5					10					15			
Thr	Ile	Ala	Ile	Asn	Leu	Ile	Asp	Ile	Leu	Ile	Val	Ala	Tyr	Ile	Leu		
			20					25					30				
Tyr	His	Phe	Thr	Lys	Gly	Ile	Ala	Gly	Thr	Lys	Ile	Met	Ile	Leu	Val		
		35				40						45					
Arg	Gly	Val	Leu	Val	Phe	Ile	Phe	Ser	Ser	Asn	Pro	Cys	Lys	Tyr	Asp		
	50				55					60							
Trp	Phe	Asp	Tyr	Asp	Leu	Leu	Val	Ile	Gln	Ser	Asn	Tyr	Tyr	Leu	Trp		
65				70					75					80			
Gly	Tyr	Cys	Gly	Gly	Cys	Tyr	Leu	Leu	Ser	Arg	Asp	Ser	Asp	Trp	Phe		
			85					90					95				
Gly	Thr	Phe	Gly	Lys	Ser	Asp	Arg	Phe	Leu	Phe	Gln	Cys	Pro	Tyr			
			100				105						110				

(2) INFORMATION FOR SEQ ID NO:3468:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...71

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3468:

Thr	Ile	Pro	Asn	Pro	Ser	Asn	Arg	Arg	Tyr	Asp	Arg	Val	Glu	Leu	Ser		
1				5				10					15				
His	Gln	Val	Ile	Asp	Thr	Cys	Phe	Arg	Leu	Val	Asn	Glu	Pro	Leu	Val		
		20				25					30						
Met	Phe	Asp	Val	Phe	Ile	Thr	Arg	Asp	Lys	Thr	Phe	Met	Arg	Tyr	Gln		
	35			40				45									
Thr	His	Asp	Gln	Leu	Lys	Gln	Lys	Ala	Val	Val	Arg	Ser	Phe	Arg	Lys		
	50			55				60									
Leu	Ser	Ser	Asp	Trp	Arg	Lys											
65				70													

(2) INFORMATION FOR SEQ ID NO:3469:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...62

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3469:

Asn	Ser	Pro	Lys	Val	Arg	Val	Leu	Phe	Leu	Thr	Phe	Glu	Arg	Thr	Ser
1				5					10					15	
Phe	Leu	Ile	Gln	Thr	Phe	Ser	Thr	Ala	Ile	Pro	Tyr	Ala	Met	Lys	Ser
			20					25					30		
Asp	Lys	Phe	Phe	Phe	Ile	Thr	Ser	Pro	Leu	Gly	Asn	Leu	Asn	Ser	Ile
		35				40					45				
Val	Pro	Ser	Ile	Leu	Asn	Ile	Thr	Leu	Ser	Lys	Pro	Asn	Pro		
	50					55					60				

(2) INFORMATION FOR SEQ ID NO:3470:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 308 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...308

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3470:

Ile	Val	Thr	Lys	Glu	Leu	Leu	Lys	Val	Trp	Leu	Leu	Met	Glu	Asp	Gln
1				5					10					15	
Met	Lys	Ser	Lys	Asn	Gly	Val	Pro	Phe	Gly	Leu	Leu	Ser	Gly	Ile	Phe
			20					25					30		
Trp	Gly	Leu	Gly	Leu	Thr	Val	Ser	Ala	Tyr	Ile	Phe	Ser	Ile	Phe	Thr
		35				40					45				
Asp	Leu	Ser	Pro	Phe	Val	Val	Ala	Ala	Ala	His	Asp	Phe	Leu	Ser	Ile
	50					55				60					
Phe	Ile	Leu	Leu	Ala	Phe	Leu	Leu	Val	Lys	Glu	Gly	Lys	Val	Arg	Leu
65				70					75					80	
Ser	Ile	Phe	Leu	Asn	Ile	Arg	Asn	Val	Ser	Val	Ile	Ile	Gly	Ala	Leu
			85					90					95		
Leu	Ala	Gly	Pro	Ile	Gly	Met	Gln	Ala	Asn	Leu	Tyr	Ala	Val	Lys	Tyr
		100					105						110		
Ile	Gly	Ser	Ser	Leu	Ala	Ser	Ser	Val	Ser	Ala	Ile	Tyr	Pro	Ala	Ile
	115					120					125				
Ser	Val	Leu	Leu	Ala	Phe	Phe	Phe	Leu	Lys	His	Lys	Ile	Ser	Lys	Asn
	130				135						140				
Thr	Val	Phe	Gly	Ile	Val	Leu	Ile	Ile	Gly	Gly	Ile	Ile	Ala	Gln	Thr
145					150				155						160

Tyr Lys Val Glu Gln Val Asn Ser Phe Tyr Ile Gly Ile Leu Cys Ala
 165 170 175
 Leu Val Cys Ala Ile Ala Trp Gly Ser Glu Ser Val Leu Ser Ser Phe
 180 185 190
 Ala Met Glu Ser Glu Leu Ser Glu Ile Glu Ala Leu Leu Ile Arg Gln
 195 200 205
 Val Thr Ser Phe Leu Ser Tyr Leu Val Ile Val Leu Phe Ser His Gln
 210 215 220
 Ser Phe Thr Ala Val Val Asn Gly Gln Leu Leu Gly Leu Met Ile Val
 225 230 235 240
 Phe Ala Ala Phe Asp Met Ile Ser Tyr Leu Ala Tyr Tyr Ile Ala Ile
 245 250 255
 Asn Arg Leu Ala Thr Ser Gln Gly Tyr Arg Leu Glu Arg Glu Leu Cys
 260 265 270
 Ser Ile Gly Arg Val Leu Phe Gly Asn Cys Phe Phe Arg Gly Ala Pro
 275 280 285
 Ala Arg Tyr Ala Asp His Tyr Asp Val Thr Cys Arg His Cys Trp Ser
 290 295 300
 Leu Tyr Tyr Tyr
 305

(2) INFORMATION FOR SEQ ID NO:3471:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 239 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...239

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3471:

Asp Phe Thr Asn Ile Trp Phe Ile Leu Pro Lys Ala Ile Arg Ser Ile
 1 5 10 15
 Ile Gly Asn Asp Asp Leu Ile Lys Ile Asp Asn Thr Leu Gln Tyr Pro
 20 25 30
 Tyr Ser Thr Ser Ala Met Val Leu Ser Lys Tyr Tyr Gly Val Ala Asp
 35 40 45
 Gly Met Asn Val Glu Gly Arg Gly Ser Ala Asn Phe Ile Lys Asp Asn
 50 55 60
 Val Leu Ile Thr Ala Ala His Asn Tyr Tyr Arg His Asp Tyr Gly Lys
 65 70 75 80
 Glu Ala Asp Asp Ile Tyr Val Leu Pro Ala Val Ser Pro Ser Gln Glu
 85 90 95
 Pro Phe Gly Lys Ile Lys Val Lys Glu Val Arg Tyr Leu Lys Glu Phe
 100 105 110
 Arg Asn Leu Asn Ser Lys Asp Ala Arg Glu Tyr Asp Leu Ala Leu Leu
 115 120 125

Ile	Leu	Glu	Lys	Pro	Ile	Gly	Ala	Lys	Leu	Gly	Thr	Leu	Gly	Leu	Pro
130						135					140				
Thr	Ser	Gln	Lys	Asn	Leu	Thr	Gly	Ile	Thr	Val	Thr	Ile	Thr	Gly	Tyr
145					150					155					160
Pro	Ser	Tyr	Asn	Phe	Lys	Ile	Tyr	Gln	Met	Tyr	Thr	Asp	Lys	Lys	Gln
			165						170					175	
Val	Leu	Ser	Asp	Asp	Gly	Met	Phe	Leu	Asp	Tyr	Gln	Val	Asp	Thr	Leu
			180					185					190		
Glu	Gly	Ser	Ser	Gly	Ser	Thr	Val	Tyr	Asp	Ala	Ser	His	Arg	Val	Val
		195					200					205			
Gly	Val	His	Thr	Leu	Gly	Asp	Gly	Ala	Asn	Gln	Ile	Asn	Ser	Ala	Val
	210					215					220				
Lys	Leu	Asn	Glu	Arg	Asn	Leu	Ser	Phe	Ile	Tyr	Leu	Phe	Gly	Ser	
225					230					235					

(2) INFORMATION FOR SEQ ID NO:3472:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...140

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3472:

Ser	Thr	Thr	Asn	Leu	Phe	Ser	Asn	Phe	Val	His	Ser	Thr	Arg	Phe	Lys
1				5					10					15	
Thr	Lys	Glu	Val	Lys	Thr	Val	Ile	Ser	Lys	Pro	Asp	Lys	Asn	Lys	Leu
		20					25						30		
Arg	Gln	Lys	Arg	His	Arg	Arg	Val	Arg	Gly	Lys	Leu	Ser	Gly	Thr	Ala
	35					40					45				
Asp	Arg	Pro	Arg	Leu	Asn	Val	Phe	Arg	Ser	Asn	Thr	Gly	Ile	Tyr	Ala
	50				55					60					
Gln	Val	Ile	Asp	Asp	Val	Ala	Gly	Val	Thr	Leu	Ala	Ser	Ala	Ser	Thr
65				70					75					80	
Leu	Asp	Lys	Glu	Val	Ser	Lys	Gly	Thr	Lys	Thr	Glu	Gln	Ala	Val	Ala
			85					90					95		
Val	Gly	Lys	Leu	Val	Ala	Glu	Arg	Ala	Asn	Ala	Lys	Gly	Ile	Ser	Glu
		100					105					110			
Val	Val	Phe	Asp	Arg	Gly	Gly	Tyr	Leu	Tyr	His	Gly	Arg	Val	Lys	Ala
	115					120					125				
Leu	Ala	Asp	Ala	Ala	Arg	Glu	Asn	Gly	Leu	Lys	Phe				
	130					135					140				

(2) INFORMATION FOR SEQ ID NO:3473:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 76 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...76

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3473:

```
Lys Ala Thr Lys Pro Glu Ala Ser Phe Lys Ser Pro Ser Pro Leu Arg
1          5          10          15
Ile Leu Asp Thr Arg Leu Gly Lys Leu Lys Arg Ser Glu Arg Glu Ala
20          25          30

Lys Ala Thr Lys Ser Val Gly Pro Arg Ala Ala Pro Thr Ala Lys Gln
35          40          45
Ala Ala Lys Gly Arg Leu Asn Gln Arg Arg Trp Ala Lys Pro Pro Lys
50          55          60
Leu Arg Val Glu Ile Lys Ile Thr Gly Asn Met Arg
65          70          75
```

(2) INFORMATION FOR SEQ ID NO:3474:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 289 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...289

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3474:

```
Ser Val Thr Lys Thr Arg His Gly Val Val Ser Met Phe Met Arg Met
1          5          10          15
Ala Arg Arg Trp Ala Met Leu Ser Leu Leu Ser Tyr Asp Phe Ile Gln
20          25          30
Arg Ala Phe Leu Ala Val Ile Ala Met Ser Leu Phe Ser Pro Val Leu
35          40          45
Gly Thr Phe Leu Ile Leu Arg Arg Gln Ser Leu Met Ser Asp Thr Leu
50          55          60
```

Ser	His	Val	Ser	Leu	Ser	Gly	Val	Ala	Phe	Gly	Leu	Val	Leu	Gly	Ile
65					70					75					80
Ser	Pro	Thr	Val	Ser	Thr	Ile	Ala	Ile	Val	Leu	Ile	Ala	Ala	Val	Phe
			85						90					95	
Leu	Glu	Tyr	Leu	Arg	Thr	Val	Tyr	Lys	Ser	Phe	Met	Glu	Ile	Gly	Thr
			100					105					110		
Ala	Ile	Leu	Met	Ser	Thr	Gly	Leu	Ala	Val	Ser	Leu	Ile	Val	Met	Ser
			115				120					125			
Lys	Gly	Lys	Ser	Ser	Ser	Ser	Met	Ser	Leu	Asp	Gln	Tyr	Leu	Phe	Gly
	130					135					140				
Ser	Ile	Val	Thr	Ile	Ser	Glu	Glu	Gln	Val	Ile	Ser	Leu	Phe	Val	Ile
145					150					155					160
Ala	Ala	Val	Val	Leu	Ile	Leu	Thr	Phe	Leu	Phe	Leu	Arg	Pro	Met	Tyr
				165					170					175	
Ile	Leu	Thr	Phe	Asp	Glu	Asp	Thr	Ala	Phe	Val	Asp	Gly	Leu	Pro	Val
			180					185					190		
Arg	Thr	Met	Ser	Ile	Leu	Phe	Asn	Met	Val	Thr	Gly	Val	Ala	Ile	Ala
			195				200					205			
Leu	Met	Ile	Pro	Ala	Ala	Gly	Ala	Leu	Leu	Val	Ser	Thr	Ile	Met	Val
	210					215					220				
Leu	Pro	Ala	Ser	Ile	Ala	Leu	Arg	Leu	Gly	Lys	Asn	Phe	Lys	Ser	Val
225					230					235					240
Met	Leu	Leu	Ala	Ser	Ala	Ile	Gly	Phe	Leu	Gly	Met	Val	Ala	Gly	Leu
				245					250					255	
Tyr	Ile	Ser	Tyr	Tyr	Ala	Glu	Thr	Pro	Ala	Ser	Ala	Ser	Ile	Thr	Ile
			260					265					270		
Ile	Phe	Val	Thr	Val	Phe	Ile	Leu	Ile	Ser	Leu	Val	Arg	Arg	Phe	Ile
		275					280						285		

Lys

(2) INFORMATION FOR SEQ ID NO:3475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...93

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3475:

Glu	Ala	Thr	Lys	Ser	Ala	Ala	Lys	Asn	Asn	Gln	Asn	Val	Val	Gln	Gly
1				5				10						15	
Val	Met	Thr	Thr	Leu	Ala	Glu	Ile	Phe	Thr	Pro	Ile	Ile	Pro	Ala	Leu
			20					25					30		
Ile	Val	Gly	Gly	Leu	Ile	Leu	Gly	Phe	Arg	Asn	Val	Leu	Glu	Gly	Val
		35					40						45		

His	Trp	Ser	Met	Leu	Asp	Gly	Lys	Thr	Ile	Thr	Glu	Ser	Ser	Gln	Phe
50						55					60				
Trp	Ala	Gly	Val	Asn	His	Phe	Leu	Trp	Leu	Pro	Gly	Glu	Ala	Ile	Phe
65				70						75					80
Gln	Phe	Leu	Pro	Val	Arg	Asp	Tyr	Leu	Val	Cys	Phe	Ser			
				85					90						

(2) INFORMATION FOR SEQ ID NO:3476:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 183 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3476:

Lys	Ala	Thr	Lys	Gln	Leu	Ile	Arg	Lys	Ile	His	Met	Glu	Gln	Leu	His
1				5					10					15	
Phe	Ile	Thr	Lys	Leu	Leu	Asp	Ile	Lys	Asp	Pro	Asn	Ile	Gln	Ile	Leu
			20					25					30		
Asp	Ile	Ile	Asn	Lys	Asp	Thr	His	Lys	Glu	Ile	Ile	Ala	Lys	Leu	Asp
			35				40					45			
Tyr	Asp	Ala	Pro	Ser	Cys	Pro	Glu	Cys	Gly	Asn	Gln	Leu	Lys	Lys	Tyr
			50			55					60				
Asp	Phe	Gln	Lys	Pro	Ser	Lys	Ile	Pro	Tyr	Leu	Glu	Thr	Thr	Gly	Met
65					70					75					80
Pro	Thr	Arg	Ile	Leu	Leu	Arg	Lys	Arg	Arg	Phe	Lys	Cys	Tyr	His	Cys
				85					90					95	
Ser	Lys	Met	Met	Val	Ala	Glu	Thr	Ser	Ile	Val	Lys	Lys	Asn	His	Gln
			100					105					110		
Ile	Pro	Arg	Ile	Ile	Asn	Gln	Lys	Ile	Ala	Gln	Lys	Leu	Ile	Glu	Lys
			115				120					125			
Ile	Ser	Met	Thr	Asp	Ile	Ala	His	Gln	Leu	Phe	Ile	Ser	Thr	Ser	Thr
						135					140				
Val	Ile	Arg	Lys	Leu	Asn	Asp	Phe	His	Phe	Lys	His	Asp	Phe	Ser	Cys
145					150					155					160
Leu	Pro	Glu	Ile	Met	Ser	Trp	Asp	Val	Glu	Thr	Val	Arg	Val	Val	Thr
				165					170					175	
Val	Ser	Ile	Gly	Arg	Trp	Arg									
				180											

(2) INFORMATION FOR SEQ ID NO:3477:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 209 amino acids

(B) TYPE: amino acid

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...209
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3477:

```

Thr Leu Ala Lys Gln Phe Tyr Pro Asn Phe Pro Ile Arg Asn His Gln
1      5      10      15
Tyr Arg Phe His Leu Ser Pro Gln Ala His Ala Lys Arg Ser Gly Arg
      20      25      30
Asn Phe Leu Glu Lys Arg Lys Leu His Leu Leu Phe Thr Pro Leu Ser
      35      40      45
Lys Asn His Gln Gly Glu Ile Arg Thr Met Lys Lys Gln Val Phe His
50      55      60
Asp Ala Ala Thr Gly Val Leu Ile Gly Leu Ile Leu Ser Ile Leu Phe
65      70      75      80
Ser Leu Ile Tyr Ala Pro Asn Thr Tyr Ala Pro Leu Asn Pro Tyr Ser
      85      90      95
Leu Ile Gly Gln Val Met Asp Gln His Gln Val His Gly Ala Leu Val
      100     105     110
Leu Leu Tyr Cys Thr Leu Ile Trp Ala Thr Ile Gly Met Leu Phe Asn
      115     120     125
Phe Gly Asn Arg Leu Phe Ser Arg Asp Trp Ser Met Leu Arg Ala Thr
      130     135     140
Leu Thr His Phe Phe Leu Met Leu Ala Gly Phe Val Pro Leu Ala Thr
      145     150     155     160
Leu Ala Gly Trp Phe Pro Phe His Trp Ile Phe Tyr Leu Gln Leu Ile
      165     170     175
Ile Glu Phe Ala Ile Val Tyr Leu Ile Ile Trp Ala Ile Leu Tyr Lys
      180     185     190
Arg Glu Ala Lys Lys Val Asp His Ile Asn Gln Leu Leu Glu His Arg
      195     200     205
Lys

```

(2) INFORMATION FOR SEQ ID NO:3478:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 159 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...159

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3478:

```
Ile Cys Ala Lys Ile Gly Trp Val Asp Ser Gln Met Leu Arg Leu Glu
1      5      10      15
Asp Gly Lys Lys Glu Gly Lys Ser Asn Arg Glu Ile Ala Ser Leu Leu
20      25      30
Gly Lys Ala Pro Gln Thr Ile His Thr Glu Ile Lys Tyr Gly Thr Val
35      40      45
Arg Lys Cys Leu Gly Lys Gly Arg Phe Lys Glu Val Tyr Ser Ala Asp
50      55      60
Tyr Ala Gln Gln Ser Tyr Glu Asn Asn Arg Lys His Ser Val Lys Arg
65      70      75      80
Ser Ser Leu Thr Lys Glu Leu Lys Glu Lys Ile Leu His Tyr His Asn
85      90      95
Gln Lys Phe Leu Pro Glu Met Met Val Met Ala Lys Gly Val Asn Val
100     105     110
Gly Ile Ser Thr Ile Tyr Tyr Trp Ile His His Gly Lys Leu Gly Leu
115     120     125
Ser Lys Gln Asp Leu Leu Tyr Pro Arg Lys Gly Lys Ser Val Lys Lys
130     135     140
Gln Val Ser Pro Asn Phe Lys Pro Ala Asp Gln Ser Ile Glu Ser
145     150     155
```

(2) INFORMATION FOR SEQ ID NO:3479:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 572 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...572

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3479:

```
Asn Pro Ala Lys Ser Ile Val Lys Ser Met His Pro Asn Met Glu Arg
1      5      10      15
Arg Thr Arg Met Lys Arg Gln Thr Val Asn Gln Thr Leu Lys Arg Leu
20      25      30
Ala Val Asp Leu Ala Ser His Pro Phe Leu Leu Phe Leu Ala Phe Leu
35      40      45
Gly Thr Ile Ala Gln Val Gly Leu Ser Ile Tyr Leu Pro Ile Leu Ile
50      55      60
```

Gly	Gln	Val	Ile	Asp	Gln	Val	Leu	Val	Ala	Gly	Ser	Ser	Pro	Val	Phe
65					70					75					80
Trp	Gln	Ile	Phe	Leu	Gln	Met	Leu	Leu	Val	Val	Ile	Gly	Asn	Thr	Leu
				85					90					95	
Val	Gln	Trp	Ala	Asn	Pro	Leu	Leu	Tyr	Asn	Arg	Leu	Ile	Phe	Ser	Tyr
			100					105					110		
Thr	Arg	Asp	Leu	Arg	Glu	Arg	Ile	Ile	His	Lys	Leu	His	Arg	Leu	Pro
		115					120					125			
Ile	Ala	Phe	Val	Asp	Arg	Gln	Gly	Ser	Gly	Glu	Met	Val	Ser	Arg	Val
	130					135					140				
Thr	Thr	Asp	Ile	Glu	Gln	Leu	Ala	Ala	Gly	Leu	Thr	Met	Ile	Phe	Asn
145					150					155					160
Gln	Phe	Phe	Ile	Gly	Val	Leu	Met	Ile	Leu	Val	Ser	Ile	Leu	Ala	Met
			165						170					175	
Leu	Gln	Ile	His	Leu	Leu	Met	Thr	Leu	Leu	Val	Leu	Leu	Leu	Thr	Pro
		180						185					190		
Leu	Ser	Met	Val	Ile	Ser	Arg	Phe	Ile	Ala	Lys	Lys	Ser	Tyr	His	Leu
		195					200					205			
Phe	Gln	Lys	Gln	Thr	Glu	Thr	Arg	Gly	Ile	Gln	Thr	Gln	Leu	Ile	Glu
	210					215					220				
Glu	Ser	Leu	Ser	Gln	Gln	Thr	Ile	Ile	Gln	Ser	Phe	Asn	Ala	Gln	Thr
225					230					235					240
Glu	Phe	Ile	Gln	Arg	Leu	Arg	Glu	Ala	His	Asp	Asn	Tyr	Ser	Gly	Tyr
			245						250					255	
Ser	Gln	Ser	Ala	Ile	Phe	Tyr	Ser	Ser	Thr	Val	Asn	Pro	Ser	Thr	Arg
		260						265				270			
Phe	Val	Asn	Ala	Leu	Ile	Tyr	Ala	Leu	Leu	Ala	Gly	Val	Gly	Ala	Tyr
		275					280					285			
Arg	Ile	Met	Met	Gly	Ser	Ala	Leu	Thr	Val	Gly	Arg	Leu	Val	Thr	Phe
	290					295					300				
Leu	Asn	Tyr	Val	Gln	Gln	Tyr	Thr	Lys	Pro	Phe	Asn	Asp	Ile	Ser	Ser
305					310					315					320
Val	Leu	Ala	Glu	Leu	Gln	Ser	Ala	Leu	Ala	Cys	Val	Glu	Arg	Ile	Tyr
			325						330					335	
Gly	Val	Leu	Asp	Ser	Pro	Glu	Val	Ala	Glu	Thr	Gly	Lys	Glu	Val	Leu
		340						345					350		
Thr	Thr	Ser	Asp	Gln	Val	Lys	Gly	Ala	Ile	Ser	Phe	Lys	His	Val	Ser
		355					360					365			
Phe	Gly	Tyr	His	Pro	Glu	Lys	Ile	Leu	Ile	Lys	Asp	Leu	Ser	Ile	Asp
	370					375					380				
Ile	Pro	Ala	Gly	Ser	Lys	Val	Ala	Ile	Val	Gly	Pro	Thr	Gly	Ala	Gly
385					390					395					400
Lys	Ser	Thr	Leu	Ile	Asn	Leu	Leu	Met	Arg	Phe	Tyr	Pro	Ile	Ser	Ser
				405					410					415	
Gly	Asp	Ile	Leu	Leu	Asp	Gly	Gln	Ser	Ile	Tyr	Asp	Tyr	Thr	Arg	Val
			420					425					430		
Ser	Leu	Arg	Gln	Gln	Phe	Gly	Met	Val	Leu	Gln	Glu	Thr	Trp	Leu	Thr
		435					440					445			
Gln	Gly	Thr	Ile	His	Asp	Asn	Ile	Ala	Phe	Gly	Asn	Pro	Glu	Ala	Ser
	450					455					460				
Arg	Glu	Gln	Val	Ile	Ala	Ala	Ala	Lys	Ala	Ala	Asn	Ala	Asp	Phe	Phe
465					470					475					480
Ile	Gln	Gln	Leu	Pro	Gln	Gly	Tyr	Asp	Thr	Lys	Leu	Glu	Asn	Ala	Gly
			485						490					495	
Glu	Ser	Leu	Ser	Val	Gly	Gln	Ala	Gln	Leu	Leu	Thr	Ile	Ala	Arg	Val
			500					505					510		

Phe	Leu	Ala	Ile	Pro	Lys	Ile	Leu	Ile	Leu	Asp	Glu	Ala	Thr	Ser	Ser
		515					520					525			
Ile	Asp	Thr	Arg	Thr	Glu	Val	Leu	Val	Gln	Asp	Ala	Phe	Ala	Lys	Xaa
	530					535					540				
His	Glu	Gly	Pro	His	Lys	Phe	His	His	Cys	Ser	Pro	Phe	Val	Asn	His
545					550					555					560
Ser	Gly	Cys	Gly	Phe	Asn	Ser	Cys	Leu	Ser	Arg	Trp				
			565						570						

(2) INFORMATION FOR SEQ ID NO:3480:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 81 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...81
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3480:

Val	Gln	Val	Leu	Gln	Gly	Pro	Phe	Glu	Tyr	Trp	Arg	Ile	Thr	Gln	Val
1				5					10					15	
Arg	Leu	Lys	Gly	Thr	Val	Leu	Lys	Thr	Val	Arg	Arg	Val	Lys	Ala	Cys
			20					25					30		
Val	Gly	Ser	Asn	Pro	Thr	Ser	Ser	Phe	Tyr	Ile	Ile	Asn	Ala	Gly	Trp
		35					40					45			
Ser	Ser	Ser	Val	Ala	Arg	Arg	Ala	His	Asn	Pro	Lys	Val	Val	Gly	Ser
	50					55				60					
Asn	Pro	Ala	Pro	Ala	Ile	Arg	Leu	Gly	Ser	Ser	Val	Gly	Arg	Ala	Met
65					70				75						80
Asp															

(2) INFORMATION FOR SEQ ID NO:3481:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 62 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...62

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3481:

Ser	Glu	Val	Leu	Asp	Ser	Arg	Gly	Asn	Pro	Thr	Leu	Glu	Val	Glu	Val
1				5				10						15	
Tyr	Thr	Glu	Ser	Gly	Ala	Phe	Gly	Arg	Gly	Met	Val	Pro	Ser	Arg	Ser
			20				25						30		
Phe	Leu	Leu	Val	Asn	Thr	Lys	Gln	Leu	Asn	Phe	Ala	Thr	Val	Thr	Asn
		35				40					45				
Leu	Val	Thr	Val	Val	Leu	Val	His	Lys	Lys	Leu	Leu	Thr	Thr		
	50					55					60				

(2) INFORMATION FOR SEQ ID NO:3482:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 61 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...61

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3482:

Thr	Gln	Tyr	Lys	Lys	Ser	Leu	Leu	Pro	Ser	Ser	Leu	Tyr	Ser	Met	Lys
1				5				10						15	
Ile	Lys	Glu	Gln	Thr	Arg	Lys	Leu	Ala	Thr	Gly	Cys	Ser	Lys	His	Arg
			20				25						30		
Phe	Glu	Val	Val	Asp	Lys	Thr	Asp	Glu	Val	Ser	Ser	Lys	His	Cys	Phe
		35				40					45				
Glu	Val	Ala	Asp	Ile	Arg	Gln	Gly	Asp	Ala	Asp	Val	Val			
	50					55					60				

(2) INFORMATION FOR SEQ ID NO:3483:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 360 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...360

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3483:

Leu	Leu	Tyr	Lys	Ile	Phe	Phe	Leu	Phe	Cys	Ile	Trp	Ser	Leu	Ser	Phe
1			5						10				15		
Ile	Lys	His	Ile	Ser	Val	Ile	Gln	Ile	Thr	Ile	Asn	Thr	Glu	Ile	Phe
			20					25					30		
Met	Pro	Val	Thr	Ile	Lys	Asp	Val	Ala	Lys	Ala	Ala	Gly	Val	Ser	Pro
		35					40					45			
Ser	Thr	Val	Thr	Arg	Val	Ile	Gln	Asn	Lys	Ser	Thr	Ile	Ser	Asp	Glu
	50					55					60				
Thr	Lys	Lys	Arg	Val	Arg	Lys	Ala	Met	Lys	Glu	Leu	Asn	Tyr	His	Pro
65					70					75					80
Asn	Leu	Asn	Ala	Arg	Ser	Leu	Val	Ser	Ser	Tyr	Thr	Gln	Val	Ile	Gly
			85						90					95	
Leu	Val	Leu	Pro	Asp	Asp	Ser	Asp	Ala	Phe	Tyr	Gln	Asn	Pro	Phe	Phe
			100					105					110		
Pro	Ser	Val	Leu	Arg	Gly	Ile	Ser	Gln	Val	Ala	Ser	Glu	Asn	His	Tyr
		115					120					125			
Ala	Ile	Gln	Ile	Ala	Thr	Gly	Lys	Asp	Glu	Lys	Glu	Arg	Leu	Asn	Ala
	130					135					140				
Ile	Ser	Gln	Met	Val	Tyr	Gly	Lys	Arg	Val	Asp	Gly	Leu	Ile	Phe	Leu
145					150					155					160
Tyr	Ala	Gln	Glu	Glu	Asp	Pro	Leu	Val	Lys	Leu	Val	Ala	Glu	Glu	Gln
				165					170					175	
Phe	Pro	Phe	Leu	Ile	Leu	Gly	Lys	Ser	Leu	Ser	Pro	Phe	Ile	Pro	Leu
			180					185					190		
Val	Asp	Asn	Asp	Asn	Val	Gln	Ala	Gly	Phe	Asp	Ala	Thr	Glu	Tyr	Phe
		195					200					205			
Ile	Lys	Lys	Gly	Cys	Lys	Arg	Ile	Ala	Phe	Ile	Gly	Gly	Ser	Lys	Lys
	210					215					220				
Leu	Phe	Val	Thr	Lys	Asp	Arg	Leu	Thr	Gly	Tyr	Glu	Gln	Ala	Leu	Lys
225					230					235					240
His	Tyr	Lys	Leu	Thr	Thr	Asp	Asn	Asn	Arg	Ile	Tyr	Phe	Ala	Asp	Glu
				245					250					255	
Phe	Leu	Glu	Glu	Lys	Gly	Tyr	Lys	Phe	Ser	Lys	Arg	Leu	Phe	Lys	His
		260					265						270		
Asp	Pro	Gln	Ile	Asp	Ala	Ile	Ile	Thr	Thr	Asp	Ser	Leu	Leu	Ala	Glu
		275					280						285		
Gly	Val	Cys	Asn	Tyr	Ile	Ala	Lys	His	Gln	Leu	Asp	Val	Pro	Val	Leu
	290					295					300				
Ser	Phe	Asp	Ser	Val	Asn	Pro	Lys	Leu	Asn	Leu	Ala	Ala	Tyr	Val	Asp
305					310					315					320
Ile	Asn	Ser	Leu	Glu	Leu	Gly	Arg	Val	Ser	Leu	Glu	Thr	Ile	Leu	Gln
				325						330				335	
Ile	Ile	Asn	Asp	Asn	Lys	Asn	Asn	Lys	Gln	Ile	Cys	Tyr	Arg	Gln	Leu
			340				345						350		
Ile	Ala	His	Lys	Ile	Ile	Glu	Lys								
		355					360								

(2) INFORMATION FOR SEQ ID NO:3484:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 136 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...136

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3484:

Gln	Ser	Val	Leu	Met	Leu	Thr	Phe	Val	Gln	Ile	Gln	Val	Trp	Val	Pro
1				5				10				15			
Gln	Val	His	Ile	Gly	Asn	Phe	Val	Glu	Val	Lys	Gly	Ser	Ser	Ile	Gly
		20						25				30			
Glu	Asn	Thr	Lys	Ala	Gly	His	Leu	Thr	Tyr	Ile	Gly	Asn	Cys	Glu	Val
		35				40						45			
Gly	Ser	Asn	Val	Asn	Phe	Gly	Ala	Gly	Thr	Ile	Thr	Val	Asn	Tyr	Asp
	50					55					60				
Gly	Lys	Asn	Lys	Tyr	Lys	Thr	Val	Ile	Gly	Val	Asn	Val	Phe	Val	Gly
65				70					75					80	
Ser	Asn	Ser	Thr	Ile	Ile	Ala	Pro	Val	Glu	Leu	Gly	Asp	Asn	Ser	Leu
				85					90					95	
Val	Gly	Ala	Gly	Ser	Thr	Ile	Thr	Lys	Asp	Val	Pro	Ala	Asp	Ala	Ile
		100						105				110			
Ala	Ile	Gly	Arg	Gly	Arg	Gln	Ile	Asn	Lys	Asp	Glu	Tyr	Ala	Thr	Arg
		115				120						125			
Leu	Pro	His	His	Pro	Lys	Asn	Gln								
	130					135									

(2) INFORMATION FOR SEQ ID NO:3485:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 121 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3485:

Ile Leu Asn Lys Leu Leu Ser Tyr Ser Gln Asp Leu Lys His His Tyr

1				5					10					15		
Gln	Leu	Tyr	Gln	Leu	Leu	Leu	Phe	His	Phe	Gln	Asn	Lys	Glu	Pro	Glu	
			20					25					30			
Lys	Phe	Phe	Gly	Leu	Ile	Glu	Asp	Asn	Leu	Lys	Gln	Ala	His	Pro	Leu	
		35					40					45				
Phe	Gln	Thr	Val	Phe	Lys	Thr	Phe	Leu	Lys	Asp	Lys	Glu	Lys	Ile	Val	
				50				55					60			
Asn	Ala	Leu	Gln	Leu	His	Tyr	Ser	Asn	Ala	Lys	Leu	Glu	Ala	Thr	Asn	
65					70					75					80	
Asn	Leu	Ile	Lys	Leu	Ile	Lys	Arg	Asn	Ala	Phe	Gly	Phe	Arg	Asn	Phe	
			85					90					95			
Glu	Asn	Phe	Lys	Lys	Arg	Ile	Phe	Ile	Ala	Leu	Asn	Ile	Lys	Lys	Glu	
			100					105					110			
Arg	Thr	Lys	Phe	Val	Leu	Ser	Arg	Ala								
		115					120									

(2) INFORMATION FOR SEQ ID NO:3486:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3486:

Leu	Val	Asn	Lys	Met	Ser	Lys	Asn	Ser	Ile	Phe	Leu	Leu	Lys	Lys	Arg	
1				5					10					15		
Ser	Leu	Lys	Gly	Lys	Glu	Ser	Asp	Met	Arg	Gln	Leu	Ala	Lys	Asp	Ile	
			20					25					30			
Asn	Ala	Phe	Leu	Asn	Glu	Val	Ile	Leu	Gln	Ala	Glu	Asn	Gln	His	Glu	
		35					40					45				
Ile	Leu	Ile	Gly	His	Cys	Thr	Ser	Glu	Val	Ala	Leu	Thr	Asn	Thr	Gln	
	50					55					60					
Glu	His	Ile	Leu	Met	Leu	Leu	Ser	Glu	Glu	Ser	Leu	Thr	Asn	Ser	Glu	
65				70						75					80	
Leu	Ala	Arg	Arg	Leu	Asn	Val	Ser	Gln	Ala	Ala	Val	Thr	Lys	Ala	Ile	
			85					90					95			
Lys	Ser	Leu	Val	Lys	Glu	Gly	Met	Leu	Glu	Thr	Ser	Lys	Asp	Ser	Lys	
		100						105					110			
Asp	Ala	Arg	Val	Ile	Phe	Tyr	Gln	Leu	Thr	Asp	Leu	Ala	Arg	Pro	Ile	
		115					120					125				
Ala	Glu	Glu	His	His	His	His	His	Glu	His	Thr	Leu	Leu	Thr	Tyr	Glu	
	130					135					140					
Gln	Val	Ala	Thr	Gln	Phe	Thr	Pro	Asn	Glu	Gln	Lys	Val	Ile	Gln	Arg	
145					150					155					160	

Phe Leu Thr Ala Leu Val Gly Glu Ile Lys
165 170

(2) INFORMATION FOR SEQ ID NO:3487:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...379

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3487:

Ile	Met	Asn	Asn	Thr	Glu	Phe	Tyr	Asp	Arg	Leu	Gly	Val	Ser	Lys	Asn
1				5					10					15	
Ala	Ser	Ala	Asp	Glu	Ile	Lys	Lys	Ala	Tyr	Arg	Lys	Leu	Ser	Lys	Lys
			20					25					30		
Tyr	His	Pro	Asp	Ile	Asn	Lys	Glu	Pro	Gly	Ala	Glu	Asp	Lys	Tyr	Lys
		35					40					45			
Glu	Val	Gln	Glu	Ala	Tyr	Glu	Thr	Leu	Ser	Asp	Asp	Gln	Lys	Arg	Ala
	50					55					60				
Ala	Tyr	Asp	Gln	Tyr	Gly	Ala	Ala	Gly	Ala	Asn	Gly	Gly	Phe	Gly	Gly
65					70					75					80
Ala	Gly	Gly	Phe	Gly	Gly	Phe	Asn	Gly	Ala	Gly	Gly	Phe	Gly	Gly	Phe
			85					90						95	
Glu	Asp	Ile	Phe	Ser	Ser	Phe	Phe	Gly	Gly	Gly	Gly	Ser	Ser	Arg	Asn
		100						105					110		
Pro	Asn	Ala	Pro	Arg	Gln	Gly	Asp	Asp	Leu	Gln	Tyr	Arg	Val	Asn	Leu
	115					120						125			
Thr	Phe	Glu	Glu	Ala	Ile	Phe	Gly	Thr	Glu	Lys	Glu	Val	Lys	Tyr	His
	130					135					140				
Arg	Glu	Ala	Gly	Cys	Arg	Thr	Cys	Asn	Gly	Ser	Gly	Ala	Lys	Pro	Gly
145				150						155					160
Thr	Ser	Pro	Val	Thr	Cys	Gly	Arg	Cys	His	Gly	Ala	Gly	Val	Ile	Asn
			165						170					175	
Val	Asp	Thr	Gln	Thr	Pro	Leu	Gly	Met	Met	Arg	Arg	Gln	Val	Thr	Cys
		180						185					190		
Asp	Val	Cys	His	Gly	Arg	Gly	Lys	Glu	Ile	Lys	Tyr	Pro	Cys	Thr	Thr
	195						200					205			
Cys	His	Gly	Thr	Gly	His	Glu	Lys	Gln	Ala	His	Ser	Val	His	Val	Lys
	210					215					220				
Ile	Pro	Ala	Gly	Val	Glu	Thr	Gly	Gln	Gln	Ile	Arg	Leu	Ala	Gly	Gln
225				230						235					240
Gly	Glu	Ala	Gly	Phe	Asn	Gly	Gly	Pro	Tyr	Gly	Asp	Leu	Tyr	Val	Val
			245						250					255	
Val	Ser	Val	Glu	Ala	Ser	Asp	Lys	Phe	Glu	Arg	Glu	Gly	Thr	Thr	Ile
			260					265						270	

Phe Tyr Asn Leu Asn Leu Asn Phe Val Gln Ala Ala Leu Gly Asp Thr
 275 280 285
 Val Asp Ile Pro Thr Val His Gly Asp Val Glu Leu Val Ile Pro Glu
 290 295 300
 Gly Thr Gln Thr Gly Lys Lys Phe Arg Leu Arg Ser Lys Gly Ala Pro
 305 310 315 320
 Ser Leu Arg Gly Gly Ala Val Gly Asp Gln Tyr Val Thr Val Asn Val
 325 330 335
 Val Thr Pro Thr Gly Leu Asn Asp Arg Gln Lys Val Ala Leu Lys Glu
 340 345 350
 Phe Ala Ala Ala Gly Gly Leu Lys Val Asn Pro Lys Lys Lys Gly Phe
 355 360 365
 Phe Asp His Ile Lys Asp Ala Phe Asp Gly Glu
 370 375

(2) INFORMATION FOR SEQ ID NO:3488:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...71

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3488:

Leu Ser Asn Lys Phe Tyr Asp Ser Tyr Leu Val Gly Met Leu Leu Phe
 1 5 10 15
 Phe Ile Arg Gln Asn Lys Arg Ile Lys Gly Val Asn Phe Leu Asn Pro
 20 25 30
 Ile Val Leu Ile Leu Asp Val Val Arg Asn Leu Gln Ser Ser Ala Pro
 35 40 45
 Phe Leu Val Asp Ser Glu Trp Ser Ala Tyr Thr Gly Asn Leu Leu Glu
 50 55 60
 Val Pro Arg Arg Gln Leu Ala
 65 70

(2) INFORMATION FOR SEQ ID NO:3489:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3489:

```
Tyr Glu Asn Lys Gly Glu Tyr Met Thr Leu Glu Trp Glu Glu Phe Leu
1      5      10      15
Asp Pro Tyr Ile Gln Ala Val Gly Glu Leu Lys Ile Lys Leu Arg Gly
20      25      30
Ile Arg Lys Gln Tyr Arg Lys Gln Asn Lys His Ser Pro Ile Glu Phe
35      40      45
Val Thr Gly Arg Val Lys Pro Ile Glu Ser Ile Lys Glu Lys Met Ala
50      55      60
Arg Arg Gly Ile Thr Tyr Ala Thr Leu Glu His Asp Leu Gln Asp Ile
65      70      75      80
Ala Gly Leu Arg Val Met Val Gln Phe Val Asp Asp Val Lys Glu Val
85      90      95
Val Asp Ile Leu His Lys Arg Gln Asp Met Arg Ile Ile Gln Glu Arg
100     105     110
Asp Tyr Ile Thr His Arg Lys Ala Ser Gly Tyr Arg Ser Tyr His Val
115     120     125
Val Val Glu Tyr Thr Val Asp Thr Ile Asn Gly Ala Lys Thr Ile Leu
130     135     140
Ala Glu Ile Gln Ile Arg Thr Leu Ala Met Asn Phe Trp Ala Thr Ile
145     150     155     160
Glu His Ser Leu Asn Tyr Lys Tyr Gln Gly Asp Phe Pro Val
165     170
```

(2) INFORMATION FOR SEQ ID NO:3490:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 664 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...664

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3490:

```
Glu Val Asp Lys Met Asn Gln Thr Val Leu Asp Val Lys Asn Leu Lys
1      5      10      15
Thr Glu Phe Ile Thr Asp Lys Lys Ala Phe Pro Ile Ile Lys Asp Val
20      25      30
Asn Phe Thr Leu Glu Arg Gly Lys Val Leu Gly Ile Val Gly Glu Ser
```

		35				40				45					
Gly	Cys	Gly	Lys	Ser	Val	Thr	Val	Asn	Thr	Val	Leu	Asn	Leu	Leu	Pro
	50					55				60					
Lys	Asn	Gly	Arg	Ile	Ala	Glu	Gly	Glu	Ile	Thr	Tyr	Phe	Asp	Glu	Asp
65					70					75				80	
Lys	Pro	Ile	Glu	Leu	Gln	Lys	Leu	Lys	Gln	Tyr	Gly	Lys	Glu	Phe	Arg
			85						90					95	
Lys	Leu	Arg	Gly	Glu	Asn	Ile	Ser	Met	Ile	Phe	Gln	Asp	Pro	Met	Ser
		100						105					110		
Ala	Leu	Asn	Pro	Val	Tyr	Thr	Ile	Gly	Asn	Gln	Ile	Thr	Glu	Val	Leu
	115						120					125			
His	Glu	His	Tyr	Asp	Ile	Ser	Lys	Glu	Glu	Ala	Asn	Lys	Arg	Ala	Ile
	130					135					140				
Glu	Met	Leu	Glu	Lys	Leu	Gly	Ile	His	Asn	Ala	Ala	Glu	Arg	Met	Asn
145					150					155					160
Asp	Tyr	Pro	His	Gln	Phe	Ser	Gly	Gly	Gln	Arg	Gln	Arg	Ile	Val	Ile
				165					170					175	
Ala	Ile	Ala	Met	Val	Cys	Asn	Pro	Asp	Ile	Leu	Ile	Ala	Asp	Glu	Pro
		180						185					190		
Thr	Thr	Ala	Leu	Asp	Val	Thr	Ile	Gln	Ala	Gln	Ile	Leu	Asp	Leu	Leu
	195						200					205			
Asp	Asp	Leu	Arg	Lys	Glu	His	Gly	Thr	Ser	Ile	Ile	Leu	Ile	Thr	His
	210					215					220				
Asp	Leu	Gly	Val	Ile	Ala	Gln	Ile	Ala	Asp	Glu	Val	Ala	Val	Met	Tyr
225					230					235					240
Ala	Gly	Glu	Val	Val	Glu	Val	Gly	Thr	Val	Ala	Gln	Ile	Phe	Asp	Gln
			245						250					255	
Pro	Lys	His	Pro	Tyr	Thr	Arg	Ser	Leu	Leu	Arg	Ser	Ile	Pro	Asn	Pro
		260						265					270		
Glu	Asn	Met	Asp	Lys	Lys	Leu	His	Val	Ile	Gln	Gly	Ser	Val	Pro	Ser
	275						280					285			
Ile	Ser	Glu	Ile	Ser	Glu	Lys	Gly	Cys	Arg	Phe	Ala	Asn	Arg	Ile	Pro
	290					295				300					
Trp	Leu	Glu	Lys	Glu	His	His	Glu	Glu	Glu	Pro	Gln	Leu	His	Asp	Leu
305					310					315					320
Gly	Asp	Gly	His	Phe	Val	Arg	Cys	Ser	Cys	Tyr	Lys	His	Phe	Phe	Phe
			325						330					335	
Glu	Asp	Lys	Glu	Glu	Glu	Thr	Leu	Ala	Glu	Lys	His	Val	Gly	Asn	Val
		340						345					350		
Val	Leu	Glu	Val	Lys	Asn	Ile	Lys	Lys	Tyr	Tyr	Tyr	Pro	Lys	Lys	Gln
	355						360					365			
Leu	Phe	Lys	Pro	Leu	Gly	Ser	Pro	Leu	Lys	Ala	Leu	Asp	Asp	Val	Ser
	370					375					380				
Leu	Glu	Leu	Arg	Lys	Gly	Thr	Thr	Ile	Gly	Ile	Val	Gly	Glu	Ser	Gly
385					390					395					400
Ser	Gly	Lys	Ser	Thr	Ile	Ala	Lys	Ser	Leu	Met	Lys	Leu	His	Asp	Ile
			405						410					415	
Thr	Asp	Gly	Glu	Ile	Asn	Ile	Asp	Leu	Asn	Gly	Lys	Thr	Gln	Asn	Ile
		420						425					430		
Tyr	Gly	Ile	Lys	Arg	Lys	Glu	Asp	Leu	Asp	Phe	Arg	Lys	Lys	Val	Gln
	435						440					445			
Met	Val	Phe	Gln	Asp	Pro	Tyr	Ala	Ser	Leu	Asn	Pro	Thr	Lys	Lys	Ile
	450					455					460				
Tyr	Asn	Ser	Phe	Asp	Glu	Pro	Met	Ile	Val	His	Asn	Ile	Gly	Asn	Lys
465					470					475					480
Glu	Glu	Arg	Phe	Glu	Arg	Met	Lys	Glu	Ala	Leu	Lys	Met	Val	Asn	Val
			485						490					495	

```

Pro Val Glu Tyr Leu Glu Arg Tyr Pro His Glu Phe Ser Gly Gly Gln
      500                      505                      510
Arg Gln Arg Arg Leu Cys Ile Ala Arg Ala Leu Cys Met Lys Pro Glu Ile
      515                      520                      525
Leu Ile Leu Asp Glu Pro Val Ser Ala Leu Asp Leu Ser Val Gln Ala
      530                      535                      540
Gln Val Leu Asn Tyr Leu Val Glu Ile Gln Asn Lys Glu Asp Leu Thr
      545                      550                      555                      560
Tyr Val Phe Ile Ser His Asp Leu Gly Val Val Lys Tyr Met Cys Asp
      565                      570                      575
Tyr Leu Tyr Val Ile His Lys Gly Arg Ile Val Glu Ala Gly Ser Arg
      580                      585                      590
Glu Asp Ile Tyr Asn Asn Pro Met His Ile Tyr Thr Lys Lys Leu Leu
      595                      600                      605
Ala Ala Ile Pro Glu Val Asp Tyr His Phe Lys Glu Ala Leu Ala Thr
      610                      615                      620
Lys Arg Lys Glu Asn Glu Val Glu Phe Lys Ala Gln Tyr His Glu Phe
      625                      630                      635                      640
Tyr Asp Glu Asp Gly Arg Ala Tyr Asp Leu Lys Gln Val Ser Pro Thr
      645                      650                      655
His Phe Val Ala Leu Lys Pro Glu
      660

```

(2) INFORMATION FOR SEQ ID NO:3491:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 78 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...78
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3491:

```

Asn Tyr Asp Lys Thr His Ser Gln Glu Gly Tyr Asp Ile Leu Lys Gly
1           5           10           15
Glu Gly Gly Cys Ile Val Cys Pro Thr Lys Val Gly Tyr Ile Ile Met
      20           25           30
Thr Ser Asn Lys Ala Gly Leu Glu Arg Lys Phe Ala Ala Lys Glu Arg
      35           40           45
Lys Arg Asn Lys Pro Gly Val Val Leu Cys Gly Ser Met Asp Glu Leu
      50           55           60
Arg Ala Leu Ala Gln Leu Asn Pro Glu Ile Glu Ala Phe Tyr
      65           70           75

```

(2) INFORMATION FOR SEQ ID NO:3492:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 168 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...168

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3492:

Ser	Pro	Cys	Lys	Lys	Val	Ala	His	Arg	Val	Ala	Phe	Phe	Asp	Tyr	Ser
1				5					10					15	
Lys	Gly	Gly	Asp	Gly	Lys	Leu	Ser	Gly	Leu	Arg	Ile	Lys	Gln	Lys	Arg
			20					25					30		
Phe	Ala	Asp	Glu	Tyr	Ile	Ile	Ser	Gly	Asn	Ala	Thr	Glu	Ala	Tyr	Lys
		35					40					45			
Lys	Ala	Gly	Tyr	Arg	Val	Ser	Ser	Asp	Arg	Val	Ala	Gly	Val	Glu	Gly
	50					55				60					
His	Lys	Leu	Leu	Lys	Asn	Pro	Lys	Ile	Lys	Ser	Tyr	Ile	Asp	Glu	Arg
65					70					75				80	
Leu	Lys	Gln	Leu	Asp	Ser	Glu	Lys	Ile	Ala	Asp	Gln	Gln	Glu	Val	Leu
			85						90					95	
Gly	Tyr	Leu	Thr	Ser	Val	Met	Arg	Gly	Glu	Thr	Gln	Glu	Gln	Thr	Leu
		100						105					110		
Ile	Ser	Ile	Gly	Glu	Leu	Gly	Gln	Thr	Ile	Thr	Asp	Ile	Asp	Val	Gly
	115					120						125			
Ala	Lys	Asp	Arg	Ile	Lys	Ala	Ala	Glu	Leu	Leu	Gly	Lys	Arg	His	Arg
	130					135					140				
Leu	Trp	Thr	Asp	Lys	Val	Glu	Ala	Asp	Val	Ser	Gly	Thr	Val	Val	Phe
145					150					155					160
Ala	Asn	Glu	Ser	Asp	Ile	Ser	Asp								
				165											

(2) INFORMATION FOR SEQ ID NO:3493:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 87 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...87

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3493:

Cys	Val	Cys	Lys	Ala	Arg	Gln	Lys	Gly	Phe	Asp	Val	Val	Val	Glu	Ile
1				5					10					15	
Leu	His	His	Ile	Leu	Gln	Glu	Asp	Val	Gln	Ile	Val	Leu	Leu	Gly	Thr
			20					25					30		
Gly	Asp	Pro	Ala	Phe	Glu	Gly	Ala	Phe	Ser	Trp	Phe	Ala	Gln	Ile	Tyr
		35					40					45			
Pro	Asp	Lys	Leu	Ser	Ala	Asn	Ile	Thr	Phe	Asp	Val	Lys	Leu	Ala	Gln
		50				55					60				
Glu	Ile	Tyr	Gly	Ala	Cys	Asp	Leu	Phe	Leu	Met	Pro	Ser	Arg	Phe	Glu
65					70				75						80
Pro	Tyr	Gly	Leu	Ser	Tyr	Met									
					85										

(2) INFORMATION FOR SEQ ID NO:3494:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...79

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3494:

Gly	Leu	Cys	Lys	Arg	Ser	Ile	Gly	Phe	Asn	Glu	Val	Glu	Glu	Asn	Ile
1				5					10					15	
Asn	Gln	Gly	Thr	Gly	Gln	Ile	Thr	Thr	Phe	Asn	Gln	Leu	Gly	Phe	Lys
			20					25					30		
Gly	Tyr	Ser	Asp	Lys	Pro	Asp	Gly	Trp	Tyr	Leu	Pro	Lys	Asn	Met	Asn
		35					40					45			
Asp	Val	Ala	Ile	Ile	Leu	Glu	Thr	Lys	Ser	Glu	Glu	Arg	Asp	Ile	Ser
		50				55					60				
Lys	Gln	Ile	Phe	Ile	Asp	Glu	Leu	Met	Lys	Asn	Ile	Asp	Ile	Ile	
65					70				75						

(2) INFORMATION FOR SEQ ID NO:3495:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3495:

Gly	Lys	Cys	Asn	Gly	Lys	Pro	Asn	Phe	Arg	Arg	Lys	Lys	Val	Asn	Thr
1				5					10					15	
Asp	Tyr	Ile	Ala	Arg	Tyr	Gly	Val	Tyr	Ala	Val	Ile	Pro	Asn	Pro	Glu
			20					25					30		
Gln	Lys	Gln	Ile	Val	Leu	Val	Gln	Glu	Pro	Asn	Gly	Ala	Trp	Phe	Leu
		35					40					45			
Pro	Cys	Gly	Lys	Ile	Glu	Ala	Gly	Glu	Asn	His	Gln	Glu	Ala	Leu	Lys
	50					55					60				
Arg	Glu	Leu	Ile	Glu	Glu	Leu	Gly	Phe	Thr	Ala	Glu	Ile	Gly	Thr	Tyr
65					70					75					80
Tyr	Gly	Gln	Ala	Asp	Glu	Tyr	Phe	Tyr	Ser	Arg	His	Arg	Asp	Ala	Tyr
			85						90					95	
Tyr	Tyr	Asn	Pro	Ala	Tyr	Leu	Tyr	Glu	Ala	Thr	Pro	Phe	Lys	Glu	Val
			100					105					110		
Gln	Lys	Pro	Leu	Glu	Asn	Phe	Asn	His	Ile	Ala	Trp	Phe	Pro	Ile	Asp
		115					120					125			
Glu	Ala	Ile	Lys	Asn	Leu	Lys	Arg	Gly	Ser	His	Lys	Trp	Ala	Ile	Glu
	130					135					140				
Ser	Trp	Lys	Lys	Gln	His	Lys	Ile	Asp							
145					150										

(2) INFORMATION FOR SEQ ID NO:3496:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...72

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3496:

Ala	Tyr	Arg	Lys	Gly	Thr	Val	Phe	Ser	Ser	Ala	Lys	Pro	His	Ser	Val
1				5					10					15	
Leu	Thr	Thr	Met	Cys	Pro	Cys	His	His	Glu	Leu	Pro	Asn	Gly	Leu	Thr
			20					25					30		

Arg	Lys	Tyr	Ser	Arg	Leu	Lys	Gln	Asp	Val	Asn	Lys	Ser	Ile	Arg	Lys
	35						40					45			
Val	Lys	Leu	Ile	Ser	Arg	Asn	Ile	Leu	Thr	Val	Ile	Thr	Asp	Tyr	Ser
	50					55					60				
Arg	Phe	Asn	Leu	Leu	Tyr	Tyr	Phe								
65					70										

(2) INFORMATION FOR SEQ ID NO:3497:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...406

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3497:

Cys	Arg	Arg	Lys	Ala	Ser	Thr	Ile	Ile	Tyr	Ser	Ile	Asn	Lys	Glu	Asn
1			5						10					15	
Val	Met	Asn	Pro	Asn	Leu	Phe	Arg	Ser	Val	Glu	Phe	Tyr	Gln	Arg	Arg
			20					25					30		
Tyr	His	Asn	Tyr	Ala	Thr	Val	Phe	Ile	Ile	Pro	Leu	Ser	Leu	Leu	Phe
		35					40					45			
Thr	Phe	Ile	Leu	Ile	Phe	Ser	Leu	Val	Ala	Thr	Lys	Glu	Ile	Thr	Val
	50					55					60				
Thr	Ser	Gln	Gly	Glu	Ile	Ala	Pro	Thr	Ser	Val	Ile	Ala	Ser	Ile	Gln
65					70				75					80	
Ser	Thr	Ser	Asp	Asn	Pro	Ile	Leu	Ala	Asn	His	Leu	Val	Ala	Asn	Gln
				85					90					95	
Val	Val	Glu	Lys	Gly	Asp	Leu	Leu	Ile	Lys	Tyr	Ser	Glu	Thr	Met	Glu
			100					105					110		
Glu	Ser	Gln	Lys	Thr	Ala	Leu	Ala	Thr	Gln	Leu	Gln	Arg	Leu	Glu	Lys
		115					120					125			
Gln	Lys	Glu	Gly	Leu	Gly	Ile	Leu	Lys	Gln	Ser	Leu	Glu	Lys	Ala	Thr
		130				135					140				
Asp	Leu	Phe	Ser	Ser	Glu	Asp	Glu	Phe	Gly	Tyr	His	Asn	Thr	Phe	Met
145					150					155					160
Asn	Phe	Thr	Lys	Gln	Ser	His	Asp	Ile	Glu	Leu	Gly	Ile	Ser	Lys	Thr
				165					170					175	
Asn	Thr	Glu	Val	Ser	Asn	Gln	Ala	Asn	Leu	Thr	Asn	Ser	Ser	Ser	Ser
			180					185					190		
Ala	Ile	Glu	Gln	Glu	Ile	Thr	Lys	Val	Gln	Gln	Gln	Ile	Gly	Glu	Tyr
		195					200					205			
Gln	Glu	Leu	Arg	Asp	Ala	Ile	Ile	Asn	Asn	Arg	Ala	Arg	Leu	Pro	Thr
	210					215					220				
Gly	Asn	Pro	His	Gln	Ser	Ile	Leu	Asn	Arg	Tyr	Leu	Ile	Ala	Ser	Gln

225		230		235		240									
Gly	Gln	Thr	Gln	Gly	Thr	Ala	Glu	Glu	Pro	Phe	Leu	Ser	Gln	Ile	Asn
		245		250		255									
Gln	Ser	Ile	Ala	Gly	Leu	Glu	Ser	Ser	Ile	Ala	Ser	Leu	Lys	Ile	Gln
		260		265		270									
Gln	Ala	Gly	Ile	Gly	Ser	Val	Ala	Thr	Tyr	Asp	Asn	Ser	Leu	Ala	Thr
		275		280		285									
Lys	Ile	Glu	Val	Leu	Arg	Thr	Gln	Phe	Leu	Gln	Thr	Ala	Ser	Gln	Gln
		290		295		300									
Gln	Leu	Thr	Val	Glu	Asn	Gln	Leu	Thr	Glu	Leu	Lys	Val	Gln	Leu	Asp
305				310		315									
Gln	Ala	Thr	Gln	Arg	Leu	Glu	Asn	Asn	Thr	Leu	Thr	Ala	Pro	Ser	Lys
				325		330									
Gly	Ile	Val	His	Leu	Asn	Ser	Glu	Phe	Glu	Gly	Lys	Asn	Arg	Ile	Pro
				340		345									
Thr	Gly	Thr	Glu	Ile	Ala	Gln	Ile	Phe	Pro	Val	Ile	Thr	Asp	Thr	Arg
				355		360									
Glu	Val	Leu	Ile	Thr	Tyr	Tyr	Val	Ser	Ser	Asp	Tyr	Leu	Pro	Leu	Leu
				370		375									
Asp	Lys	Gly	Gln	Thr	Val	Arg	Leu	Lys	Leu	Glu	Lys	Asn	Gly	Asn	His
385				390		395									
Gly	Thr	Thr	Ile	Ile	Gly										
				405											

(2) INFORMATION FOR SEQ ID NO:3498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...63

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3498:

Leu	Arg	Arg	Asn	Ile	Pro	Glu	Gly	Tyr	Phe	Gly	Lys	Ile	Asn	Gln	Phe
1			5					10					15		
Met	Glu	Gln	Val	Tyr	Ser	Gln	Gly	Ile	Ile	Tyr	Pro	Pro	Lys	Glu	Lys
			20					25					30		
Val	Phe	Gln	Ala	Leu	Leu	Thr	Thr	Leu	Leu	Glu	Glu	Val	Lys	Val	Val
			35					40					45		
Ile	Leu	Gly	Lys	Thr	Pro	Ile	Thr	Asp	Gln	Val	Lys	Arg	Arg	Ala	
50						55						60			

(2) INFORMATION FOR SEQ ID NO:3499:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...306

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3499:

```

Leu Leu Ser Lys Val Gln Pro Met Leu Lys Ile Leu Thr Thr Asn Glu
1      5      10      15
Phe Arg Asn Tyr Leu Asp Glu Leu Gly Asp Ser Leu Leu Val Val Asn
20      25      30
Asp Asp Glu Ile Val Lys Val His Val His Thr Glu Asp Pro Gly Leu
35      40      45
Val Met Gln Glu Gly Leu Lys Tyr Gly Ser Leu Val Lys Val Lys Val
50      55      60
Asp Asn Met Arg Asn Gln His Glu Ala Gln Val Glu Lys Glu Ala Thr
65      70      75      80
Gln Val Ile Lys Ser Ala Glu Glu Lys Glu Tyr Ala Leu Ile Ala Val
85      90      95
Val Ala Gly Lys Gly Leu Ala Asp Ile Phe Cys Ser Gln Gly Val Asp
100     105     110
Tyr Val Ile Glu Gly Gly Gln Thr Met Asn Pro Ser Thr Glu Asp Phe
115     120     125
Ile Lys Ala Val Glu Gln Val Asn Ala Arg Asn Ile Ile Phe Leu Pro
130     135     140
Asn Asn Lys Asn Ile Phe Met Ala Ala Gln Ser Ala Ala Glu Val Leu
145     150     155     160
Glu Gln Pro Ala Val Val Val Glu Ala Arg Thr Leu Pro Gln Gly Met
165     170     175
Thr Ser Leu Leu Ala Phe Asp Pro Ser Lys Ser Ile Glu Glu Asn Gln
180     185     190
Glu Arg Met Thr Ala Ala Leu Ser Asp Val Val Ser Gly Ser Val Thr
195     200     205
Thr Ala Val Arg Asp Thr Thr Ile Asp Gly Leu Glu Ile His Glu Asn
210     215     220
Asp Asn Leu Gly Met Val Asp Gly Lys Ile Leu Val Ser Asn Pro Asp
225     230     235     240
Met His Gln Thr Leu Thr Glu Thr Leu Lys His Met Leu Asp Glu Asp
245     250     255
Ser Glu Ile Val Thr Phe Tyr Val Gly Glu Asp Gly Ser Glu Glu Leu
260     265     270
Ala Asn Glu Ile Ala Gln Glu Ile Val Glu Glu Phe Glu Asp Val Glu
275     280     285
Val Glu Ile His Gln Gly Gln Gln Pro Val Tyr Pro Tyr Leu Phe Ser
290     295     300
Val Glu
305

```

(2) INFORMATION FOR SEQ ID NO:3500:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 98 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...98

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3500:

```
Lys Arg Ser Lys Leu Met Lys Lys Glu Thr Phe Thr Glu Lys Leu Ile
1          5          10          15
Lys Arg Thr Tyr Gly Ile Ser Gly Pro Leu Asp Glu Tyr Lys Arg Arg
          20          25          30
Glu Ala Asp Ser Ile Gly Asn Gln Val Phe Ile Val Leu Phe Tyr Leu
          35          40          45
Met Ile Phe Gly Asn Leu Ile Pro Leu Leu Leu Ala Tyr Lys Tyr Pro
          50          55          60
Gln Glu Val Ala Leu Ile Tyr Pro Pro Leu Ile Leu Val Ile Ala Leu
65          70          75          80
Ile Ala Ala Gly Tyr Val Thr Tyr Gln Met Lys Lys Asn Arg His His
          85          90          95
Ser His
```

(2) INFORMATION FOR SEQ ID NO:3501:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...71

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3501:

```
Val Phe Leu Asn Phe Phe Ser Ser Ser Val Pro Thr Ala Thr Tyr His
1          5          10          15
```

Ser Pro Tyr Gly Ile Arg Thr Arg Val Thr Ala Val Lys Arg Arg Cys
 20 25 30
 Leu Asn Pro Leu Thr Asn Gly Pro Glu Leu Leu Phe Ser Thr Leu Thr
 35 40 45
 Ile Ile Gln Ser Phe Gln Thr Leu Ser Thr Thr Phe Ser Asn Phe Phe
 50 55 60
 His Phe Phe Cys Met Thr Tyr
 65 70

(2) INFORMATION FOR SEQ ID NO:3502:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...69

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3502:

Ala Phe Leu Asn Phe Phe Ser Ser Ser Val Pro Thr Ala Thr Tyr His
 1 5 10 15
 Ser Pro Tyr Gly Ile Arg Thr Arg Val Thr Ala Val Lys Arg Arg Cys
 20 25 30
 Leu Asn Pro Leu Thr Asn Gly Pro Glu Leu Leu Phe Ser Thr Leu Thr
 35 40 45
 Ile Ile Gln Ser Phe Tyr Val Leu Ser Thr Thr Phe Ser Asn Phe Phe
 50 55 60
 Tyr Phe Phe Asn Leu
 65

(2) INFORMATION FOR SEQ ID NO:3503:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3503:

Met	Asn	Leu	Asn	Gln	Leu	Asp	Ile	Ile	Val	Ser	Asn	Val	Pro	Gln	Val
1			5						10					15	
Cys	Ala	Asp	Leu	Glu	His	Ile	Leu	Asp	Lys	Lys	Ala	Asp	Tyr	Ala	Asp
			20					25					30		
Asp	Gly	Phe	Ala	Gln	Phe	Thr	Ile	Gly	Ser	His	Cys	Leu	Met	Leu	Ser
		35					40					45			
Gln	Asn	His	Leu	Val	Pro	Leu	Glu	Asn	Phe	Gln	Ser	Gly	Ile	Ile	Ile
	50					55					60				
His	Ile	Glu	Val	Glu	Asp	Val	Asp	Gln	Asn	Tyr	Lys	Arg	Leu	Asn	Glu
65					70					75					80
Leu	Gly	Ile	Lys	Val	Leu	His	Gly	Pro	Thr	Val	Thr	Asp	Trp	Gly	Thr
			85						90					95	
Glu	Ser	Leu	Leu	Val	Gln	Gly	Pro	Ala	Gly	Leu	Val	Leu	Asp	Phe	Tyr
			100					105						110	
Arg	Met	Lys													
			115												

(2) INFORMATION FOR SEQ ID NO:3504:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...63

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3504:

Ile	Asp	Leu	Asn	Ser	Gln	Ile	Ile	Leu	Phe	Ser	Ser	Tyr	Phe	Ile	Leu
1			5					10						15	
Leu	Tyr	Asn	Pro	Val	Glu	Lys	Thr	Arg	Val	His	Ile	Lys	Lys	Val	Leu
			20					25					30		
Ala	Ser	Cys	Asn	Thr	Phe	Leu	Arg	Gly	Ser	Phe	Ile	Leu	Phe	Leu	Phe
		35					40					45			
Gln	Leu	Thr	Ile	Ser	Pro	Met	Val	Leu	Val	Gln	Lys	Ala	Arg	Leu	
	50					55						60			

(2) INFORMATION FOR SEQ ID NO:3505:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...267

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3505:

Gln	Ile	Ser	Leu	Lys	Leu	Ala	Ser	Ser	Ile	Ala	Cys	Leu	Tyr	Trp	Leu	
1				5					10					15		
Lys	Thr	Gly	Tyr	Phe	Lys	Phe	Ser	Phe	Arg	Pro	Ser	Gly	Met	Glu	Lys	
			20					25					30			
Ser	Val	Ile	Ile	Ile	Glu	Lys	Glu	Lys	Arg	Met	His	Lys	Ile	Leu	Leu	
			35					40					45			
Ile	Glu	Asp	Asp	Gln	Val	Ile	Arg	Gln	Gln	Val	Gly	Lys	Met	Leu	Ser	
	50						55					60				
Glu	Trp	Gly	Phe	Glu	Val	Val	Leu	Val	Glu	Asp	Phe	Met	Lys	Val	Leu	
65					70					75					80	
Ser	Leu	Phe	Val	Gln	Ser	Glu	Pro	His	Leu	Val	Leu	Met	Asp	Ile	Gly	
				85					90					95		
Leu	Pro	Leu	Phe	Asn	Gly	Tyr	His	Trp	Cys	Gln	Glu	Ile	Arg	Lys	Ile	
			100					105					110			
Ser	Lys	Val	Pro	Ile	Met	Phe	Leu	Ser	Ser	Arg	Asp	Gln	Ala	Met	Asp	
			115				120					125				
Ile	Val	Met	Ala	Ile	Asn	Met	Gly	Ala	Asp	Asp	Phe	Val	Thr	Lys	Pro	
	130					135					140					
Phe	Asp	Gln	Gln	Val	Leu	Leu	Ala	Lys	Val	Gln	Gly	Leu	Leu	Arg	Arg	
145					150					155					160	
Ser	Tyr	Glu	Phe	Gly	Arg	Asp	Glu	Ser	Leu	Leu	Glu	Tyr	Ala	Gly	Val	
				165					170					175		
Ile	Leu	Asn	Thr	Lys	Ser	Met	Asp	Leu	His	Tyr	Gln	Gly	Gln	Val	Leu	
			180					185					190			
Asn	Leu	Thr	Lys	Asn	Glu	Phe	Gln	Ile	Leu	Arg	Val	Leu	Phe	Glu	His	
		195					200					205				
Ala	Gly	Asn	Ile	Val	Ala	Arg	Asp	Asp	Leu	Met	Arg	Glu	Leu	Trp	Asn	
	210					215					220					
Ser	Asp	Phe	Phe	Ile	Asp	Asp	Asn	Thr	Leu	Ser	Val	Asn	Val	Ala	Arg	
225					230					235					240	
Leu	Arg	Lys	Lys	Leu	Glu	Glu	Gln	Gly	Leu	Val	Gly	Phe	Ile	Glu	Thr	
				245					250					255		
Lys	Lys	Gly	Ile	Gly	Tyr	Gly	Leu	Lys	His	Ala						
			260					265								

(2) INFORMATION FOR SEQ ID NO:3506:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 463 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...463

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3506:

Lys	Ser	Leu	Lys	Thr	Met	Leu	Gln	Trp	Ile	Lys	Asn	Phe	Ser	Ile	Pro
1				5					10					15	
Leu	Ile	Tyr	Leu	Ser	Phe	Leu	Leu	Leu	Trp	Leu	Tyr	Tyr	Ala	Ile	Phe
			20					25					30		
Ser	Ala	Ser	Tyr	Leu	Ala	Leu	Leu	Gly	Phe	Val	Phe	Leu	Leu	Val	Cys
		35					40					45			
Leu	Phe	Phe	Gln	Phe	Pro	Trp	Lys	Ser	Ala	Ser	Lys	Val	Leu	Val	Ile
	50					55					60				
Cys	Gly	Ile	Phe	Gly	Phe	Trp	Phe	Val	Phe	Gln	Asn	Trp	Gln	Gln	Ser
65					70					75					80
Gln	Ala	Ser	Gln	Asn	Leu	Ala	Asp	Ser	Val	Glu	Arg	Val	Arg	Ile	Leu
				85					90					95	
Pro	Asp	Thr	Ile	Lys	Val	Asn	Gly	Asp	Ser	Leu	Ser	Phe	Arg	Gly	Lys
			100					105					110		
Ser	Asn	Gly	Arg	Ala	Phe	Gln	Val	Tyr	Tyr	Lys	Leu	Gln	Ser	Glu	Glu
		115					120					125			
Glu	Lys	Glu	Ala	Phe	Gln	Ala	Leu	Thr	Asp	Leu	His	Glu	Ile	Gly	Leu
	130					135					140				
Glu	Gly	Lys	Leu	Ser	Glu	Pro	Glu	Gly	Gln	Arg	Asn	Phe	Gly	Gly	Phe
145					150					155					160
Asn	Tyr	Gln	Ala	Tyr	Leu	Lys	Thr	Gln	Gly	Ile	Tyr	Gln	Thr	Leu	Asn
				165					170					175	
Ile	Lys	Arg	Ile	Gln	Ser	Leu	Gln	Lys	Val	Gly	Ser	Trp	Asp	Ile	Gly
			180					185					190		
Glu	Lys	Leu	Ser	Ser	Leu	Arg	Arg	Lys	Ala	Val	Val	Trp	Ile	Lys	Met
		195					200					205			
His	Phe	Pro	Asp	Pro	Met	Arg	Asn	Tyr	Met	Thr	Gly	Leu	Leu	Leu	Gly
	210					215					220				
His	Leu	Asp	Thr	Asp	Phe	Glu	Glu	Met	Asn	Glu	Leu	Tyr	Ser	Ser	Leu
225					230					235					240
Gly	Ile	Ile	His	Xaa	Phe	Ala	Leu	Ser	Gly	Met	Gln	Val	Gly	Phe	Phe
				245					250					255	
Met	Asn	Gly	Phe	Lys	Lys	Leu	Leu	Leu	Arg	Leu	Gly	Leu	Thr	Gln	Glu
		260						265					270		
Lys	Leu	Lys	Trp	Leu	Thr	Tyr	Pro	Phe	Ser	Leu	Ile	Tyr	Ala	Gly	Leu
		275					280						285		
Thr	Gly	Phe	Ser	Ala	Ser	Val	Ile	Arg	Ser	Leu	Leu	Gln	Lys	Leu	Leu
	290					295						300			
Ala	Gln	His	Gly	Val	Lys	Gly	Leu	Asp	Asn	Phe	Ala	Leu	Thr	Val	Leu
305					310					315					320
Val	Leu	Phe	Ile	Val	Met	Pro	Asn	Phe	Phe	Leu	Thr	Ala	Gly	Gly	Val
				325					330					335	
Leu	Ser	Cys	Ala	Tyr	Ala	Phe	Ile	Leu	Thr	Met	Thr	Ile	Lys	Glu	Gly
			340					345					350		
Lys	Gly	Leu	Lys	Ala	Val	Ala	Ser	Glu	Ser	Leu	Val	Ile	Ser	Leu	Gly
		355					360						365		

```

Ile Leu Pro Ile Ile Ser Phe Tyr Phe Ala Glu Phe Gln Pro Trp Ser
370                      375                      380
Ile Leu Leu Thr Phe Val Phe Ser Phe Leu Phe Asp Leu Thr Leu Leu
385                      390                      395                      400
Pro Leu Leu Ser Ile Leu Phe Val Leu Ser Phe Leu Tyr Pro Val Ile
                      405                      410                      415
Gln Leu Asn Phe Ile Phe Glu Trp Leu Glu Gly Ile Ile Arg Leu Val
                      420                      425                      430
Ser Gln Val Thr Ser Arg Pro Leu Val Phe Gly Gln Pro Asn Glu Trp
                      435                      440                      445
Leu Leu Thr Leu Leu Leu Asn Ile Leu Trp Leu Trp Ser Met Ile
                      450                      455                      460

```

(2) INFORMATION FOR SEQ ID NO:3507:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 67 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...67
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3507:

```

Asn Gln Leu Lys Thr Glu Gln Ile Tyr Trp Glu Ile Gln Ile Thr Phe
1                      5                      10                      15
Leu Lys Tyr Phe Arg Asn Arg Ser Val Ile Phe Gln Ile Gln Phe Thr
                      20                      25                      30
Ile Lys Leu Ala Phe Leu Leu Gln Lys Lys Lys Glu Arg Leu Pro Phe
                      35                      40                      45
Val Pro Phe Leu Leu Leu Ala Thr Cys Leu Ile Ile Phe Gly Lys Leu
                      50                      55                      60
Leu Leu Val
65

```

(2) INFORMATION FOR SEQ ID NO:3508:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 192 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3508:

Asn	Lys	Leu	Asn	Lys	Glu	Lys	Ile	Met	Val	Lys	Val	Ala	Val	Ile	Leu
1				5					10					15	
Ala	Gln	Gly	Phe	Glu	Glu	Ile	Glu	Ala	Leu	Thr	Val	Val	Asp	Val	Leu
			20					25					30		
Arg	Arg	Ala	Asn	Ile	Thr	Cys	Asp	Met	Val	Gly	Phe	Glu	Glu	Gln	Val
			35				40					45			
Thr	Gly	Ser	His	Ala	Ile	Gln	Val	Arg	Ala	Asp	His	Val	Phe	Asp	Gly
	50					55				60					
Asp	Leu	Ser	Asp	Tyr	Asp	Met	Ile	Val	Leu	Pro	Gly	Gly	Met	Pro	Gly
65				70					75					80	
Ser	Ala	His	Leu	Arg	Asp	Asn	Gln	Thr	Leu	Ile	Gln	Glu	Leu	Gln	Ser
			85						90					95	
Phe	Glu	Gln	Glu	Gly	Lys	Lys	Leu	Ala	Ala	Ile	Cys	Ala	Ala	Pro	Ile
			100					105						110	
Ala	Leu	Asn	Gln	Ala	Glu	Ile	Leu	Lys	Asn	Lys	Arg	Tyr	Thr	Cys	Tyr
		115					120					125			
Asp	Gly	Val	Gln	Glu	Gln	Ile	Leu	Asp	Gly	His	Tyr	Val	Lys	Glu	Thr
	130					135					140				
Val	Val	Val	Asp	Gly	Gln	Leu	Thr	Thr	Ser	Arg	Gly	Pro	Ser	Thr	Ala
145					150					155					160
Leu	Ala	Phe	Ala	Tyr	Glu	Leu	Val	Glu	Gln	Leu	Gly	Gly	Asp	Ala	Glu
				165					170					175	
Ser	Leu	Arg	Thr	Gly	Met	Leu	Tyr	Gln	Asp	Val	Phe	Gly	Lys	Asn	Gln
			180					185					190		

(2) INFORMATION FOR SEQ ID NO:3509:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...249

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3509:

Glu	Arg	Leu	Lys	Cys	Glu	Lys	Arg	Arg	Phe	Leu	Met	Gly	Arg	Lys	Trp
1				5					10					15	
Ala	Asn	Ile	Val	Ala	Lys	Lys	Thr	Ala	Lys	Asp	Gly	Ala	Asn	Ser	Lys
			20					25					30		
Val	Tyr	Ala	Lys	Phe	Gly	Val	Glu	Ile	Tyr	Val	Ala	Ala	Lys	Lys	Gly

65		70		75		80								
Tyr	Lys	Asp	Asp	Gln	Val	Lys	Ile	Asp	Phe	Met	Asn	Ser	Glu	Arg
				85					90				95	

(2) INFORMATION FOR SEQ ID NO:3511:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 95 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...95
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3511:

Ile	Met	Leu	Lys	Ile	Gly	Thr	Ala	Cys	Gly	Ser	Gly	Leu	Gly	Ser	Ser
1				5					10				15		
Phe	Met	Val	Gln	Met	Asn	Ile	Glu	Ser	Val	Leu	Ser	Asp	Leu	Asn	Val
			20				25					30			
Ser	Asp	Val	Glu	Val	Glu	His	Tyr	Asp	Leu	Gly	Gly	Ala	Asp	Pro	Asn
		35				40					45				
Ala	Ala	Asp	Ile	Trp	Ile	Val	Gly	Arg	Asp	Leu	Ala	Asp	Ser	Ala	Ser
	50				55				60						
His	Leu	Gly	Asp	Val	Arg	Ile	Leu	Asn	Ser	Ile	Ile	Asp	Met	Asp	Glu
65				70				75					80		
Leu	Arg	Glu	Leu	Ile	Thr	Lys	Ile	Cys	Glu	Glu	Lys	Gly	Leu	Ile	
			85					90					95		

(2) INFORMATION FOR SEQ ID NO:3512:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 66 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...66
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3512:

Lys	Met	Leu	Asn	Leu	Gln	Phe	Ala	Glu	Thr	Met	Glu	Leu	Thr	Glu	Ala
1			5						10					15	
Glu	Leu	Glu	Thr	Val	Tyr	Gly	Gly	Glu	Phe	Gly	Asn	Asn	Ala	Val	Ile
			20					25					30		
Pro	Ala	Gly	Ala	Trp	Gly	Gly	Leu	Gly	Thr	Ser	Trp	Ser	Ile	Thr	Asn
		35					40					45			
Phe	Trp	Lys	Lys	Tyr	Phe	Asn	His	Asp	Ser	Ser	Thr	Val	Asn	Arg	Arg
	50					55					60				
His	Tyr														
65															

(2) INFORMATION FOR SEQ ID NO:3513:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 126 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3513:

Met	Ala	Leu	Lys	Tyr	Thr	Thr	Trp	Lys	Val	Thr	Asp	Glu	Lys	Glu	Leu
1			5						10					15	
Lys	Leu	Arg	Leu	Thr	Ser	His	Gln	Thr	Ala	Thr	Val	Glu	Glu	Lys	Ile
			20					25					30		
Gly	Met	Asn	Leu	Leu	Lys	Ile	Phe	Met	Pro	Glu	Ala	Gly	Glu	Glu	Phe
		35					40					45			
Thr	Leu	Pro	Pro	Leu	Lys	Val	Met	Leu	Leu	Leu	Val	His	Gly	Ala	Leu
	50					55					60				
Gln	Gln	Tyr	Glu	His	Gly	Tyr	Ser	Leu	Glu	Asp	Val	Tyr	Asp	Leu	Tyr
65				70						75				80	
Asp	Glu	Tyr	Val	Asp	Asn	Gly	Gly	Asp	Gln	Thr	Thr	Phe	Met	Thr	Glu
			85						90					95	
Val	Leu	Met	Pro	Leu	Phe	Glu	Val	Ser	Gly	Phe	Thr	Pro	Arg	Gly	Ser
			100					105					110		
Lys	Asp	Lys	Lys	Thr	Ser	Lys	Lys	Lys	Met	Thr	Val	Asp	Lys		
		115					120					125			

(2) INFORMATION FOR SEQ ID NO:3514:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...114

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3514:

Arg	Lys	Leu	Lys	Lys	Glu	Glu	Asn	Lys	Met	Asn	Lys	Thr	Thr	Glu	Met
1			5						10					15	
Ile	Val	Phe	Arg	Ser	Arg	Lys	Thr	Gly	Glu	Phe	Leu	Asn	Ser	Tyr	Lys
			20					25					30		
Asp	Arg	Ser	Ser	Leu	Ala	Phe	Ala	Ala	Asp	Phe	Cys	Ser	Leu	Glu	Tyr
			35				40					45			
Cys	Leu	Lys	Leu	Pro	Arg	Lys	Lys	Tyr	Glu	Asp	Asn	Lys	Lys	Thr	Tyr
			50				55				60				
Lys	Ala	Leu	Ala	Ala	Ala	Phe	Asp	Cys	Glu	Ile	Val	Ala	Val	Glu	Ala
65					70					75				80	
Glu	Tyr	Lys	Leu	Thr	Tyr	Pro	Asn	Gly	Ser	Glu	Val	Glu	Pro	Ile	Lys
				85				90						95	
Arg	Asp	Arg	Ser	Ser	Ile	Glu	Asp	Met	Ile	Lys	Asp	Ile	Ile	Gly	Gly
			100					105					110		
Val	Leu														

(2) INFORMATION FOR SEQ ID NO:3515:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 650 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...650

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3515:

Leu	His	Ser	Leu	Val	Ile	Phe	Val	Lys	Ile	Asn	Ala	Asn	Thr	Asn	Glu
1			5					10						15	
Ser	Glu	Asn	Lys	Met	Thr	Arg	Tyr	Gln	Asp	Asp	Phe	Tyr	Asp	Ala	Ile
			20					25					30		
Asn	Gly	Glu	Trp	Gln	Gln	Thr	Ala	Glu	Ile	Pro	Ala	Asp	Lys	Ser	Gln
			35				40					45			
Thr	Gly	Gly	Phe	Val	Asp	Leu	Asp	Gln	Glu	Ile	Glu	Asp	Leu	Met	Leu
			50				55				60				

Ala	Thr	Thr	Asp	Lys	Trp	Leu	Ala	Gly	Glu	Glu	Val	Pro	Glu	Asp	Ala
65					70					75					80
Ile	Leu	Glu	Asn	Phe	Val	Lys	Tyr	His	Arg	Leu	Val	Arg	Asp	Phe	Asp
				85					90					95	
Lys	Arg	Glu	Ala	Asp	Gly	Ile	Thr	Pro	Val	Leu	Pro	Leu	Leu	Lys	Glu
			100					105					110		
Phe	Gln	Glu	Leu	Glu	Thr	Phe	Ala	Asp	Phe	Thr	Ala	Lys	Leu	Ala	Glu
		115					120					125			
Phe	Glu	Leu	Ala	Gly	Lys	Pro	Asn	Phe	Leu	Pro	Phe	Gly	Val	Ser	Pro
	130					135					140				
Asp	Phe	Met	Asp	Ala	Arg	Ile	Asn	Val	Leu	Trp	Ala	Ser	Ala	Pro	Ser
145					150					155					160
Thr	Ile	Leu	Pro	Asp	Thr	Thr	Tyr	Tyr	Ala	Glu	Glu	His	Pro	Gln	Arg
				165					170					175	
Glu	Glu	Leu	Leu	Thr	Leu	Trp	Lys	Glu	Ser	Ser	Ala	Asn	Leu	Leu	Lys
			180					185					190		
Ala	Tyr	Asp	Phe	Ser	Asp	Glu	Glu	Ile	Glu	Asp	Leu	Leu	Glu	Lys	Arg
		195					200					205			
Leu	Glu	Leu	Asp	Arg	Arg	Val	Ala	Ala	Val	Val	Leu	Ser	Asn	Glu	Glu
	210					215					220				
Ser	Ser	Glu	Tyr	Ala	Lys	Leu	Tyr	His	Pro	Tyr	Ser	Tyr	Glu	Asp	Phe
225					230					235					240
Lys	Lys	Phe	Ala	Pro	Ala	Leu	Pro	Leu	Asp	Asp	Phe	Phe	Lys	Ala	Val
				245					250					255	
Ile	Gly	Gln	Leu	Pro	Asp	Lys	Val	Ile	Val	Asp	Glu	Glu	Arg	Phe	Trp
			260					265					270		
Gln	Ala	Ala	Glu	Gln	Phe	Tyr	Ser	Glu	Glu	Ala	Trp	Ser	Leu	Leu	Lys
		275					280					285			
Ala	Thr	Leu	Ile	Leu	Ser	Val	Val	Asn	Leu	Ser	Thr	Ser	Tyr	Leu	Thr
	290					295					300				
Glu	Asp	Ile	Arg	Val	Leu	Ser	Gly	Ala	Tyr	Ser	Arg	Thr	Leu	Ser	Gly
305					310					315					320
Val	Pro	Glu	Ala	Lys	Asp	Lys	Val	Lys	Ala	Ala	Tyr	His	Leu	Ala	Gln
				325					330					335	
Glu	Pro	Phe	Lys	Gln	Ala	Leu	Gly	Leu	Trp	Tyr	Ala	Arg	Glu	Lys	Phe
			340				345						350		
Ser	Pro	Glu	Ala	Lys	Ala	Asp	Val	Glu	Lys	Lys	Val	Ala	Thr	Met	Ile
		355				360						365			
Asp	Val	Tyr	Lys	Glu	Arg	Leu	Leu	Lys	Asn	Asp	Trp	Leu	Thr	Pro	Glu
370						375					380				
Thr	Cys	Lys	Gln	Ala	Ile	Val	Lys	Leu	Asn	Val	Ile	Lys	Pro	Tyr	Ile
385					390					395					400
Gly	Tyr	Pro	Glu	Glu	Leu	Pro	Ala	Arg	Tyr	Lys	Asp	Lys	Val	Val	Asn
				405					410					415	
Glu	Thr	Ala	Ser	Leu	Phe	Glu	Asn	Ala	Leu	Ala	Phe	Ala	Arg	Val	Glu
			420				425						430		
Ile	Lys	His	Ser	Trp	Ser	Lys	Trp	Asn	Gln	Pro	Val	Asn	Tyr	Lys	Glu
	435						440					445			
Trp	Gly	Met	Pro	Ala	His	Met	Val	Asn	Ala	Tyr	Tyr	Asn	Pro	Gln	Lys
	450					455					460				
Asn	Leu	Ile	Val	Phe	Pro	Ala	Ala	Ile	Leu	Gln	Ala	Pro	Phe	Tyr	Asp
465					470					475					480
Leu	His	Gln	Ser	Ser	Ser	Ala	Asn	Tyr	Gly	Gly	Ile	Gly	Ala	Val	Ile
				485					490					495	
Ala	His	Glu	Ile	Ser	His	Ala	Phe	Asp	Thr	Asn	Gly	Ala	Ser	Phe	Asp
			500					505				510			
Glu	Asn	Gly	Ser	Leu	Lys	Asp	Trp	Trp	Thr	Glu	Ser	Asp	Tyr	Ala	Ala

145		150		155		160									
Leu	Tyr	Val	Ala	Leu	Phe	Phe	Thr	Ile	Tyr	Ser	Gly	Tyr	Asp	Tyr	Phe
		165				170								175	
Lys	Gly	Ser	Ala	Tyr	Val	Phe	Lys	Gly	Thr	Phe	Gly	Ser	Lys		
		180					185						190		

(2) INFORMATION FOR SEQ ID NO:3517:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 77 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...77
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3517:

Pro	Lys	Leu	Asn	Phe	Lys	Lys	Arg	Gly	Trp	Leu	Phe	Ser	Gln	Ser	Phe
1			5				10						15		
Glu	Gly	Ala	Lys	Ala	Thr	Ala	Ile	Ile	Met	Ser	Leu	Leu	Glu	Thr	Ala
		20				25						30			
Lys	Arg	His	Gln	Leu	Asn	Ser	Glu	Lys	Tyr	Leu	Phe	Tyr	Leu	Leu	Glu
	35				40				45						
Cys	Leu	Pro	Asn	Glu	Glu	Thr	Leu	Val	Asn	Lys	Glu	Val	Leu	Glu	Ala
	50				55				60						
Tyr	Leu	Pro	Trp	Thr	Lys	Val	Val	Gln	Glu	Lys	Cys	Lys			
65			70						75						

(2) INFORMATION FOR SEQ ID NO:3518:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 445 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...445
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3518:

Asn	Asn	Ile	Asn	Lys	Met	Lys	Glu	Ile	Glu	Asn	Asn	Gln	Trp	Ile	Ala
1				5					10					15	
Asn	Tyr	Arg	Thr	Asp	Gln	Pro	His	Phe	Gly	Leu	Glu	Arg	Met	Val	Glu
			20					25					30		
Leu	Leu	Ala	Leu	Arg	Gly	Asn	Pro	His	Leu	Lys	Leu	Lys	Val	Leu	His
		35					40					45			
Ile	Gly	Gly	Thr	Asn	Gly	Lys	Gly	Ser	Thr	Ile	Ala	Phe	Leu	Lys	Lys
	50					55					60				
Met	Leu	Glu	Lys	Leu	Gly	Leu	Arg	Val	Gly	Val	Phe	Ser	Ser	Pro	Tyr
65					70					75					80
Leu	Ile	His	Tyr	Thr	Asp	Gln	Ile	Ser	Ile	Asn	Gly	Glu	Ser	Ile	Ser
				85					90					95	
Glu	Val	Arg	Leu	Glu	Ala	Leu	Met	Ala	Asp	Tyr	Gln	Ser	Leu	Leu	Glu
			100					105					110		
Gly	Glu	Ala	Val	Ala	Asn	Leu	Gln	Gly	Thr	Thr	Glu	Phe	Glu	Ile	Ile
		115					120					125			
Thr	Ala	Leu	Ala	Tyr	Asp	Tyr	Phe	Ala	Ser	Glu	Gln	Val	Asp	Val	Ala
	130					135						140			
Ile	Met	Glu	Val	Gly	Met	Gly	Gly	Leu	Leu	Asp	Ser	Thr	Asn	Val	Cys
145					150					155					160
Gln	Pro	Ile	Leu	Thr	Gly	Ile	Thr	Thr	Ile	Gly	Leu	Asp	His	Val	Ala
			165						170					175	
Leu	Leu	Gly	Asp	Thr	Leu	Glu	Ala	Ile	Ala	Glu	Gln	Lys	Ala	Gly	Ile
			180					185					190		
Ile	Lys	Gln	Gly	Met	Pro	Leu	Val	Thr	Gly	Arg	Ile	Ala	Pro	Glu	Ala
	195					200						205			
Leu	Ala	Val	Ile	Asp	Arg	Ile	Ala	Glu	Gly	Lys	Asp	Ala	Pro	Arg	Leu
	210					215					220				
Ala	Tyr	Gly	Thr	Asp	Tyr	Gln	Val	Arg	His	Gln	Glu	Ser	Val	Val	Thr
225					230					235					240
Gly	Glu	Val	Phe	Asp	Tyr	Thr	Ser	Ala	Val	Arg	Gln	Gly	Arg	Phe	Gln
			245						250					255	
Thr	Ser	Leu	Leu	Gly	Leu	Tyr	Gln	Ile	Glu	Asn	Ala	Gly	Met	Ala	Ile
		260						265					270		
Ala	Leu	Leu	Asp	Thr	Phe	Cys	Gln	Glu	Asp	Gly	Arg	Glu	Leu	Ala	Ser
	275						280					285			
Asn	Asp	Phe	Leu	Gly	Gln	Ala	Leu	Glu	Glu	Thr	Ser	Trp	Pro	Gly	Arg
	290					295						300			
Leu	Glu	Ile	Val	Ser	Arg	Asp	Pro	Leu	Met	Ile	Leu	Asp	Gly	Ala	His
305					310					315					320
Asn	Pro	His	Ala	Ile	Lys	Ala	Leu	Leu	Val	Thr	Leu	Gln	Glu	Arg	Phe
			325						330					335	
Ala	Asp	Tyr	His	Lys	Glu	Ile	Leu	Phe	Thr	Cys	Ile	Lys	Thr	Lys	Ala
		340						345					350		
Leu	Glu	Asp	Met	Leu	Asp	Leu	Leu	Gly	Ala	Met	Pro	Asp	Thr	Glu	Leu
	355						360					365			
Thr	Leu	Thr	His	Phe	Ala	Asp	Ser	Arg	Ala	Thr	Asp	Glu	Asn	Val	Leu
	370					375						380			
Lys	Glu	Ala	Ala	Lys	Ser	Arg	Asn	Leu	Ser	Tyr	Gln	Asp	Trp	His	Asp
385					390					395					400
Phe	Leu	Glu	Gln	Asn	Leu	Thr	Asp	Lys	Lys	Glu	Glu	Lys	Gln	Thr	Val
			405						410					415	
Arg	Ile	Val	Thr	Gly	Ser	Leu	Tyr	Phe	Leu	Ser	Gln	Val	Arg	Ala	Tyr
		420						425					430		
Leu	Met	Glu	Arg	Lys	Asn	Glu	Asn	Gly	Tyr	Thr	Lys	Asp			
	435						440					445			

(2) INFORMATION FOR SEQ ID NO:3519:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...118

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3519:

Thr	Ile	Ile	Lys	Leu	Ser	Phe	Asn	Val	Asn	His	Trp	Val	Thr	Cys	Lys
1			5					10						15	
Asn	Thr	Val	Ser	His	Arg	Phe	Tyr	Gln	Thr	Phe	Phe	Asn	Arg	Trp	Asp
			20					25					30		
Lys	Phe	Thr	Arg	Asn	His	Thr	Thr	Asp	Asp	Cys	Val	Phe	Glu	Phe	Glu
			35				40					45			
Ser	Phe	Thr	Phe	Phe	Val	Trp	Ser	Lys	Phe	Asn	Pro	Tyr	Ile	Thr	Glu
			50			55				60					
Leu	Thr	Phe	Thr	Thr	Arg	Leu	Thr	Phe	Glu	Glu	Ser	Thr	Cys	Leu	Ser
65					70				75					80	
Arg	Ser	Ala	Glu	Cys	Phe	Thr	Val	Arg	Tyr	Leu	Arg	Arg	Thr	Tyr	Val
				85				90						95	
Arg	Phe	Asn	Phe	Glu	Leu	Thr	Thr	His	Thr	Ile	Asn	Lys	Asp	Val	Lys
			100					105					110		
Val	Lys	Phe	Thr	His	Thr										
			115												

(2) INFORMATION FOR SEQ ID NO:3520:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...78

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3520:

Tyr	Ser	Ile	Lys	Ile	Lys	Glu	Gln	Thr	Arg	Lys	Leu	Ala	Ala	Val	Ser
1				5					10					15	
Ser	Lys	His	Cys	Phe	Glu	Val	Val	Asp	Arg	Thr	Asp	Glu	Val	Ser	Ser
			20					25					30		
Lys	His	Cys	Phe	Glu	Val	Val	Asp	Arg	Thr	Asp	Glu	Val	Ser	Asn	His
		35					40					45			
Ile	Tyr	Ser	Lys	Ala	Lys	Leu	Thr	Trp	Phe	Glu	Glu	Ile	Phe	Lys	Glu
	50					55					60				
Tyr	Lys	Leu	Tyr	Phe	Tyr	Asn	Leu	Asn	Leu	Val	Phe	Thr	Glu		
65					70					75					

(2) INFORMATION FOR SEQ ID NO:3521:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3521:

Lys	Ala	Ile	Asn	Asn	Arg	Lys	Glu	Arg	Lys	Ala	Met	Thr	Val	Gln	Met
1				5					10					15	
Glu	Tyr	Glu	Lys	Asp	Val	Lys	Val	Ala	Ala	Leu	Asp	Gly	Lys	Lys	Ile
			20					25					30		
Ala	Val	Ile	Gly	Tyr	Gly	Ser	Gln	Gly	His	Ala	His	Ala	Gln	Asn	Leu
		35				40					45				
Arg	Asp	Ser	Gly	Arg	Asp	Val	Ile	Ile	Gly	Val	Arg	Pro	Gly	Lys	Ser
	50				55						60				
Phe	Asp	Lys	Ala	Lys	Glu	Asp	Gly	Phe	Asp	Thr	Tyr	Thr	Val	Ala	Glu
65				70					75					80	
Ala	Thr	Lys	Leu	Ala	Asp	Val	Ile	Met	Ile	Leu	Ala	Pro	Asp	Glu	Ile
			85				90						95		
Gln	Gln	Glu	Leu	Tyr	Glu	Ala	Glu	Ile	Ala	Pro	Asn	Leu	Glu	Ala	Gly
		100					105						110		
Asn	Ala	Val	Gly	Phe	Ala	His	Gly	Phe	Asn	Ile	His	Phe	Glu	Phe	Ile
	115					120					125				
Lys	Val	Pro	Ala	Asp	Val	Asp	Val	Phe	Met	Cys	Ala	Pro	Lys	Gly	Pro
	130				135				140						
Gly	His	Leu	Val	Arg	Arg	Thr	Tyr	Glu	Glu	Gly	Phe	Gly	Val	Pro	Ala
145				150					155					160	
Leu	Tyr	Ala	Val	Tyr	Gln	Asp	Ala	Thr	Gly	Asn	Ala	Lys	Asn	Ile	Ala
			165				170						175		
Met	Asp	Trp	Cys	Lys	Gly	Val	Gly	Ala	Ala	Arg	Val	Gly	Leu	Leu	Glu
	180					185					190				
Thr	Thr	Tyr	Lys	Glu	Glu	Thr	Glu	Glu	Asp	Leu	Phe	Gly	Glu	Gln	Ala

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...77
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3523:

```

Asp Lys Ile Asn Ile Thr Gly Glu Ile Ile Met Ser Val Glu Glu Lys
 1             5             10             15
Leu Asn Gln Ala Lys Gly Ser Ile Lys Glu Gly Val Gly Lys Ala Ile
      20             25             30
Gly Asp Glu Lys Met Glu Lys Glu Gly Ala Ala Glu Lys Val Val Ser
      35             40             45
Lys Val Lys Glu Val Ala Glu Asp Ala Lys Asp Ala Val Glu Gly Ala
 50             55             60
Val Glu Gly Val Lys Asn Met Leu Ser Gly Asp Asp Lys
65             70             75

```

(2) INFORMATION FOR SEQ ID NO:3524:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 257 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...257
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3524:

```

Glu Lys Ile Lys Glu Val Glu Gly Ser Ile Pro Cys Arg Pro Ser Leu
 1             5             10             15
Leu Phe Asn Gly Asp Arg Lys Met Met Asn Glu Leu Phe Gly Glu Phe
      20             25             30
Leu Gly Thr Leu Ile Leu Ile Leu Leu Gly Asn Gly Val Val Ala Gly
      35             40             45
Val Val Leu Pro Lys Thr Lys Ser Asn Ser Ser Gly Trp Ile Val Ile
 50             55             60
Thr Met Gly Trp Gly Ile Ala Val Ala Val Ala Val Phe Val Ser Gly
65             70             75             80
Lys Leu Ser Pro Ala His Leu Asn Pro Ala Val Thr Ile Gly Val Ala
      85             90             95

```

Leu	Lys	Gly	Gly	Leu	Pro	Trp	Ala	Ser	Val	Leu	Pro	Tyr	Ile	Leu	Ala
			100					105					110		
Gln	Phe	Ala	Gly	Ala	Met	Leu	Gly	Gln	Ile	Leu	Val	Trp	Leu	Gln	Phe
		115					120					125			
Lys	Pro	His	Tyr	Glu	Ala	Glu	Glu	Asn	Ala	Gly	Asn	Ile	Leu	Ala	Thr
	130					135					140				
Phe	Ser	Thr	Gly	Pro	Ala	Ile	Lys	Asp	Thr	Val	Ser	Asn	Leu	Ile	Ser
145					150					155					160
Glu	Ile	Leu	Gly	Thr	Phe	Val	Leu	Val	Leu	Thr	Ile	Phe	Ala	Leu	Gly
			165						170						175
Leu	Tyr	Asp	Phe	Gln	Ala	Gly	Ile	Gly	Thr	Phe	Ala	Val	Gly	Thr	Leu
		180						185					190		
Ile	Val	Gly	Ile	Gly	Leu	Ser	Leu	Gly	Gly	Thr	Thr	Gly	Tyr	Ala	Leu
	195						200					205			
Asn	Pro	Ala	Arg	Asp	Leu	Gly	Pro	Arg	Ile	Met	His	Ser	Ile	Leu	Pro
	210					215					220				
Ile	Pro	Asn	Lys	Gly	Asp	Gly	Asp	Trp	Ser	Tyr	Ala	Trp	Ile	Pro	Val
225				230						235					240
Val	Gly	Pro	Val	Ile	Gly	Ala	Ala	Leu	Ala	Val	Leu	Val	Phe	Ser	Leu
				245				250						255	

Phe

(2) INFORMATION FOR SEQ ID NO:3525:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...113

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3525:

Ala	Glu	Ile	Asn	Gly	Ile	Ile	Ala	Val	Leu	Ala	Gly	Ile	Leu	Val	Tyr
1				5					10					15	
Gly	Gly	Val	Gln	Leu	Ile	Gly	Leu	Thr	Ala	Asn	His	Glu	Met	Arg	Ile
			20					25					30		
Phe	Ile	Leu	Ile	Ile	Leu	Thr	Ser	Leu	Val	Phe	Met	Ser	Met	Val	Thr
		35				40						45			
Thr	Leu	Ala	Thr	Trp	Asn	Ser	Arg	Ile	Gly	Ala	Phe	Phe	Ser	Leu	Ile
	50				55						60				
Leu	Leu	Leu	Leu	Gln	Leu	Ala	Ser	Ser	Ala	Gly	Thr	Tyr	Pro	Leu	Ala
65				70						75					80
Leu	Thr	Asn	Asp	Phe	Phe	Arg	Ser	Ile	Asn	Pro	Trp	Leu	Pro	Met	Ser
			85					90						95	
Tyr	Ser	Val	Ser	Gly	Leu	Arg	Gln	Thr	Ile	Ser	Ile	Asn	Lys	Ser	Phe
			100					105						110	

Ser

(2) INFORMATION FOR SEQ ID NO:3526:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...233

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3526:

Lys	Glu	Ile	Asn	Met	Phe	Ala	Ser	Lys	Ser	Glu	Arg	Lys	Val	His	Tyr
1				5				10						15	
Ser	Ile	Arg	Lys	Phe	Ser	Ile	Gly	Val	Ala	Ser	Val	Ala	Val	Ala	Ser
			20					25					30		
Leu	Val	Met	Gly	Ser	Val	Val	His	Ala	Thr	Glu	Lys	Glu	Val	Thr	Thr
		35					40					45			
Gln	Val	Ala	Thr	Ser	Ser	Asn	Arg	Ala	Asn	Glu	Ser	Gln	Ala	Gly	His
	50					55				60					
Arg	Lys	Ala	Ala	Glu	Gln	Phe	Asp	Glu	Tyr	Ile	Lys	Thr	Met	Ile	Gln
65					70				75					80	
Leu	Asp	Arg	Arg	Lys	His	Thr	Gln	Asn	Phe	Ala	Leu	Asn	Ile	Lys	Leu
			85						90					95	
Ser	Arg	Ile	Lys	Thr	Glu	Tyr	Leu	Arg	Lys	Leu	Asn	Val	Leu	Glu	Glu
			100					105					110		
Lys	Ser	Lys	Ala	Glu	Leu	Pro	Ser	Glu	Thr	Lys	Lys	Glu	Ile	Asp	Ala
		115					120					125			
Ala	Phe	Glu	Gln	Phe	Lys	Lys	Asp	Thr	Asn	Arg	Thr	Lys	Lys	Thr	Val
	130					135					140				
Ala	Glu	Ala	Glu	Lys	Lys	Val	Glu	Glu	Ala	Lys	Lys	Lys	Ala	Lys	Ala
145					150					155					160
Gln	Lys	Glu	Glu	Asp	His	Arg	Asn	Tyr	Pro	Thr	Asn	Thr	Tyr	Lys	Thr
			165						170					175	
Leu	Glu	Leu	Glu	Ile	Ala	Glu	Ser	Asp	Val	Glu	Val	Lys	Lys	Ala	Glu
		180					185						190		
Leu	Glu	Leu	Val	Lys	Glu	Glu	Ala	Lys	Glu	Ser	Arg	Asp	Asp	Glu	Lys
		195					200					205			
Ile	Lys	Gln	Ala	Glu	Ala	Lys	Val	Glu	Ser	Lys	Lys	Ala	Glu	Ala	Thr
	210					215						220			
Arg	Leu	Asp	Lys	His	Gln	Asp	Arg	Ser							
225					230										

(2) INFORMATION FOR SEQ ID NO:3527:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 158 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...158
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3527:

```

Ser Arg Ile Asn Asp Asn Arg Lys Glu Lys Ile Met Lys Ile Arg Gly
1      5      10      15
Phe Glu Leu Val Ser Ser Phe Thr Asp Glu Asn Leu Leu Pro Lys Arg
      20      25      30
Glu Thr Ala His Ala Ala Gly Tyr Asp Leu Lys Val Ala Val Arg Thr
      35      40      45
Val Val Ala Pro Gly Glu Ile Val Leu Val Pro Thr Gly Val Lys Ala
      50      55      60
Tyr Met Gln Pro Thr Glu Val Leu Tyr Leu Tyr Asp Arg Ser Ser Asn
65      70      75      80
Pro Arg Lys Lys Gly Leu Val Leu Ile Asn Ser Val Gly Val Ile Asp
      85      90      95
Gly Asp Tyr Tyr Gly Asn Pro Gly Asn Glu Gly His Ile Phe Ala Gln
      100     105     110
Met Lys Asn Ile Thr Asp Gln Glu Val Val Leu Glu Val Gly Glu Arg
      115     120     125
Ile Val Gln Ala Val Phe Ala Thr Phe Leu Ile Ala Asp Gly Asp Ala
      130     135     140
Ala Asp Gly Val Arg Thr Gly Gly Phe Gly Ser Thr Gly His
145      150      155

```

(2) INFORMATION FOR SEQ ID NO:3528:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 447 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...447

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3528:

Leu	Met	Ile	Lys	Asn	Pro	Lys	Leu	Leu	Thr	Lys	Ser	Phe	Leu	Arg	Ser
1			5					10						15	
Phe	Ala	Ile	Leu	Gly	Gly	Val	Gly	Leu	Val	Ile	His	Ile	Ala	Ile	Tyr
		20					25						30		
Leu	Thr	Phe	Pro	Phe	Tyr	Tyr	Ile	Gln	Leu	Glu	Gly	Glu	Lys	Phe	Asn
	35					40					45				
Glu	Ser	Ala	Arg	Val	Phe	Thr	Glu	Tyr	Leu	Lys	Thr	Lys	Thr	Ser	Asp
	50				55					60					
Glu	Ile	Pro	Ser	Leu	Leu	Gln	Ser	Tyr	Ser	Lys	Ser	Leu	Thr	Ile	Ser
65				70					75					80	
Ala	His	Leu	Lys	Arg	Asp	Ile	Val	Asp	Lys	Arg	Leu	Pro	Leu	Val	His
			85					90						95	
Asp	Leu	Asp	Ile	Lys	Asp	Gly	Lys	Leu	Ser	Asn	Tyr	Ile	Val	Met	Leu
	100							105					110		
Asp	Met	Ser	Val	Ser	Thr	Ala	Asp	Gly	Lys	Gln	Val	Thr	Val	Gln	Phe
	115						120					125			
Val	His	Gly	Val	Asp	Val	Tyr	Lys	Glu	Ala	Lys	Asn	Ile	Leu	Leu	Leu
	130					135					140				
Tyr	Leu	Pro	Tyr	Thr	Phe	Leu	Val	Thr	Ile	Ala	Phe	Ser	Phe	Val	Phe
145					150				155					160	
Ser	Tyr	Phe	Tyr	Thr	Lys	Arg	Leu	Leu	Asn	Pro	Leu	Phe	Tyr	Ile	Ser
			165					170						175	
Glu	Val	Thr	Ser	Lys	Met	Gln	Asp	Leu	Asp	Asp	Asn	Ile	Arg	Phe	Asp
	180						185						190		
Glu	Ser	Arg	Lys	Asp	Glu	Val	Gly	Glu	Val	Gly	Glu	Ile	Gly	Lys	Gln
	195					200						205			
Ile	Asn	Gly	Met	Tyr	Glu	His	Leu	Leu	Lys	Val	Ile	His	Glu	Leu	Glu
	210					215						220			
Ser	Arg	Asn	Glu	Gln	Ile	Val	Lys	Leu	Gln	Asn	Gln	Lys	Val	Ser	Phe
225				230					235					240	
Val	Arg	Gly	Ala	Ser	His	Glu	Leu	Lys	Thr	Pro	Leu	Ala	Ser	Leu	Arg
			245					250						255	
Ile	Ile	Leu	Glu	Asn	Met	Gln	His	Asn	Ile	Gly	Asp	Tyr	Lys	Asp	His
	260						265						270		
Pro	Lys	Tyr	Ile	Ala	Lys	Ser	Ile	Asn	Lys	Ile	Asp	Gln	Met	Ser	His
	275						280					285			
Leu	Leu	Glu	Glu	Val	Leu	Glu	Ser	Ser	Lys	Phe	Gln	Glu	Trp	Thr	Glu
	290					295					300				
Cys	Arg	Glu	Thr	Leu	Thr	Val	Lys	Pro	Val	Leu	Val	Asp	Ile	Leu	Ser
305				310					315					320	
Arg	Tyr	Gln	Glu	Leu	Ala	His	Ser	Ile	Gly	Val	Thr	Ile	Glu	Asn	Gln
			325						330					335	
Leu	Thr	Asp	Ala	Thr	Arg	Val	Val	Met	Ser	Leu	Arg	Ala	Leu	Asp	Lys
	340						345						350		
Val	Leu	Thr	Asn	Leu	Ile	Ser	Asn	Ala	Ile	Lys	Tyr	Ser	Asp	Lys	Asn
	355						360					365			
Gly	Arg	Val	Ile	Ile	Ser	Glu	Gln	Asp	Gly	Tyr	Leu	Ser	Ile	Lys	Asn
	370					375					380				
Thr	Cys	Ala	Pro	Leu	Ser	Asp	Gln	Glu	Leu	Glu	His	Leu	Phe	Asp	Ile
385				390						395				400	
Phe	Tyr	His	Ser	Gln	Ile	Val	Thr	Asp	Lys	Asp	Glu	Ser	Ser	Gly	Leu
			405						410					415	
Gly	Leu	Tyr	Ile	Val	Ser	Asn	Ile	Leu	Glu	Ser	Tyr	Gln	Met	Asp	Tyr
		420					425						430		
Ser	Phe	Leu	Pro	Tyr	Glu	His	Gly	Met	Glu	Phe	Lys	Ile	Ser	Leu	

(2) INFORMATION FOR SEQ ID NO:3529:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 223 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...223

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3529:

```

Met Asn Val Lys Glu Asn Thr Glu Leu Val Phe Arg Glu Val Ala Glu
1      5      10      15
Ala Ser Leu Ser Ala Asn Arg Glu Ser Gly Ser Val Ser Val Ile Ala
      20      25      30
Val Thr Lys Tyr Val Asp Val Pro Thr Ala Glu Ala Leu Leu Pro Leu
      35      40      45
Gly Val His His Ile Gly Glu Asn Arg Val Asp Lys Phe Leu Glu Lys
      50      55      60
Tyr Glu Ala Leu Lys Asp Arg Asp Val Thr Trp His Leu Ile Gly Thr
65      70      75      80
Leu Gln Arg Arg Lys Val Lys Asp Val Ile Gln Tyr Val Asp Tyr Phe
      85      90      95
His Ala Leu Asp Ser Val Lys Leu Ala Gly Glu Ile Gln Lys Arg Ser
      100     105     110
Asp Arg Val Ile Lys Cys Phe Leu Gln Val Asn Ile Ser Lys Glu Glu
      115     120     125
Ser Lys His Gly Phe Ser Arg Glu Glu Leu Leu Glu Ile Leu Pro Glu
      130     135     140
Leu Ala Gly Leu Asp Lys Ile Glu Tyr Val Gly Leu Met Thr Met Ala
145     150     155     160
Pro Phe Glu Ala Ser Ser Glu Gln Leu Lys Glu Ile Phe Lys Ala Ala
      165     170     175
Gln Asp Leu Gln Arg Glu Ile Gln Glu Lys Gln Ile Pro Asn Ile Pro
      180     185     190
Met Thr Glu Leu Ser Met Gly Met Ser Arg Asp Tyr Lys Glu Ala Ile
      195     200     205
Gln Phe Gly Ser Thr Phe Val Arg Ile Gly Thr Ser Phe Phe Lys
210     215     220

```

(2) INFORMATION FOR SEQ ID NO:3530:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 246 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...246
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3530:

```

Asn Asp Val Lys Val Phe Leu Asn Ala Arg Lys Tyr Tyr Arg Ile Leu
1      5      10      15
Phe His Gln Leu Met Gly Phe Ser Pro Gly Ile Ala Val Phe Tyr Lys
      20      25      30
Glu Ser Gln Thr Thr Lys Asn Leu Phe Lys Phe Tyr Tyr Phe Leu Tyr
      35      40      45
Phe Thr Thr Leu Ile Ser Tyr Tyr Phe Phe Phe Thr Phe Val Tyr Asp
      50      55      60
Lys Pro Leu Leu Leu Pro Leu Ile Pro Phe Ser Ile Ile Ile Ala Leu
      65      70      75      80
Val Gln Lys Leu Tyr Arg Ile Glu Asn Gln Gln Leu Phe Leu Leu Lys
      85      90      95
Ser Lys Val Leu Thr Ile Leu Glu Ser Lys Lys Asn Cys Glu Phe Asn
      100     105     110
Leu Gln Asp Tyr His Glu Ile Trp Lys Leu Gln Ser Lys Ser Glu Leu
      115     120     125
Pro Cys Val Ala Leu Ser Tyr Ile Ser Leu Ile Lys Pro Tyr Leu Ser
      130     135     140
Glu Ser Val Arg Glu Gln Ile Asp Leu Leu Glu Val Lys Arg Phe Lys
      145     150     155     160
Lys Ile Asn His Pro Ile Ser Leu Tyr Gly Met Leu Asp Val Ile Lys
      165     170     175
Leu Asn Leu Tyr Leu Arg His Tyr Asn Glu Lys Asn Lys Tyr Glu Ser
      180     185     190
Met Leu Lys Lys Ile Leu Glu Val Arg Pro Asp Phe Val Leu Ile Glu
      195     200     205
Gln Asn Ile Asp Asp Ser Leu Asn Ser Ser Gln Pro Leu Ser Leu Ser
      210     215     220
Leu Ala Ile Ser Glu Ile Gln Leu Leu Leu Glu Val Tyr Met Gly Ile
      225     230     235     240
Lys His Val Ser Thr Lys
      245

```

(2) INFORMATION FOR SEQ ID NO:3531:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 139 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...139

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3531:

```

Gln Ile Val Lys Ser Met Ile Lys Ala Phe Thr Met Leu Glu Ser Leu
1           5           10           15
Leu Ala Leu Ser Leu Val Ser Ile Leu Ala Leu Gly Leu Ser Gly Ser
          20           25           30
Val Gln Ser Thr Phe Ala Ala Val Glu Glu Gln Ile Phe Phe Met Glu
          35           40           45
Phe Glu Glu Leu Tyr Arg Glu Thr Gln Lys Arg Ser Val Ala Ser Gln
          50           55           60
Gln Lys Thr Ser Leu Asn Leu Asp Gly Gln Thr Ile Ser Asn Gly Ser

65           70           75           80
Gln Lys Leu Pro Val Pro Lys Gly Ile Gln Ala Pro Ser Gly Gln Ser
          85           90           95
Ile Thr Phe Asp Arg Ala Gly Gly Asn Ser Ser Leu Ala Lys Val Glu
          100          105          110
Phe Gln Thr Ser Lys Gly Ala Ile Arg Tyr Gln Leu Tyr Leu Gly Asn
          115          120          125
Gly Lys Ile Lys Arg Ile Lys Glu Thr Lys Asn
130           135

```

(2) INFORMATION FOR SEQ ID NO:3532:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 174 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3532:

```

Ser Gln Val Lys Arg Asn Glu Lys His Met Tyr Ile Glu Met Val Asp
1           5           10           15
Glu Thr Gly Gln Val Ser Lys Glu Met Leu Gln Gln Thr Gln Glu Ile
          20           25           30
Leu Glu Phe Ala Ala Lys Lys Leu Gly Lys Glu Asp Lys Glu Met Ala
          35           40           45
Val Thr Phe Val Thr Asn Glu Arg Ser His Glu Leu Asn Leu Glu Tyr

```

50		55		60											
Arg	Asp	Thr	Asp	Arg	Pro	Thr	Asp	Val	Ile	Ser	Leu	Glu	Tyr	Lys	Pro
65					70					75					80
Glu	Leu	Glu	Ile	Ala	Phe	Asp	Glu	Glu	Asp	Leu	Leu	Glu	Asn	Pro	Glu
				85					90					95	
Leu	Ala	Glu	Met	Met	Ser	Glu	Phe	Asp	Ala	Tyr	Ile	Gly	Glu	Leu	Phe
			100					105					110		
Ile	Ser	Ile	Asp	Lys	Ala	His	Glu	Gln	Ala	Glu	Glu	Tyr	Gly	His	Ser
			115				120					125			
Phe	Glu	Arg	Glu	Met	Gly	Phe	Leu	Ala	Val	His	Gly	Phe	Leu	His	Ile
	130					135					140				
Asn	Gly	Tyr	Asp	His	Tyr	Thr	Pro	Glu	Glu	Glu	Ala	Glu	Met	Phe	Gly
145					150				155						160
Leu	Gln	Glu	Glu	Ile	Leu	Thr	Ala	Tyr	Gly	Leu	Thr	Arg	Gln		
				165					170						

(2) INFORMATION FOR SEQ ID NO:3533:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 256 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...256

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3533:

Ser	Pro	Ser	Lys	Val	Ala	Cys	Met	Gly	Gly	Phe	Tyr	Phe	Ile	Ile	His
1				5					10					15	
Asp	Ile	Ile	Glu	Ala	Asn	Gly	Gly	Arg	Lys	Met	Val	Lys	Val	Arg	Leu
			20					25					30		
Tyr	Leu	Val	Arg	His	Gly	Lys	Thr	Met	Phe	Asn	Thr	Ile	Gly	Arg	Ala
		35				40						45			
Gln	Gly	Trp	Ser	Asp	Thr	Pro	Leu	Thr	Ala	Glu	Gly	Glu	Arg	Gly	Ile
	50					55				60					
Gln	Glu	Leu	Gly	Ile	Gly	Leu	Arg	Glu	Ser	Asp	Leu	Gln	Phe	Glu	Arg
65					70				75						80
Ala	Tyr	Ser	Ser	Asp	Ser	Gly	Arg	Thr	Ile	Gln	Thr	Met	Gly	Ile	Ile
				85					90					95	
Leu	Glu	Glu	Leu	Gly	Leu	Gln	Gly	Lys	Ile	Pro	Tyr	Arg	Met	Asp	Lys
			100					105					110		
Arg	Ile	Arg	Glu	Trp	Cys	Phe	Gly	Ser	Phe	Asp	Gly	Ala	Tyr	Asp	Gly
		115					120					125			
Asp	Leu	Phe	Met	Gly	Ile	Ile	Pro	Arg	Ile	Phe	Asn	Val	Asp	His	Val
	130					135					140				
His	Gln	Leu	Ser	Tyr	Ala	Glu	Leu	Ala	Glu	Gly	Leu	Val	Glu	Val	Asp
145					150					155					160
Thr	Ala	Gly	Trp	Ala	Glu	Gly	Trp	Glu	Lys	Leu	Ser	Gly	Arg	Ile	Lys

				165					170					175			
Glu	Gly	Phe	Glu	Ile	Ile	Ala	Lys	Glu	Met	Glu	Asp	Gln	Gly	Gly	Gly		
			180					185					190				
Asn	Ala	Leu	Val	Val	Ser	His	Gly	Met	Thr	Ile	Gly	Thr	Ile	Val	Tyr		
		195					200					205					
Leu	Ile	Asn	Gly	Met	His	Pro	His	Gly	Leu	Asp	Asn	Gly	Ser	Val	Thr		
	210					215				220							
Ile	Leu	Glu	Tyr	Glu	Asp	Gly	Gln	Phe	Arg	Val	Glu	Val	Val	Gly	Asp		
225					230				235						240		
Arg	Ser	Tyr	Arg	Glu	Leu	Gly	Arg	Glu	Lys	Met	Glu	Glu	Gly	Ser	Ile		
			245					250						255			

(2) INFORMATION FOR SEQ ID NO:3534:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 856 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...856

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3534:

Val	Pro	Ser	Lys	Gln	Lys	Ile	Ser	Gln	Gly	Lys	Leu	Asn	Ser	Ala	Ser		
1				5				10						15			
Gly	Gln	Ser	Pro	Val	Ser	Glu	His	Phe	Lys	Lys	Pro	Lys	Arg	Pro	Arg		
			20					25					30				
Ile	Thr	Asn	Leu	Ser	Leu	Phe	Phe	Tyr	Arg	Glu	Lys	Met	Ile	Gly	Asn		
		35				40						45					
Tyr	Leu	Asn	Leu	Pro	Glu	Gln	Lys	His	Leu	Asn	Ser	His	Leu	Phe	Met		
	50					55					60						
Gln	Arg	Asn	Phe	Met	Glu	Val	Tyr	Phe	Ser	Gly	Thr	Ile	Glu	Arg	Ile		
65					70					75					80		
Ile	Phe	Glu	Asn	Pro	Ser	Asn	Phe	Tyr	Arg	Ile	Leu	Leu	Leu	Glu	Ile		
			85					90						95			
Asp	Asp	Thr	Asp	Ala	Glu	Asp	Phe	Asp	Asp	Phe	Glu	Ile	Ile	Val	Thr		
		100						105						110			
Gly	Thr	Met	Ala	Asp	Val	Ile	Glu	Gly	Glu	Asp	Tyr	Thr	Phe	Trp	Gly		
		115						120					125				
Gln	Ile	Val	Gln	His	Ser	Lys	Tyr	Gly	Glu	Gln	Leu	Gln	Ile	Ser	Arg		
	130					135						140					
Tyr	Asp	Arg	Ala	Lys	Pro	Thr	Ser	Lys	Gly	Leu	Val	Lys	Tyr	Phe	Ser		
145					150						155				160		
Ser	Ser	His	Phe	Lys	Gly	Ile	Gly	Leu	Lys	Thr	Ala	Gln	Lys	Ile	Val		
			165					170						175			
Asp	Thr	Tyr	Gly	Glu	Asn	Thr	Ile	Asp	Glu	Ile	Leu	Gln	His	Pro	Glu		
		180						185					190				
Lys	Leu	Glu	Gly	Ile	Ala	Gly	Leu	Ser	Ala	Lys	Asn	Arg	Glu	Ala	Phe		

		195				200				205					
Val	Ser	Thr	Leu	Arg	Leu	Asn	Tyr	Gly	Thr	Glu	Met	Ile	Leu	Ala	Lys
	210					215					220				
Leu	Ala	Asn	Tyr	Gly	Ile	Pro	Asn	Lys	Leu	Ala	Phe	Gln	Ile	Gln	Asp
225					230					235					240
Phe	Tyr	Lys	Glu	Glu	Thr	Leu	Asp	Val	Val	Glu	Asn	Tyr	Pro	Tyr	Gln
			245						250					255	
Leu	Val	Glu	Asp	Ile	Lys	Gly	Leu	Gly	Phe	Thr	Ile	Ala	Asp	Gln	Leu
		260						265					270		
Ala	Glu	Glu	Leu	Gly	Ile	Glu	Ser	Gln	Ala	Pro	Glu	Arg	Phe	Arg	Ala
	275						280					285			
Gly	Leu	Val	His	Ser	Leu	Phe	Gln	Thr	Cys	Met	Glu	Thr	Gly	Asp	Thr
	290					295					300				
Tyr	Val	Glu	Ala	Arg	Asp	Leu	Leu	Glu	Gln	Thr	Leu	Thr	Leu	Leu	Glu
305					310					315					320
Ser	Ser	Arg	Pro	Val	Glu	Leu	Asp	Pro	Ser	Gln	Val	Ala	Gln	Glu	Leu
			325						330					335	
Ser	Tyr	Leu	Ile	Glu	Glu	Asp	Lys	Val	Gln	Gln	Ile	Asp	Thr	Lys	Ile
		340						345					350		
Phe	Asp	Asn	Ser	Leu	Phe	Phe	Ala	Glu	Glu	Gly	Ile	Arg	Ser	His	Leu
	355						360					365			
Ile	Arg	Ile	Leu	Glu	Lys	Gly	Lys	Gln	Lys	Ser	Gln	Asp	Leu	Glu	Thr
	370					375					380				
Ile	Gln	Lys	His	Ile	Thr	Thr	Val	Glu	Gln	Glu	Leu	Gly	Ile	Glu	Tyr
385					390					395					400
Asp	Asn	Ile	Gln	Lys	Gln	Ala	Ile	Cys	Asp	Ala	Ile	Gln	Asn	Lys	Val
			405					410					415		
Phe	Ile	Leu	Thr	Gly	Gly	Pro	Gly	Thr	Gly	Lys	Thr	Thr	Val	Ile	Asn
		420						425					430		
Gly	Ile	Ile	Ala	Val	Tyr	Ala	Leu	Leu	Glu	Gly	Leu	Asp	Phe	Arg	Lys
	435					440					445				
Lys	Asn	Asn	Leu	Pro	Ile	Leu	Leu	Ala	Ala	Pro	Thr	Gly	Arg	Ala	Ala
	450					455				460					
Arg	Arg	Met	Asn	Glu	Leu	Thr	Gly	Leu	Pro	Ser	Ala	Thr	Ile	His	Arg
465					470					475					480
His	Leu	Gly	Met	Thr	Gly	Asp	Asp	Asp	Thr	Ser	His	Leu	Glu	Asp	Tyr
			485						490					495	
Leu	Asp	Ala	Asp	Phe	Ile	Ile	Val	Asp	Glu	Phe	Ser	Met	Val	Asp	Thr
	500							505					510		
Trp	Leu	Ala	Asn	Gln	Leu	Phe	Ser	Asn	Ile	Ser	Ser	Asn	Ser	Lys	Ile
	515						520					525			
Leu	Ile	Val	Gly	Asp	Ser	Asp	Gln	Leu	Pro	Ser	Val	Ser	Pro	Gly	Gln
	530					535					540				
Val	Leu	Ala	Asp	Leu	Leu	His	Ile	Pro	Leu	Ile	Pro	Gln	Thr	Arg	Leu
545					550					555					560
Glu	Lys	Ile	Tyr	Arg	Gln	Ser	Lys	Glu	Ser	Thr	Ile	Val	Thr	Leu	Ala
			565						570					575	
Ser	Gln	Ile	Arg	Gln	Gly	Ile	Leu	Pro	Ala	Asp	Phe	Thr	Gln	Lys	Lys
		580						585					590		
Ala	Asp	Arg	Ser	Tyr	Phe	Glu	Ile	Ala	Ser	Gly	His	Ile	Pro	Ala	Thr
	595					600						605			
Ile	Glu	Lys	Ile	Leu	Gly	Ala	Ala	Leu	Arg	Asn	Gly	Ile	Pro	Ala	Arg
	610					615					620				
Asp	Ile	Gln	Val	Leu	Ala	Pro	Met	Tyr	Arg	Gly	Thr	Ala	Gly	Ile	Asp
625					630					635					640
Ala	Ile	Asn	Gln	Leu	Met	Gln	Asp	Leu	Leu	Asn	Pro	Pro	Gln	Lys	Asp
			645						650					655	

Gln	Leu	Ser	Phe	Glu	Ala	Pro	Gln	Cys	His	Tyr	Arg	Lys	Arg	Asp	Lys
			660					665					670		
Val	Ile	His	Leu	Val	Asn	Asp	Ala	Glu	Ile	Asn	Val	Phe	Asn	Gly	Asp
		675					680					685			
Leu	Gly	Ala	Ile	Thr	Asp	Leu	Ile	Pro	Gly	Lys	Tyr	Thr	Glu	Ser	Lys
	690					695					700				
Gln	Asp	Glu	Ile	Val	Ile	Asp	Phe	Asp	Gly	Asn	Glu	Val	Ser	Tyr	Pro
705					710					715					720
Arg	Asn	Glu	Trp	Tyr	Lys	Ile	Arg	Leu	Ala	Tyr	Ala	Met	Ser	Ile	His
				725					730					735	
Lys	Ser	Gln	Gly	Ser	Glu	Phe	Pro	Val	Val	Ile	Leu	Pro	Ile	Thr	Ser
			740					745					750		
Ala	Ser	Arg	Arg	Met	Leu	Glu	Arg	Asn	Leu	Ile	Tyr	Thr	Ala	Ile	Thr
		755					760					765			
Arg	Ala	Lys	Ser	Lys	Leu	Ile	Leu	Leu	Gly	Glu	Leu	Gln	Ala	Phe	Asp
	770				775						780				
Tyr	Ala	Thr	Gln	His	Ile	Gly	Thr	Ala	Arg	Lys	Thr	Tyr	Leu	Ile	Glu
785					790					795					800
Arg	Phe	Ser	Asp	Leu	Leu	Glu	Asn	Val	Glu	Glu	Lys	Gln	Gln	Ala	Val
				805					810					815	
Ser	Glu	Thr	Val	Thr	Ser	Ser	Ala	Ser	Glu	Gln	Ser	Tyr	Ile	Leu	Thr
			820					825					830		
Glu	Glu	Asn	Trp	Asp	Arg	Ile	Pro	Ala	Met	Ile	Gly	Ile	Thr	Asp	Thr
		835					840					845			
Asp	Leu	Lys	Glu	Ile	Phe	Gly	Lys								
	850					855									

(2) INFORMATION FOR SEQ ID NO:3535:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 249 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...249
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3535:

Val	Phe	Ser	Lys	Phe	Asp	Asn	Leu	Ser	Gly	Leu	Ala	Val	Gly	Ser	Phe
1				5					10					15	
Gly	Pro	Ile	Asp	Ile	Asp	Lys	Asn	Ser	Lys	Thr	Tyr	Gly	Phe	Ile	Thr
			20					25					30		
Thr	Thr	Pro	Lys	Pro	Asn	Trp	Ala	Asn	Val	Asp	Leu	Leu	Gly	Ala	Phe
		35					40					45			
Arg	Arg	Ala	Leu	Asn	Val	Pro	Met	Tyr	Phe	Thr	Thr	Asp	Val	Asn	Ser
	50					55					60				

Ser	Ala	Tyr	Gly	Glu	Met	Val	Ala	Arg	Asn	Asn	Ala	Gly	Gly	Arg	Ile
65					70				75						80
Glu	Asn	Leu	Val	Tyr	Tyr	Thr	Ile	Gly	Thr	Gly	Ile	Gly	Ala	Gly	Val
			85						90					95	
Ile	Gln	Arg	Gly	Glu	Phe	Ile	Gly	Gly	Val	Gly	His	Pro	Glu	Met	Gly
			100					105					110		
His	Tyr	Tyr	Val	Ala	Arg	His	Pro	Met	Asp	Ile	Glu	Lys	Glu	Phe	Lys
			115				120					125			
Gly	Val	Cys	Pro	Phe	His	Lys	Gly	Cys	Leu	Glu	Gly	Tyr	Ala	Ala	Gly
	130					135					140				
Pro	Ser	Leu	Glu	Ala	Arg	Thr	Gly	Val	Arg	Gly	Glu	Asn	Ile	Glu	Leu
145					150					155					160
Asn	Asn	Pro	Val	Trp	Asp	Val	Gln	Ala	Tyr	Tyr	Ile	Ala	Gln	Ala	Ala
				165					170					175	
Val	Asn	Ala	Thr	Val	Thr	Phe	Arg	Pro	Asp	Val	Ile	Val	Phe	Gly	Gly
			180					185					190		
Gly	Val	Met	Ala	Gln	Gln	His	Met	Leu	Asp	Arg	Val	Arg	Glu	Lys	Phe
		195					200					205			
Thr	Ser	Leu	Leu	Asn	Gly	Tyr	Leu	Pro	Val	Pro	Asp	Val	Arg	Asp	Tyr
	210				215						220				
Ile	Val	Thr	Pro	Ala	Val	Ala	Gly	Asn	Gly	Ser	Ala	Thr	Leu	Gly	Asn
225					230					235					240
Phe	Val	Leu	Ala	Lys	Glu	Val	Ser	Lys							
				245											

(2) INFORMATION FOR SEQ ID NO:3536:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...66

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3536:

Met	Ile	Ser	Lys	Ile	Ser	Trp	Met	Lys	Ile	Gly	Ala	Ser	Pro	Ile	Asp
1			5					10					15		
Gly	Ser	Ser	Lys	Arg	Arg	Ser	Phe	Gly	Val	Asp	Ile	Arg	Ala	Arg	Pro
			20					25					30		
Met	Ala	Ser	Ile	Cys	Cys	Ser	Pro	Pro	Glu	Arg	Val	Ala	Ala	Ser	Trp
			35				40						45		
Phe	Phe	Arg	Ser	Ser	Arg	Arg	Gly	Lys	Arg	Glu	Lys	Thr	Phe	Phe	Lys
	50					55					60				
Leu	Ala														
65															

(2) INFORMATION FOR SEQ ID NO:3537:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 217 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...217
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3537:

```

Ile Pro Ser Lys Glu Arg Phe Met Asn Arg Glu Ala Leu Arg Leu Tyr
1      5      10      15
Leu Val Thr Asn Arg Tyr Gln Asp Ser Val Glu Ser Phe Leu Ala Lys
      20      25      30
Val Glu Thr Ala Cys Arg Ser Gly Val Thr Ile Val Gln Leu Arg Glu
      35      40      45
Lys Asn Leu Thr Thr Asn Gln Tyr Tyr Gln Leu Ala Lys Gln Val Lys
      50      55      60
Glu Ile Thr Asp Ala Tyr Gln Val Pro Leu Ile Ile Asp Asp Arg Leu
65      70      75      80
Asp Val Cys Leu Ala Val Asp Ala Ala Gly Leu His Ile Gly Asp Asp
      85      90      95
Glu Leu Pro Val Ser Val Ala Arg Gln Val Leu Gly Pro Glu Lys Ile
      100     105     110
Leu Gly Val Thr Ala Lys Thr Val Lys Arg Ala Leu Glu Ala Glu Lys
      115     120     125
Ser Gly Ala Asp Tyr Leu Gly Thr Gly Ala Ile Phe Pro Thr Thr Thr
      130     135     140
Lys Glu Asn Ala Pro Ile Thr Leu Ile Ser Thr Leu Lys Thr Ile Cys
145     150     155     160
Gln Thr Val Ala Ile Pro Ile Val Ala Ile Gly Gly Leu Thr Ser Glu
      165     170     175
Asn Ile Asp Gln Leu Met Gly Thr Gly Ile Ala Gly Val Ala Val Val
      180     185     190
Arg Asp Leu Met Gln Ala Glu Asp Ile Glu Ala Lys Thr Gln Ala Phe
      195     200     205
Leu Thr Lys Leu His Asp Ile Leu Ser
210      215

```

(2) INFORMATION FOR SEQ ID NO:3538:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 140 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...140

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3538:

Val	Pro	Ser	Asn	Pro	Arg	Pro	Val	Tyr	Gly	Leu	Ala	Ser	Phe	Lys	Ile
1				5					10					15	
Ile	Phe	Phe	Pro	Ser	Ser	Phe	Ser	Leu	Ala	Leu	Tyr	Ile	Pro	Pro	Leu
			20					25					30		
Phe	Glu	Asn	Leu	Ile	Ala	Leu	Ser	Ile	Ile	Lys	Gly	Lys	Ser	Pro	Cys
		35					40					45			
Phe	Leu	Ser	Phe	Leu	Ser	Ser	His	Leu	Phe	Lys	Lys	Ser	Gly	Gly	Thr
	50					55					60				
Ile	Pro	Phe	Gly	Ile	Leu	Asn	Thr	Gly	Lys	Arg	Ser	Ser	Leu	Thr	Thr
65					70				75					80	
Ser	Ser	Pro	Thr	Ile	Asn	Ser	Ser	Ile	Ala	Thr	Phe	Phe	Ser	Ser	Ser
			85						90					95	
Leu	Asp	Gly	Leu	Asn	Thr	Pro	Tyr	Leu	Arg	Tyr	Ile	Gly	Ala	Ser	Ser
		100						105					110		
Gln	Arg	Leu	Ser	Leu	Lys	Ile	Tyr	Gly	Pro	Leu	Tyr	Cys	Phe	Lys	Ala
		115					120					125			
Leu	Ser	Asn	Leu	Cys	Lys	Thr	Asp	Ser	Asn	Ser	Phe				
	130					135					140				

(2) INFORMATION FOR SEQ ID NO:3539:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 232 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...232

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3539:

Lys	Pro	Ser	Asn	Ser	Gln	Gly	Glu	Gln	Ala	Arg	Ile	Gln	Glu	Gln	Gly
1				5					10					15	
Leu	Ser	Leu	Ala	Tyr	Gln	Gln	Thr	Ser	Gln	Gln	Val	Glu	Glu	Leu	Glu
			20					25					30		
Thr	Leu	Trp	Lys	Leu	Gln	Glu	Glu	Glu	Ile	Asp	Arg	Leu	Ser	Glu	Gly

				85					90					95					
Asn	Trp	Asn	Lys	Glu	Asn	Gly	Lys	Asp	Leu	Val	Ala	Ile	Ala	Asp	Thr				
			100					105					110						
Tyr	Ile	Ser	Pro	Ile	Arg	Leu	Tyr	Ser	Gly	Leu	Asn	Gly	Ser	Ala	Asn				
		115					120					125							
Lys	Tyr	Thr	Lys	Val	Glu	Asp	Ile	Pro	Ala	Asn	Gly	Glu	Ile	Ala	Val				
	130					135					140								
Pro	Asn	Asp	Ala	Thr	Asn	Glu	Ser	Arg	Ala	Leu	Tyr	Leu	Leu	Gln	Ser				
145					150					155					160				
Ala	Gly	Leu	Ile	Lys	Leu	Asp	Val	Ser	Gly	Thr	Ala	Leu	Ala	Thr	Val				
				165					170										
Ala	Asn	Ile	Lys	Glu	Asn	Pro	Lys	Asn	Leu	Lys	Ile	Thr	Glu	Leu	Asp				
			180					185					190						
Ala	Ser	Gln	Thr	Ala	Arg	Ser	Leu	Ser	Ser	Val	Asp	Ala	Ala	Val	Val				
		195					200					205							
Asn	Asn	Thr	Phe	Val	Thr	Glu	Ala	Lys	Leu	Asp	Tyr	Lys	Lys	Ala	Leu				
	210					215					220								
Phe	Lys	Glu	Gln	Ala	Asp	Lys	Asn	Ser	Lys	Gln	Trp	Tyr	Asn	Ile	Ile				
225					230					235					240				
Val	Ala	Lys	Lys	Asp	Trp	Glu	Thr	Ser	Pro	Lys	Ala	Asp	Ala	Ile	Lys				
				245					250					255					
Ile	Val	Ile	Ala	Ala															
				260															

(2) INFORMATION FOR SEQ ID NO:3541:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3541:

Thr	Leu	Ser	Asn	Gly	Trp	Cys	Ser	Met	Ser	Asp	Ser	Arg	Gly	Lys	Ser				
1				5				10					15						
Thr	Leu	Ala	Gln	Leu	Ile	Pro	Arg	Leu	Phe	Asp	Pro	Gln	Asn	Gly	Ala				
		20					25					30							
Ile	Lys	Ile	Gly	Gly	Thr	Asp	Ile	Arg	Asp	Val	Ser	Glu	Gly	Asn	Leu				
	35					40						45							
Arg	Gln	Thr	Val	Ser	Ser	Phe	Ser	Lys	Arg	Ser	Ile	Leu	Phe	Ser	Val				
	50					55					60								
Thr	Ile	Ala	Asp	Asn	Leu	Arg	Gln	Gly	Lys	Gly	Asn	Ala	Thr	Leu	Phe				
65				70					75					80					
Glu	Met	Glu	Arg	Ala	Ala	Asn	Ile	Ala	Gln	Ala	Ser	Glu	Phe	Ile	His				
				85				90					95						
Arg	Met	Glu	Lys	Asn	Phe	Glu	Ser	Pro	Val	Glu	Glu	Arg	Gly	Thr	Asn				

			100					105				110			
Phe	Ser	Gly	Gly	Gln	Lys	Gln	Arg	Met	Ser	Ile	Ala	Arg	Gly	Ile	Val
		115					120					125			
Ser	Asn	Pro	Arg	Ile	Leu	Ile	Phe	Asp	Asp	Ser	Thr	Ser	Ala	Leu	Asp
	130					135					140				
Ala	Lys	Ser	Glu	Arg	Leu	Val	Gln	Glu	Ala	Leu	Asn	Lys	Asp	Leu	Lys
145					150					155					160
Gly	Thr	Thr	Thr	Ile	Ile	Ile	Ala	Gln	Lys	Ile	Ser	Ser	Val	Val	His
				165					170				175		
Ala	Asp	Lys	Ile	Leu	Val	Leu	Asn	Gln	Gly	Arg	Leu	Ile	Gly	Gln	Gly
		180						185					190		
Thr	His	Ala	Asp	Leu	Val	Ala	Asn	Asn	Ala	Val	Tyr	Arg	Glu	Ile	Tyr
	195						200					205			
Glu	Thr	Gln	Lys												
	210														

(2) INFORMATION FOR SEQ ID NO:3542:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 239 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...239

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3542:

Ile	Ser	Ser	Lys	Gln	Thr	Leu	Leu	Asn	Val	Phe	Leu	Asp	Lys	Leu	Ala
1			5					10					15		
Gly	Val	Ser	Asp	Pro	Glu	Gln	Lys	Arg	Lys	Ile	Ile	Gly	Asn	Glu	Ser
		20					25					30			
Val	Tyr	Val	Phe	Asp	Asp	Glu	Ala	Gly	Lys	Leu	Lys	Asp	Val	Lys	Phe
	35					40					45				
Leu	Ala	Gln	Gly	Thr	Leu	Tyr	Thr	Asp	Val	Val	Glu	Ser	Gly	Thr	Asp
	50				55					60					
Thr	Ala	Gln	Thr	Ile	Lys	Ser	His	His	Asn	Val	Gly	Gly	Leu	Pro	Glu
65				70					75					80	
Asp	Met	Gln	Phe	Glu	Leu	Ile	Glu	Pro	Leu	Asn	Thr	Leu	Tyr	Lys	Asp
		85						90					95		
Glu	Val	Arg	Ala	Leu	Gly	Thr	Glu	Leu	Gly	Met	Pro	Asp	His	Ile	Val
	100						105				110				
Trp	Arg	Gln	Pro	Phe	Pro	Gly	Pro	Gly	Leu	Ala	Ile	Arg	Val	Met	Gly
	115					120					125				
Glu	Ile	Thr	Glu	Glu	Lys	Leu	Glu	Thr	Val	Arg	Glu	Ser	Asp	Ala	Ile
	130				135				140						
Leu	Arg	Glu	Glu	Ile	Ala	Lys	Ala	Gly	Leu	Asp	Arg	Asp	Ile	Trp	Gln
145				150				155						160	
Tyr	Phe	Thr	Val	Asn	Thr	Gly	Val	Arg	Ser	Val	Gly	Val	Met	Gly	Asp

				165				170					175				
Gly	Arg	Thr	Tyr	Asp	Tyr	Thr	Ile	Ala	Ile	Arg	Ala	Ile	Thr	Ser	Ile		
			180					185					190				
Asp	Gly	Met	Thr	Ala	Asp	Phe	Ala	Lys	Ile	Pro	Trp	Glu	Val	Leu	Gln		
		195					200					205					
Lys	Ile	Ser	Val	Arg	Ile	Val	Asn	Glu	Val	Asp	His	Val	Asn	Arg	Ile		
	210					215					220						
Val	Tyr	Asp	Ile	Thr	Ser	Lys	Pro	Pro	Ala	Thr	Val	Glu	Trp	Glu			
225					230					235							

(2) INFORMATION FOR SEQ ID NO:3543:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 88 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...88
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3543:

Asn	Ala	Ser	Lys	Ala	Ile	Ser	Phe	Ile	Leu	Phe	Leu	Leu	Ile	Leu	Phe		
1				5				10					15				
Glu	Asn	Leu	Phe	Lys	Pro	Arg	Gln	Arg	Arg	Leu	Thr	Val	Arg	Met	Leu		
		20					25					30					
Pro	Thr	Ser	Ser	Val	Leu	Ser	Ala	Thr	Ser	Lys	Leu	Tyr	Phe	Glu	Gln		
		35				40					45						
Pro	Thr	Thr	Ser	Phe	Leu	Val	Cys	Ser	Leu	Ile	Phe	Ile	Asp	Tyr	Lys		
	50				55				60								
Met	Val	Leu	Ile	Leu	Phe	Phe	Lys	Ser	Gly	Thr	Thr	Ser	Ala	Ser	Asn		
65				70				75							80		
Gln	Gly	Phe	Leu	Ala	Ile	Gln	Ile										
				85													

(2) INFORMATION FOR SEQ ID NO:3544:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 101 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3544:

```

Leu Pro Pro Lys Phe Ala Ala Leu Ala Gln Ile Ile Pro Ser Pro Val
1          5          10          15
Leu Gly Gly Ala Met Leu Val Met Phe Val Phe Val Ser Ile Gln Gly
          20          25          30
Met Gln Ile Leu Ala Arg Val Asp Phe Ala Asn Asn Glu His Asn Phe
          35          40          45
Leu Ile Ala Ala Val Ser Ile Ala Ala Gly Val Gly Leu Asn Asn Ser
          50          55          60
Asn Leu Phe Val Ser Met Pro Thr Ala Phe Gln Met Phe Phe Ser Asn
65          70          75          80
Gly Ile Val Val Ala Ser Leu Leu Ala Ile Val Leu Asn Ala Val Leu
          85          90          95
Asn His Lys Lys Lys
          100

```

(2) INFORMATION FOR SEQ ID NO:3545:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 89 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...89

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3545:

```

Trp Pro Pro Lys Leu Asp Cys Pro Phe Pro Leu Gln Arg Ala Gln Asn
1          5          10          15
Leu Ser Leu Ile Leu Ser Phe Leu Thr Pro Gln Asn Gln Phe Asn Glu
          20          25          30
Thr Phe Phe Leu Lys Thr Ser Ile Thr Tyr Phe Pro Tyr Ser Gly Leu
          35          40          45
Lys Arg Ile Ser Glu Ile Arg Ile Asp Leu Gln Val Tyr Leu Lys Ser
          50          55          60
Lys Ile Leu Ile Lys Ala Lys Ile Ala Asp Pro Pro Cys Phe Lys Ile
65          70          75          80
Ile Phe Leu Ser Ala Val Lys Glu Pro
          85

```

(2) INFORMATION FOR SEQ ID NO:3546:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 130 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3546:

Lys	Tyr	Pro	Lys	Ser	Ser	Glu	Phe	Glu	Asp	Ile	Thr	Asp	Asp	Ile	Phe
1				5				10						15	
Lys	Phe	Thr	Thr	Asn	Phe	Thr	Glu	Glu	Thr	Leu	Glu	Ala	Gly	Glu	Ala
			20				25						30		
Trp	Val	Asn	Asp	Asn	Val	Pro	Gly	Val	Lys	Ala	Met	Thr	Thr	Gly	Phe
		35				40					45				
Glu	Ser	Ile	Asp	Ile	Val	Leu	Asp	Tyr	Val	Asp	Lys	Gly	Val	Ala	Ile
	50				55					60					
Val	Glu	Leu	Val	Lys	Lys	Leu	Gly	Ile	Thr	Met	Asp	Gln	Val	Met	Ala
65				70					75					80	
Phe	Gly	Asp	Asn	Leu	Asn	Asp	Leu	His	Met	Met	Gln	Val	Val	Gly	His
			85					90						95	
Pro	Val	Ala	Pro	Glu	Asn	Ala	Arg	Pro	Glu	Ile	Leu	Glu	Leu	Ala	Lys
			100					105						110	
Thr	Val	Ile	Gly	His	His	Lys	Asp	Gln	Ser	Val	Ile	Ala	Cys	Met	Glu
			115				120						125		

Gly Leu
130

(2) INFORMATION FOR SEQ ID NO:3547:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...96

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3547:

Pro	Pro	Pro	Lys	Ala	Gly	Gly	Lys	Ser	Lys	Ser	Thr	Asn	Ser	Arg	Leu
1				5					10					15	
Leu	Arg	His	Trp	Ser	Thr	His	Tyr	Leu	Met	Leu	Asp	Asn	Asn	Ala	Lys
			20					25					30		
Lys	Leu	Leu	Ile	Lys	Ala	Cys	Leu	Ser	Ala	Leu	Ser	Thr	Thr	Phe	Ser
		35					40					45			
Cys	His	Thr	Pro	Ser	Phe	Ile	Ile	Leu	Tyr	Ser	Met	Lys	Ile	Lys	Glu
	50					55					60				
Gln	Thr	Arg	Lys	Leu	Ala	Ala	Ser	Cys	Ser	Lys	His	Cys	Phe	Glu	Val
65					70					75					80
Val	Asp	Lys	Thr	Asp	Glu	Val	Ser	His	Ile	His	Thr	Val	Arg	Arg	Arg
				85					90					95	

(2) INFORMATION FOR SEQ ID NO:3548:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3548:

His	Phe	Thr	Lys	Glu	Glu	Lys	Ile	Lys	Met	Lys	Leu	His	Glu	Leu	Lys
1				5					10					15	
Pro	Ala	Glu	Gly	Ser	Arg	Lys	Val	Arg	Asn	Arg	Val	Gly	Arg	Gly	Thr
			20					25					30		
Ser	Ser	Gly	Asn	Gly	Lys	Thr	Ser	Gly	Arg	Gly	Gln	Lys	Gly	Gln	Lys
		35				40					45				
Ala	Arg	Ser	Gly	Gly	Gly	Val	Arg	Leu	Gly	Phe	Glu	Gly	Gly	Gln	Thr
	50					55					60				
Pro	Leu	Phe	Arg	Arg	Leu	Pro	Lys	Arg	Gly	Phe	Thr	Asn	Ile	Asn	Ala
65					70					75					80
Lys	Glu	Tyr	Ala	Ile	Val	Asn	Leu	Asp	Gln	Leu	Asn	Val	Phe	Glu	Asp
				85				90						95	
Gly	Ala	Glu	Val	Thr	Pro	Val	Val	Leu	Ile	Glu	Ala	Gly	Ile	Val	Lys
			100					105					110		
Ala	Glu	Lys	Ser	Gly	Ile	Lys	Ile	Leu	Gly	Asn	Gly	Glu	Leu	Thr	Lys
		115				120						125			
Lys	Leu	Thr	Val	Lys	Ala	Ala	Lys	Phe	Ser	Lys	Ser	Ala	Glu	Glu	Ala
	130					135					140				
Ile	Thr	Ala	Lys	Gly	Gly	Ser	Val	Glu	Val	Ile					
145					150					155					

(2) INFORMATION FOR SEQ ID NO:3549:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 290 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...290
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3549:

```

Pro Asn Thr Lys  Thr Arg Arg Ile Lys  Gln Ile Met Lys Leu Ala Gln
1      5      10      15
Leu Phe Ser  Asn Phe Glu Glu Glu Leu Ile Arg Gln Gly Glu Glu Ala
20     25     30
Glu Ser Leu Ser Phe Val Tyr Arg Ser Leu Lys Asn Leu Ser Phe Thr
35     40     45
Asp Phe Ile Phe Ala Leu Gln Gln Glu Val Thr Thr Glu Glu Glu Lys
50     55     60
Gln Phe Val Glu Asp  Ile Tyr Gln Gln Leu Ala Ala His Lys Pro Ala
65     70     75     80
Gln Tyr Ile Ile Gly Gln Ala Asp Phe Tyr Gly Met His Leu Lys Val
85     90     95
Asp Glu Arg Val Leu Ile Pro Arg Pro Glu Thr Glu Glu Leu Val Glu
100    105    110
Leu Ile Leu Thr Glu Asn Leu Glu Thr Asn Leu Ser Val Leu Asp Ile
115    120    125
Gly Thr Gly Ser Gly Ala  Ile Ala Leu Ala Leu Ala Lys Asn Arg Pro
130    135    140
Asp Trp Ser Val Thr  Ala Ala Asp Val Ser  Gln Glu Ala Leu Glu Leu
145    150    155    160
Ala Ser Glu Asn Ala Ser Asp Gln Asn Leu Asn Ile Phe Phe Lys Lys
165    170    175
Ser Asp Cys Phe Ala Glu Ile Ser Glu Lys Tyr Asp Ile Ile Val Ser
180    185    190
Asn Pro Pro Tyr Ile Ser Arg Glu Asp Glu Ser Glu Val Gly Leu Asn
195    200    205
Val Leu His Ser Glu Pro His Leu Ala Leu Phe Ala Asp Glu Asp Gly
210    215    220
Leu Ala Ile Tyr Cys Arg Ile Ala Glu Asp Ala Lys Asp Tyr Leu Lys
225    230    235    240
Asp Gly Gly Lys Ile Tyr Leu Glu Ile Gly Tyr Lys Gln Gly Gln Ser
245    250    255
Val Pro Glu Leu Phe Arg Lys His Leu Pro Glu Lys Lys Val Arg Thr
260    265    270
Leu Lys Asp Gln Phe Gly Gln Asp Arg Met Val Val Val Asp Asp Gly
275    280    285
Gln Asp
290

```

(2) INFORMATION FOR SEQ ID NO:3550:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...91

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3550:

Cys	Ile	Thr	Lys	Ser	Ser	Thr	Leu	Pro	Ser	Arg	Ala	Gln	Ser	Leu	Cys
1				5					10					15	
Gln	Lys	Asn	Ser	Ile	Asn	Met	Pro	Glu	Lys	Glu	His	Lys	Arg	Ala	His
			20					25					30		
Lys	Lys	Arg	Gln	Lys	Gln	Asp	Leu	Leu	Asn	Lys	Gly	Ser	Leu	Phe	Asp
			35				40					45			
Arg	Leu	Ser	Cys	Ser	Cys	Leu	Pro	Tyr	Leu	Arg	Val	Leu	Val	Ser	Leu
			50				55				60				
Tyr	Tyr	Thr	Phe	Lys	Glu	Ile	Leu	Ser	Thr	Glu	Asn	Trp	Lys	Phe	Tyr
65					70					75					80
Ala	Leu	Lys	Ser	Lys	Asn	Arg	Ser	Ile	Lys	Thr					
				85					90						

(2) INFORMATION FOR SEQ ID NO:3551:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 414 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...414

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3551:

Asn	Val	Thr	Asn	Ser	Phe	Thr	Thr	Asn	Arg	Asn	Leu	Asn	Glu	Met	Glu
1				5					10					15	
Phe	Ser	Met	Lys	Ser	Val	Lys	Gly	Leu	Leu	Phe	Ile	Ile	Ala	Ser	Phe

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...488

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3552:

Glu	Leu	Thr	Asn	Asp	Leu	Tyr	Arg	His	Ile	Leu	Ser	Leu	Pro	Lys	His
1				5					10					15	
Ser	Arg	Asp	Arg	Leu	Thr	Thr	Ser	Ser	Leu	Val	Thr	Arg	Leu	Thr	Ser
			20					25					30		
Asp	Thr	Tyr	Gln	Ile	Gln	Thr	Gly	Ile	Asn	Gln	Phe	Leu	Arg	Leu	Phe
			35				40					45			
Leu	Arg	Ala	Pro	Ile	Ile	Val	Phe	Gly	Ala	Ile	Phe	Met	Ala	Tyr	Arg
			50			55					60				
Ile	Ser	Ala	Glu	Leu	Thr	Phe	Trp	Phe	Leu	Val	Met	Val	Ala	Ile	Leu
65					70					75					80
Thr	Ile	Val	Ile	Val	Gly	Leu	Ser	Arg	Leu	Val	Asn	Pro	Leu	Tyr	Ser
				85					90					95	
Ser	Leu	Arg	Lys	Lys	Thr	Asp	Gln	Leu	Val	Gln	Glu	Thr	Arg	Gln	Gln
			100				105						110		
Leu	Gln	Gly	Met	Arg	Val	Ile	Arg	Ala	Phe	Gly	Gln	Glu	Lys	Arg	Glu
			115				120					125			
Leu	Gln	Ile	Phe	Gln	Thr	Leu	Asn	Gln	Val	Tyr	Ala	Arg	Leu	Gln	Glu
			130			135					140				
Lys	Thr	Gly	Phe	Trp	Ser	Ser	Leu	Leu	Thr	Pro	Leu	Thr	Tyr	Leu	Ile
145					150					155					160
Val	Asn	Gly	Thr	Leu	Leu	Val	Ile	Ile	Trp	Gln	Gly	Tyr	Ile	Ser	Ile
				165					170					175	
Gln	Gly	Gly	Val	Leu	Ser	Gln	Gly	Ala	Leu	Ile	Ala	Leu	Ile	Asn	Tyr
			180				185						190		
Leu	Leu	Gln	Ile	Leu	Val	Glu	Leu	Val	Lys	Leu	Ala	Met	Leu	Ile	Asn
			195				200					205			
Ser	Leu	Asn	Gln	Ser	Tyr	Ile	Ser	Val	Lys	Arg	Ile	Glu	Glu	Val	Phe
			210			215					220				
Val	Glu	Ala	Pro	Glu	Asp	Ile	His	Ser	Glu	Leu	Glu	Gln	Lys	Gln	Ala
225					230					235					240
Thr	Arg	Asp	Lys	Val	Leu	Gln	Val	Gln	Glu	Leu	Thr	Phe	Thr	Tyr	Pro
			245						250					255	
Asp	Ala	Ala	Gln	Pro	Ser	Leu	Arg	Tyr	Ile	Ser	Phe	Asp	Met	Thr	Gln
			260					265					270		
Gly	Gln	Ile	Leu	Gly	Ile	Ile	Gly	Gly	Thr	Gly	Ser	Gly	Lys	Ser	Ser
			275				280					285			
Leu	Val	Gln	Leu	Leu	Leu	Gly	Leu	Tyr	Pro	Val	Asp	Lys	Gly	Asn	Ile
			290			295					300				
Asp	Leu	Tyr	Gln	Asn	Gly	Arg	Ser	Pro	Leu	Asn	Leu	Glu	Gln	Trp	Arg
305					310					315					320
Ser	Trp	Ile	Ala	Tyr	Val	Pro	Gln	Lys	Val	Glu	Leu	Phe	Lys	Gly	Thr
			325						330					335	
Ile	Arg	Ser	Asn	Leu	Thr	Leu	Gly	Phe	Asn	Gln	Glu	Val	Ser	Asp	Gln
			340				345						350		

Glu	Leu	Trp	Gln	Ala	Leu	Glu	Ile	Ala	Gln	Ala	Lys	Asp	Phe	Val	Ser
		355					360					365			
Glu	Lys	Glu	Gly	Leu	Leu	Asp	Ala	Leu	Val	Glu	Ala	Gly	Gly	Arg	Asn
	370					375					380				
Phe	Ser	Gly	Gly	Gln	Lys	Gln	Arg	Leu	Ser	Ile	Ala	Arg	Ala	Val	Leu
385					390					395					400
Arg	Gln	Ala	Pro	Phe	Leu	Ile	Leu	Asp	Asp	Ala	Thr	Ser	Ala	Leu	Asp
			405						410					415	
Thr	Ile	Thr	Glu	Ser	Lys	Leu	Leu	Lys	Ala	Ile	Arg	Glu	Asn	Phe	Pro
			420					425					430		
Asn	Thr	Ser	Leu	Ile	Leu	Ile	Ser	Gln	Arg	Thr	Ser	Thr	Leu	Gln	Met
		435					440					445			
Ala	Asp	Gln	Ile	Leu	Leu	Leu	Glu	Lys	Gly	Glu	Leu	Leu	Ala	Val	Gly
	450					455				460					
Lys	His	Asp	Asp	Leu	Met	Lys	Ser	Ser	Gln	Val	Tyr	Cys	Glu	Ile	Asn
465					470					475					480
Ala	Ser	Gln	His	Gly	Lys	Glu	Asp								
				485											

(2) INFORMATION FOR SEQ ID NO:3553:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...317

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3553:

Asp	Met	Thr	Lys	Glu	Phe	His	His	Val	Thr	Val	Leu	Leu	His	Glu	Thr
1			5					10					15		
Ile	Asp	Met	Leu	Asp	Val	Lys	Pro	Asp	Gly	Ile	Tyr	Val	Asp	Ala	Thr
		20					25					30			
Leu	Gly	Gly	Ala	Gly	His	Ser	Glu	Tyr	Leu	Leu	Ser	Lys	Leu	Ser	Glu
	35					40						45			
Lys	Gly	His	Leu	Tyr	Ala	Phe	Asp	Gln	Asp	Gln	Asn	Ala	Ile	Asp	Asn
	50					55					60				
Ala	Gln	Lys	Arg	Leu	Ala	Pro	Tyr	Ile	Glu	Lys	Gly	Val	Val	Thr	Phe
65					70				75					80	
Ile	Lys	Asp	Asn	Phe	Arg	His	Leu	Gln	Ala	Arg	Leu	Arg	Glu	Ala	Gly
			85					90					95		
Val	Gln	Glu	Ile	Asp	Gly	Ile	Cys	Tyr	Asp	Leu	Gly	Val	Ser	Ser	Pro
		100					105					110			
Gln	Leu	Asp	Gln	Arg	Glu	Arg	Gly	Phe	Ser	Tyr	Lys	Lys	Asp	Ala	Pro
	115					120					125				
Leu	Asp	Met	Arg	Met	Asn	Gln	Asp	Ala	Ser	Leu	Thr	Ala	Tyr	Glu	Val

130		135		140											
Val	Asn	His	Tyr	Asp	Tyr	His	Asp	Leu	Val	Arg	Ile	Phe	Phe	Lys	Tyr
145					150					155					160
Gly	Glu	Asp	Lys	Phe	Ser	Lys	Gln	Ile	Ala	Arg	Lys	Ile	Glu	Gln	Ala
				165						170					175
Arg	Glu	Val	Lys	Pro	Ile	Glu	Thr	Thr	Glu	Leu	Ala	Glu	Ile	Ile	
				180						185					190
Lys	Leu	Val	Lys	Pro	Ala	Lys	Glu	Leu	Lys	Lys	Lys	Gly	His	Pro	Ala
		195					200					205			
Lys	Gln	Ile	Phe	Gln	Ala	Ile	Arg	Ile	Glu	Val	Asn	Asp	Glu	Leu	Gly
	210					215					220				
Ala	Ala	Asp	Glu	Ser	Ile	Gln	Gln	Ala	Met	Asp	Met	Leu	Ala	Leu	Asp
225					230					235					240
Gly	Arg	Ile	Ser	Val	Ile	Thr	Phe	His	Ser	Leu	Glu	Asp	Arg	Leu	Thr
				245						250					255
Lys	Gln	Leu	Phe	Lys	Glu	Ala	Ser	Thr	Val	Glu	Val	Pro	Lys	Gly	Leu
			260					265					270		
Pro	Phe	Ile	Pro	Asp	Asp	Leu	Lys	Pro	Lys	Met	Glu	Leu	Val	Ser	Arg
		275					280					285			
Lys	Pro	Ile	Leu	Pro	Ser	Ala	Glu	Glu	Leu	Glu	Ala	Asn	Asn	Arg	Ser
	290				295						300				
His	Ser	Ala	Lys	Leu	Arg	Val	Val	Arg	Lys	Ile	His	Lys			
305					310					315					

(2) INFORMATION FOR SEQ ID NO:3554:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...189

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3554:

Ser	Val	Thr	Asn	Ser	Leu	Lys	Asn	Asp	Lys	Ile	Gly	Glu	Ile	Phe	Asp
1				5					10					15	
Tyr	Gln	Ile	Phe	Lys	Glu	Gly	Ile	Val	Ser	Tyr	Phe	Glu	Gln	Phe	Met
			20				25						30		
Gln	Ala	Asn	Gln	Ala	Tyr	Val	Ala	Leu	His	Gly	Gln	Leu	Asn	Leu	Pro
		35				40					45				
Leu	Lys	Pro	Lys	Thr	Arg	Val	Ala	Ile	Val	Thr	Cys	Met	Asp	Ser	Arg
	50				55					60					
Leu	His	Val	Ala	Gln	Ala	Leu	Gly	Leu	Ala	Leu	Gly	Asp	Ala	His	Ile
65				70					75					80	
Leu	Arg	Asn	Ala	Gly	Gly	Arg	Val	Thr	Glu	Asp	Met	Ile	Arg	Ser	Leu
			85					90						95	

Val	Ile	Ser	Gln	Gln	Gln	Met	Gly	Thr	Arg	Glu	Ile	Val	Val	Leu	His
			100					105					110		
His	Thr	Asp	Cys	Gly	Ala	Gln	Thr	Phe	Glu	Asn	Glu	Pro	Phe	Gln	Glu
		115					120					125			
Tyr	Leu	Lys	Glu	Glu	Leu	Gly	Val	Asp	Val	Ser	Asp	Gln	Asp	Phe	Leu
	130					135					140				
Pro	Phe	Gln	Asp	Ile	Glu	Glu	Ser	Val	Arg	Glu	Asp	Met	Gln	Leu	Leu
145					150					155					160
Ile	Glu	Ser	Pro	Leu	Ile	Pro	Asp	Asp	Val	Ile	Ile	Ser	Gly	Ala	Ile
			165					170						175	
Tyr	Asn	Val	Asp	Thr	Gly	Ser	Met	Thr	Val	Val	Glu	Leu			
			180					185							

(2) INFORMATION FOR SEQ ID NO:3555:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3555:

Lys	Ala	Thr	Lys	Gln	Leu	Ile	Arg	Lys	Ile	His	Met	Glu	Gln	Leu	His
1				5					10					15	
Phe	Ile	Thr	Lys	Leu	Leu	Asp	Ile	Lys	Asp	Pro	Asn	Ile	Gln	Ile	Leu
			20					25					30		
Asp	Ile	Ile	Asn	Lys	Asp	Thr	His	Lys	Glu	Ile	Ile	Ala	Lys	Leu	Asp
	35					40					45				
Tyr	Asp	Ala	Pro	Ser	Cys	Pro	Glu	Cys	Gly	Asn	Gln	Leu	Lys	Lys	Tyr
	50					55					60				
Asp	Phe	Gln	Lys	Pro	Ser	Lys	Ile	Pro	Tyr	Leu	Glu	Thr	Thr	Gly	Met
65					70				75						80
Pro	Thr	Arg	Ile	Leu	Leu	Arg	Lys	Arg	Arg	Phe	Lys	Cys	Tyr	His	Cys
			85					90						95	
Ser	Lys	Met	Met	Val	Ala	Glu	Thr	Ser	Ile	Val	Lys	Asn	Asn	His	Gln
			100					105					110		
Ile	Pro	Arg	Ile	Ile	Asn	Gln	Lys	Ile	Ala	Gln	Lys	Leu	Ile	Glu	Lys
		115					120					125			
Ile	Ser	Met	Thr	Asp	Ile	Ala	His	Gln	Leu	Ser	Ile	Ser	Thr	Ser	Thr
	130					135					140				
Val	Ile	Arg	Lys	Leu	Asn	Asp	Phe	His	Phe	Lys	His	Asp	Phe	Ser	Cys
145					150					155					160
Leu	Pro	Glu	Ile	Met	Ser	Trp	Asp	Val	Glu	Thr	Val	Arg	Gly	Val	Thr
			165					170						175	
Val	Ser	Ile	Gly	Arg	Trp	Arg									

(2) INFORMATION FOR SEQ ID NO:3556:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3556:

```

Lys Ala Thr Lys Gln Leu Ile Arg Lys Asn His Met Glu Gln Leu His
1          5          10          15
Phe Ile Thr Lys Leu Leu Asp Ile Lys Asp Pro Asn Val Gln Ile Leu
          20          25          30
Asn Ile Ile Asn Lys Asp Thr His Lys Glu Ile Ile Ala Lys Leu Asp
          35          40          45
Tyr Asp Ala Pro Ser Cys Pro Glu Cys Gly Asn Gln Leu Lys Lys Tyr
          50          55          60
Asp Phe Gln Lys Pro Ser Lys Ile Pro Tyr Leu Glu Thr Thr Gly Ile
65          70          75          80
Pro Thr Arg Ile Leu Leu Arg Lys Arg Arg Phe Lys Cys Tyr His Cys
          85          90          95
Ser Lys Met Met Val Ala Glu Thr Ser Asp Asp Val Gln Ser Tyr Leu
          100          105          110

Phe Ser Phe Tyr Tyr Ile Thr Val Leu Asn Leu Ala Leu Leu Asp Ser
          115          120          125
Pro Leu Leu Ser Ile Tyr Ser Glu Lys Arg Arg Lys Asn Leu Arg Ile
          130          135          140
Ile Ser Gly Leu Val Ile Lys Phe Phe Ser Gln Tyr Arg Lys Val Glu
145          150          155          160
Lys Val Val Val Phe His Glu Tyr Val Arg
          165          170

```

(2) INFORMATION FOR SEQ ID NO:3557:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...420

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3557:

Lys	Ala	Thr	Lys	Gln	Leu	Ile	Arg	Lys	Ile	His	Met	Gly	Gln	Leu	His
1				5					10					15	
Phe	Ile	Thr	Lys	Leu	Leu	Asp	Ile	Lys	Asp	Thr	Asn	Ile	Gln	Ile	Ile
			20					25					30		
Asp	Val	Val	Asn	Arg	Asp	Ser	His	Lys	Glu	Ile	Ile	Ala	Lys	Leu	Asp
		35				40						45			
Tyr	Asp	Ala	Pro	Ser	Cys	Pro	Gly	Cys	Gly	Asn	Gln	Leu	Lys	Lys	Tyr
	50				55					60					
Asp	Phe	Gln	Lys	Pro	Ser	Lys	Ile	Pro	Tyr	Leu	Glu	Thr	Thr	Gly	Met
65					70				75						80
Pro	Thr	Arg	Ile	Leu	Leu	Arg	Lys	Arg	Arg	Phe	Lys	Cys	Tyr	Gln	Cys
			85					90						95	
Ser	Lys	Ile	Ala	Val	Ala	Glu	Thr	Ser	Leu	Val	Lys	Lys	Asn	His	Gln
			100					105					110		
Ile	Pro	Arg	Ile	Ile	Asn	Gln	Lys	Ile	Ala	Gln	Lys	Leu	Ile	Glu	Lys
	115					120						125			
Ile	Ser	Met	Thr	Asp	Ile	Ala	His	Gln	Leu	Ser	Ile	Ser	Thr	Ser	Thr
	130				135						140				
Val	Ile	Arg	Lys	Leu	Asn	Asp	Phe	His	Phe	Lys	His	Asp	Phe	Ser	Cys
145					150					155					160
Leu	Pro	Glu	Ile	Met	Ser	Trp	Asp	Glu	Tyr	Ala	Phe	Thr	Lys	Gly	Lys
			165					170						175	
Met	Ser	Phe	Ile	Ala	Gln	Asp	Phe	Asn	Asn	Leu	Asn	Ile	Ile	Thr	Val
		180				185						190			
Leu	Glu	Gly	Arg	Thr	Gln	Ala	Ile	Ile	Arg	Asn	His	Phe	Leu	Arg	Tyr
	195					200						205			
Asp	Arg	Val	Val	Arg	Cys	Arg	Val	Lys	Ile	Ile	Thr	Met	Asp	Met	Phe
	210				215						220				
Ser	Pro	Tyr	Tyr	Gly	Leu	Ala	Lys	Gln	Leu	Arg	Phe	His	Ile	Val	Gln
225					230					235					240
His	Leu	Ser	Cys	Ala	Met	Ser	Arg	Val	Arg	Val	Gln	Ile	Met	Asn	Gln
			245					250						255	
Phe	His	Arg	Lys	Ser	His	Glu	Tyr	Lys	Ala	Ile	Lys	Arg	Tyr	Trp	Lys
		260					265						270		
Leu	Ile	Gln	Asp	Ser	Arg	Lys	Leu	Ser	Asp	Lys	Arg	Phe	Tyr	Arg	
	275					280					285				
Pro	Thr	Phe	Arg	Ile	His	Leu	Thr	Asn	Lys	Glu	Ile	Leu	Asp	Lys	Leu
	290				295						300				
Leu	Ser	Tyr	Ser	Gln	Asp	Leu	Lys	His	His	Tyr	Gln	Leu	Tyr	Gln	Leu
305					310					315					320
Leu	Leu	Phe	His	Phe	Gln	Asn	Lys	Glu	Pro	Glu	Lys	Phe	Phe	Gly	Leu
			325					330						335	
Ile	Glu	Asp	Asn	Leu	Lys	Gln	Val	His	Pro	Ile	Phe	Gln	Thr	Val	Phe
		340					345					350			
Lys	Thr	Phe	Leu	Lys	Asp	Lys	Glu	Lys	Ile	Val	Asn	Ala	Leu	Gln	Leu
		355				360					365				
His	Tyr	Ser	Asn	Val	Lys	Leu	Glu	Ala	Thr	Asn	Asn	Leu	Ile	Lys	Leu
	370					375					380				

Ile	Lys	Arg	Asn	Ala	Phe	Gly	Phe	Arg	Asn	Phe	Glu	Asn	Phe	Lys	Lys
385					390					395					400
Arg	Ile	Phe	Ile	Ala	Leu	Asn	Ile	Lys	Lys	Glu	Arg	Thr	Lys	Phe	Val
				405					410					415	
Leu	Ser	Arg	Ala												
			420												

(2) INFORMATION FOR SEQ ID NO:3558:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 183 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3558:

Lys	Ala	Thr	Lys	Gln	Leu	Ile	Arg	Lys	Asn	His	Met	Glu	Gln	Leu	His
1				5					10					15	
Phe	Ile	Thr	Lys	Leu	Leu	Asp	Ile	Lys	Asp	Pro	Asn	Ile	Gln	Ile	Leu
			20					25					30		
Asp	Ile	Ile	Asn	Lys	Asp	Thr	His	Lys	Glu	Ile	Ile	Ala	Lys	Leu	Asp
			35				40					45			
Tyr	Glu	Ala	Pro	Ser	Cys	Pro	Glu	Cys	Gly	Ser	Gln	Met	Lys	Lys	Tyr
			50			55					60				
Tyr	Phe	Gln	Lys	Pro	Ser	Lys	Ile	Pro	Tyr	Leu	Glu	Thr	Thr	Gly	Met
65					70					75					80
Pro	Thr	Arg	Ile	Leu	Leu	Arg	Lys	Arg	Arg	Phe	Lys	Cys	Tyr	His	Cys
				85				90						95	
Ser	Lys	Ile	Met	Val	Ala	Glu	Thr	Ser	Ile	Val	Lys	Lys	Asn	His	Gln
			100					105					110		
Ile	Pro	Arg	Ile	Ile	Asn	Gln	Lys	Ile	Ala	Gln	Lys	Leu	Ile	Glu	Lys
			115				120					125			
Ile	Ser	Met	Thr	Asp	Ile	Ala	His	Gln	Leu	Ser	Ile	Ser	Thr	Ser	Thr
			130			135					140				
Val	Ile	Arg	Lys	Leu	Asn	Asp	Phe	His	Phe	Glu	Cys	Asn	Phe	Arg	Asn
145					150					155					160
Leu	Pro	Lys	Ile	Met	Ser	Trp	Asp	Val	Glu	Thr	Val	Arg	Gly	Val	Thr
				165					170					175	
Val	Ser	Ile	Gly	Arg	Trp	Arg									
			180												

(2) INFORMATION FOR SEQ ID NO:3559:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 61 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...61

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3559:

```

Lys Ala Thr Lys Gln Leu Ile Arg Lys Asn His Met Glu Gln Leu His
1          5          10          15
Phe Ile Thr Lys Leu Leu Asp Ile Lys Glu Pro His Ile Pro Thr Phe
          20          25          30
Tyr Ile Leu Pro Pro Gly Gly Arg Pro Arg Arg Asn Pro Pro Pro Gly
          35          40          45
Gly Arg Lys Thr Pro Leu Phe Leu Val Val Glu Phe Leu
          50          55          60

```

(2) INFORMATION FOR SEQ ID NO:3560:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 183 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3560:

```

Lys Ala Thr Lys Gln Leu Ile Arg Lys Asn His Met Glu Gln Leu His
1          5          10          15
Phe Ile Thr Lys Leu Leu Asp Ile Lys Asp Pro Asn Ile Gln Ile Leu
          20          25          30
Asp Ile Ile Asn Lys Asp Thr His Lys Glu Ile Ile Ala Lys Leu Asp
          35          40          45
Tyr Asp Ala Pro Ser Cys Pro Glu Cys Gly Asn Gln Leu Lys Lys Tyr
          50          55          60
Asp Phe Gln Lys Pro Ser Lys Ile Pro Tyr Leu Glu Thr Thr Gly Met
          65          70          75          80
Pro Ser Arg Ile Leu Leu Arg Lys Arg Arg Phe Lys Cys Tyr His Cys
          85          90          95
Ser Lys Met Met Val Ala Glu Thr Ser Ile Val Lys Lys Asn His Gln

```

			100					105				110				
Ile	Pro	Arg	Ile	Ile	Asn	Gln	Lys	Ile	Ala	Gln	Lys	Leu	Ile	Glu	Lys	
		115					120					125				
Ile	Ser	Met	Thr	Asp	Ile	Ala	His	Gln	Leu	Ala	Ile	Ser	Thr	Ser	Thr	
		130					135					140				
Val	Ile	Arg	Lys	Leu	Asn	Asp	Ser	His	Phe	Glu	His	Asp	Phe	Ser	Arg	
145					150					155					160	
Leu	Pro	Glu	Ile	Met	Ser	Trp	Asp	Val	Glu	Thr	Val	Arg	Gly	Val	Thr	
			165						170					175		
Val	Ser	Ile	Gly	Arg	Trp	Arg										
			180													

(2) INFORMATION FOR SEQ ID NO:3561:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 183 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3561:

Lys	Ala	Thr	Lys	Gln	Leu	Ile	Arg	Lys	Asn	His	Met	Glu	Gln	Leu	His	
1				5				10						15		
Phe	Ile	Thr	Lys	Leu	Leu	Asp	Ile	Lys	Asp	Pro	Asn	Ile	Gln	Ile	Leu	
			20					25					30			
Asp	Ile	Ile	Asn	Lys	Asp	Thr	His	Lys	Glu	Ile	Ile	Ala	Lys	Leu	Asp	
			35				40					45				
Tyr	Glu	Ala	Pro	Ser	Cys	Pro	Glu	Cys	Gly	Ser	Gln	Met	Lys	Lys	Tyr	
			50			55					60					
Asp	Phe	Gln	Lys	Pro	Ser	Lys	Ile	Pro	Tyr	Leu	Glu	Thr	Ile	Gly	Met	
65				70					75						80	
Pro	Ser	Arg	Ile	Leu	Leu	Arg	Lys	Arg	Arg	Phe	Lys	Cys	Tyr	His	Cys	
			85					90						95		
Ser	Lys	Met	Met	Val	Ala	Glu	Thr	Pro	Leu	Val	Lys	Lys	Asn	His	Gln	
			100					105					110			
Ile	Pro	Arg	Ile	Ile	Asn	Gln	Lys	Ile	Ala	Gln	Lys	Leu	Ile	Glu	Lys	
			115				120					125				
Ile	Ser	Met	Thr	Asp	Ile	Ala	His	Gln	Leu	Ser	Ile	Ser	Thr	Ser	Thr	
			130			135					140					
Val	Ile	Arg	Lys	Leu	Asn	Asp	Ser	His	Phe	Glu	His	Asp	Phe	Ser	Arg	
145				150						155					160	
Leu	Pro	Glu	Ile	Met	Ser	Trp	Asp	Val	Glu	Thr	Val	Arg	Gly	Val	Thr	
			165					170						175		
Val	Ser	Ile	Gly	Arg	Trp	Arg										
			180													

(2) INFORMATION FOR SEQ ID NO:3562:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 429 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...429

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3562:

Lys	Ala	Thr	Lys	Gln	Leu	Ile	Arg	Lys	Asn	His	Met	Glu	Gln	Leu	His
1			5					10					15		
Phe	Ile	Thr	Lys	Leu	Leu	Asp	Ile	Lys	Asp	Pro	Asn	Ile	Gln	Ile	Leu
			20					25					30		
Asp	Ile	Ile	Asn	Lys	Asp	Thr	His	Lys	Glu	Ile	Ile	Ala	Lys	Leu	Asp
			35				40					45			
Tyr	Asp	Ala	Pro	Ser	Cys	Pro	Glu	Cys	Gly	Ser	Gln	Met	Lys	Lys	Tyr
			50			55				60					
Asp	Phe	Gln	Lys	Pro	Ser	Lys	Ile	Pro	Tyr	Leu	Glu	Thr	Thr	Gly	Met
65					70				75						80
Pro	Thr	Arg	Ile	Leu	Leu	Arg	Lys	Arg	Arg	Phe	Lys	Cys	Tyr	Gln	Cys
				85				90						95	
Ser	Lys	Ile	Ala	Val	Ala	Glu	Thr	Ser	Leu	Val	Lys	Lys	Asn	His	Gln
			100					105					110		
Ile	Pro	Arg	Ile	Ile	Asn	Gln	Lys	Ile	Ala	Gln	Lys	Leu	Ile	Glu	Lys
			115				120					125			
Ile	Ser	Met	Thr	Asp	Ile	Ala	His	Gln	Leu	Ser	Ile	Ser	Thr	Ser	Thr
			130			135				140					
Val	Ile	Arg	Lys	Leu	Asn	Asp	Phe	His	Phe	Lys	His	Asp	Phe	Ser	Cys
145					150				155						160
Leu	Pro	Glu	Ile	Met	Ser	Trp	Asp	Glu	Tyr	Ala	Phe	Thr	Lys	Gly	Lys
				165				170						175	
Met	Ser	Phe	Ile	Ala	Gln	Asp	Phe	Asn	Asn	Leu	Asn	Ile	Ile	Thr	Val
			180				185					190			
Leu	Glu	Gly	Arg	Thr	Gln	Ala	Ile	Ile	Arg	Asn	His	Phe	Leu	Lys	Tyr
			195			200						205			
Asp	Arg	Ala	Val	Arg	Cys	Arg	Val	Lys	Ile	Ile	Thr	Met	Asp	Met	Phe
			210			215					220				
Ser	Pro	Tyr	Tyr	Asp	Leu	Ala	Arg	Gln	Leu	Phe	Pro	Cys	Ala	Lys	Ile
225					230				235						240
Val	Leu	Asp	Arg	Phe	His	Ile	Val	Gln	His	Leu	Ser	Arg	Ala	Met	Ser
				245				250						255	
Arg	Val	Arg	Val	Gln	Ile	Met	Asn	Gln	Leu	Asp	Arg	Lys	Ser	His	Glu
			260				265						270		
Tyr	Lys	Ala	Ile	Lys	Arg	Tyr	Trp	Lys	Leu	Ile	Gln	Gln	Asp	Ser	Arg
			275				280				285				
Lys	Leu	Ser	Asp	Lys	Arg	Phe	Tyr	Arg	Pro	Thr	Phe	Arg	Ile	His	Leu

290		295		300
Thr Asn Lys Glu Ile Leu Asn Lys Leu Leu Ser Tyr Ser Glu Asp Leu				
305		310		315
Lys His His Tyr Gln Leu Tyr Gln Leu Leu Phe His Phe Gln Asn				
	325		330	335
Lys Glu Pro Glu Lys Phe Phe Gly Leu Ile Glu Asp Asn Leu Lys Gln				
	340		345	350
Val His Pro Leu Phe Gln Thr Val Phe Lys Thr Phe Leu Lys Asp Lys				
	355		360	365
Glu Lys Ile Val Asn Ala Leu Gln Leu His Tyr Ser Asn Ala Lys Leu				
	370		375	380
Glu Ala Thr Asn Asn Leu Ile Lys Leu Ile Lys Arg Asn Ala Phe Gly				
385		390		395
Phe Arg Asn Phe Glu Asn Phe Lys Lys Arg Ile Phe Ile Ala Leu Asn				
	405		410	415
Ile Lys Lys Glu Arg Thr Lys Phe Val Leu Ser Arg Ala				
	420		425	

(2) INFORMATION FOR SEQ ID NO:3563:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3563:

Pro Asn Ala Asn Gly Gly Phe Glu Ile Met Thr Gln Ala Ile Leu Glu		
1	5	10
Ile Lys His Leu Lys Lys Ser Tyr Gly Gln Asn Glu Val Leu Lys Asp		
	20	25
Ile Ser Leu Thr Val His Lys Gly Glu Val Ile Ser Ile Ile Gly Ser		
	35	40
Ser Gly Ser Gly Lys Ser Thr Phe Leu Arg Ser Ile Asn Leu Leu Glu		
	50	55
Thr Pro Thr Asp Gly Gln Ile Leu Tyr His Gly Gln Asn Val Leu Glu		
65	70	75
Lys Gly Tyr Asp Leu Thr Gln Tyr Arg Glu Lys Leu Gly Met Val Phe		
	85	90
Gln Ser Phe Asn Leu Phe Glu Asn Leu Asn Val Leu Glu Asn Thr Ile		
	100	105
Val Ala Gln Thr Thr Val Leu Lys Arg Glu Arg Thr Glu Ala Glu Lys		
	115	120
Ile Ala Lys Glu Asn Leu Glu Lys Val Gly Met Gly Glu Arg Tyr Trp		
	130	135
		140

Gln	Ala	Lys	Pro	Lys	Gln	Leu	Ser	Gly	Gly	Gln	Lys	Gln	Arg	Val	Ala
145					150					155					160
Ile	Ala	Arg	Ala	Leu	Ser	Met	Asn	Pro	Asp	Ala	Ile	Leu	Phe	Asp	Glu
				165					170						175
Pro	Thr	Ser	Ala	Leu	Asp	Pro	Glu	Met	Val	Gly	Glu	Val	Leu	Lys	Ile
			180					185					190		
Met	Gln	Asp	Leu	Ala	Gln	Glu	Gly	Leu	Thr	Met	Ile	Val	Val	Thr	His
	195						200					205			
Glu	Met	Glu	Phe	Ala	Arg	Asp	Val	Ser	His	Arg	Val	Ile	Phe	Met	Asp
	210					215					220				
Lys	Gly	Val	Ile	Ala	Glu	Glu	Gly	Lys	Pro	Glu	Asp	Leu	Phe	Thr	Asn
225					230					235					240
Pro	Lys	Glu	Asp	Arg	Thr	Lys	Glu	Phe	Leu	Gln	Arg	Tyr	Leu	Lys	
				245					250						255

(2) INFORMATION FOR SEQ ID NO:3564:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...159

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3564:

Gly	Met	Ala	Lys	Glu	Pro	Trp	Gln	Glu	Asp	Ile	Tyr	Asp	Gln	Glu	Glu
1			5					10					15		
Ser	Arg	Ala	Gly	Arg	Arg	His	Arg	Asn	His	Gly	Gly	Ala	Asp	Arg	Met
		20					25					30			
Ala	Asn	Arg	Ile	Leu	Thr	Ile	Leu	Ala	Ser	Ile	Phe	Phe	Val	Ile	Val
	35					40					45				
Val	Val	Met	Val	Ile	Val	Leu	Ile	Tyr	Leu	Ser	Ser	Gly	Gly	Ser	Asn
	50				55					60					
Arg	Thr	Ala	Ala	Leu	Lys	Asp	Phe	His	Asp	Ser	Asp	Ala	Ser	Val	Val
65				70					75						80
Gln	Ile	Ser	Ser	Ser	Ser	Ser	Ser	Gln	Pro	Glu	Gln	Ser	Ser	Glu	Pro
			85					90						95	
Glu	Ser	Thr	Ser	Ser	Ser	Ser	Glu	Glu	Ala	Ala	Asn	Pro	Glu	Gly	Thr
		100					105					110			
Ile	Lys	Val	Leu	Ala	Gly	Glu	Gly	Glu	Ala	Ala	Ile	Ala	Ala	Arg	Ala
	115				120						125				
Gly	Ile	Ser	Ile	Ala	Gln	Leu	Glu	Ala	Leu	Asn	Pro	Gly	His	Met	Ala
	130				135					140					
Thr	Gly	Ser	Trp	Phe	Ala	Asn	Pro	Gly	Asp	Val	Ile	Lys	Ile	Lys	
145				150					155						

(2) INFORMATION FOR SEQ ID NO:3565:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 161 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...161
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3565:

```

Ile Met Ala Lys Lys Val Lys Ile Lys Lys Thr Leu Val Glu Gln Ile
1      5      10      15
Leu Ser Lys Ala Ala Ile Pro His Gln Gly Ile Gln Ile Asn Ala Leu
20     25     30
Glu Gly Glu Leu Pro Gln Gly Tyr Glu Arg Asp Gln Ile Phe Lys Thr
35     40     45
Leu Ala Leu Leu Gly Asp Lys Thr Gly Pro Ile Ile Gly Ile Val Pro
50     55     60
Ile Thr Gln His Leu Ser Glu Lys Lys Leu Ala Lys Ile Ser Gly Asn
65     70     75     80
Lys Lys Val Ser Met Ile Pro Gln Lys Asp Leu Glu Lys Thr Thr Gly
85     90     95
Tyr Ile His Gly Ala Asn Asn Pro Val Gly Ile Arg Gln Lys His Asn
100    105    110
Tyr Pro Ile Phe Ile Asp Lys Ile Ala Leu Asp Leu Asp Arg Met Ile
115    120    125
Val Ser Ala Gly Glu Val Gly His Ser Ile Ile Val Ala Pro Gln Asp
130    135    140
Leu Ala Ser Phe Val Lys Ala Asp Phe Val Asp Ile Leu Glu Asp Ile
145    150    155    160
Lys

```

(2) INFORMATION FOR SEQ ID NO:3566:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 472 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...472

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3566:

Lys	Met	Ala	Asn	Lys	Ala	Val	Asn	Asp	Phe	Ile	Leu	Ala	Met	Asn	Tyr
1			5						10					15	
Asp	Lys	Lys	Lys	Leu	Leu	Thr	His	Gln	Gly	Glu	Ser	Ile	Glu	Asn	Arg
			20					25					30		
Phe	Ile	Lys	Glu	Gly	Asn	Gln	Leu	Pro	Asp	Glu	Phe	Val	Val	Ile	Glu
		35				40						45			
Arg	Lys	Lys	Arg	Ser	Leu	Ser	Thr	Asn	Thr	Ser	Asp	Ile	Ser	Val	Thr
	50					55				60					
Ala	Thr	Asn	Asp	Ser	Arg	Leu	Tyr	Pro	Gly	Ala	Leu	Leu	Val	Val	Asp
65					70					75					80
Glu	Thr	Leu	Leu	Glu	Asn	Asn	Pro	Thr	Leu	Leu	Ala	Val	Asp	Arg	Ala
				85					90					95	
Pro	Met	Thr	Tyr	Ser	Ile	Asp	Leu	Pro	Gly	Leu	Ala	Ser	Ser	Asp	Ser
			100					105					110		
Phe	Leu	Gln	Val	Glu	Asp	Pro	Ser	Asn	Ser	Ser	Val	Arg	Gly	Ala	Val
		115				120						125			
Asn	Asp	Leu	Leu	Ala	Lys	Trp	His	Gln	Asp	Tyr	Gly	Gln	Val	Asn	Asn
	130					135					140				
Val	Pro	Ala	Arg	Met	Gln	Tyr	Glu	Lys	Ile	Thr	Ala	His	Ser	Met	Glu
145					150					155					160
Gln	Leu	Lys	Val	Lys	Phe	Gly	Ser	Asp	Phe	Glu	Lys	Thr	Gly	Asn	Ser
				165					170					175	
Leu	Asp	Ile	Asp	Phe	Asn	Ser	Val	His	Ser	Gly	Glu	Lys	Gln	Ile	Gln
			180					185					190		
Ile	Val	Asn	Phe	Lys	Gln	Ile	Tyr	Tyr	Thr	Val	Ser	Val	Asp	Ala	Val
		195					200						205		
Lys	Asn	Pro	Gly	Asp	Val	Phe	Gln	Asp	Thr	Val	Thr	Val	Glu	Asp	Leu
	210					215					220				
Lys	Gln	Arg	Gly	Ile	Ser	Ala	Glu	Arg	Pro	Leu	Val	Tyr	Ile	Ser	Ser
225				230						235					240
Val	Ala	Tyr	Gly	Arg	Gln	Val	Tyr	Leu	Lys	Leu	Glu	Thr	Thr	Ser	Lys
				245					250					255	
Ser	Asp	Glu	Val	Glu	Ala	Ala	Phe	Glu	Ala	Leu	Ile	Lys	Gly	Val	Lys
			260					265					270		
Val	Ala	Pro	Gln	Thr	Glu	Trp	Lys	Gln	Ile	Leu	Asp	Asn	Thr	Glu	Val
		275					280					285			
Lys	Ala	Val	Ile	Leu	Gly	Gly	Asp	Pro	Ser	Ser	Gly	Ala	Arg	Val	Val
	290					295					300				
Thr	Gly	Lys	Val	Asp	Met	Val	Glu	Asp	Leu	Ile	Gln	Glu	Gly	Ser	Arg
305				310						315					320
Phe	Thr	Ala	Asp	His	Pro	Gly	Leu	Pro	Ile	Ser	Tyr	Thr	Thr	Ser	Phe
				325					330					335	
Leu	Arg	Asp	Asn	Val	Val	Ala	Thr	Phe	Gln	Asn	Ser	Thr	Asp	Tyr	Val
			340					345					350		
Glu	Thr	Lys	Val	Thr	Ala	Tyr	Arg	Asn	Gly	Asp	Leu	Leu	Leu	Asp	His
		355					360					365			
Ser	Gly	Ala	Tyr	Val	Ala	Gln	Tyr	Tyr	Ile	Thr	Trp	Asn	Glu	Leu	Ser
	370					375					380				
Tyr	Asp	His	Gln	Gly	Lys	Glu	Val	Leu	Thr	Pro	Lys	Ala	Trp	Asp	Arg
385					390					395					400
Asn	Gly	Gln	Asp	Leu	Thr	Ala	His	Phe	Thr	Thr	Ser	Ile	Pro	Leu	Lys

				405					410					415			
Gly	Asn	Val	Arg	Asn	Leu	Ser	Val	Lys	Ile	Arg	Glu	Cys	Thr	Gly	Leu		
			420					425					430				
Ala	Trp	Glu	Trp	Trp	Arg	Thr	Val	Tyr	Glu	Lys	Thr	Asp	Leu	Pro	Leu		
		435					440					445					
Val	Arg	Lys	Arg	Thr	Ile	Ser	Ile	Trp	Gly	Thr	Thr	Leu	Tyr	Pro	Gln		
	450					455					460						
Val	Glu	Asp	Lys	Val	Glu	Asn	Asp										
465					470												

(2) INFORMATION FOR SEQ ID NO:3567:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 691 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...691

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3567:

Ile	Val	Pro	Leu	Val	Arg	Asn	Tyr	Arg	Gly	Asn	Phe	Val	Tyr	Lys	Glu		
1				5					10					15			
Ser	Thr	Met	Lys	Lys	Leu	Phe	Ile	Leu	Leu	Ser	Thr	Phe	Phe	Leu	Ser		
			20					25					30				
Phe	Phe	Leu	Ala	Trp	Ile	Ile	Val	Leu	Arg	Ala	Pro	Gln	Tyr	Leu	Tyr		
		35				40					45						
Ala	Ser	Tyr	Asp	Ser	Val	Ser	Leu	Leu	Arg	Val	Lys	Lys	Asp	Thr	Gln		
	50					55					60						
Glu	Pro	Thr	Arg	Glu	Val	Phe	Glu	Gln	Glu	Leu	Glu	Asn	Phe	Ala	Asn		
65				70					75						80		
Ser	Glu	Gln	Ser	Leu	Ile	Ala	Arg	Arg	Ile	Val	Glu	Pro	Ser	Lys	Asp		
			85						90					95			
Gly	Thr	Thr	His	Phe	Thr	Tyr	Ala	Thr	Tyr	Gly	Gln	Gly	Thr	Leu	Pro		
			100					105					110				
Lys	Glu	Phe	Gln	Glu	Ala	Ser	Gln	Glu	Ser	Arg	Glu	Arg	Ser	Asp	Pro		
	115						120					125					
Leu	Asn	Ser	Tyr	Leu	Leu	Leu	Ser	Gly	Ser	Leu	Thr	Lys	Glu	Lys	Leu		
	130					135					140						
Ala	Asp	Lys	Leu	Gly	Asp	Leu	Gly	Tyr	Lys	Ala	Ser	Ala	Asp	Arg	Lys		
145				150					155						160		
Ile	Pro	Pro	Tyr	Phe	Leu	Ala	Phe	Arg	Ile	Leu	Leu	Asn	Pro	Leu	Ile		
			165					170						175			
Leu	Ile	Ser	Leu	Ala	Ile	Phe	Gly	Leu	Ser	Phe	Phe	Ala	Leu	Val	Ile		
		180					185						190				
Ile	Thr	Arg	Ile	Lys	Glu	Met	Arg	Ala	Ala	Gly	Ile	Lys	Leu	Phe	Ser		
	195					200						205					
Gly	Gln	Thr	Leu	Leu	Ser	Ile	Met	Gly	His	Ser	Leu	Ser	Thr	Asp	Ile		

210		215		220	
Lys Trp Leu Leu Leu Ser	Ala Leu Leu Ser Phe	Leu Gly Gly Gly Val			
225	230	235	240		
Val Leu Phe Ser Gln Gly	Leu Phe Tyr Pro Ile	Leu Leu Ala Thr Tyr			
	245	250	255		
Gly Phe Gly Ile Ser Phe	Tyr Leu Leu Phe Leu	Leu Ala Ile Ser Ile			
	260	265	270		
Leu Leu Met Leu Leu Tyr	Leu Met Ser Leu Ser	Tyr Lys Ala Leu Val			
	275	280	285		
Pro Val Ile Lys Gly Arg	Leu Pro Leu Lys Arg	Leu Met Ile Leu Thr			
	290	295	300		
Leu Leu Cys Gln Leu Val	Ala Val Phe Thr Val	Gly Tyr Ala Val Lys			
305	310	315	320		
Thr Gly Leu Met Ser Tyr	Gln Arg Leu Lys Glu	Leu Glu Ile Ser Lys			
	325	330	335		
Gln Ala Trp Gln Asp Arg	Ala Asp Tyr Tyr Gln	Ile Ser Phe Gly Leu			
	340	345	350		
Gly Asp Arg Gly Lys Asp	Thr Glu Asn Gln Ser	Lys Trp Tyr Ala Phe			
	355	360	365		
Ala Lys Glu Ala Ile Glu	Glu Glu Gln Ala Leu	Tyr Val Lys Asp Asn			
	370	375	380		
Leu Leu His Phe Ala Asn	Pro Gln Gly Lys Asn	Glu Gln Gly Glu Thr			
385	390	395	400		
Leu Asp Thr Tyr Ser Pro	Asp Ala Asn Thr Leu	Tyr Val Ser Pro Ser			
	405	410	415		
Tyr Leu Asp Lys Glu Lys	Val Val Val Asp Ala	Glu Thr Lys Gln Lys			
	420	425	430		
Leu Ala His Leu Gln Lys	Gly Glu Phe Ile Leu	Leu Leu Pro Glu His			
	435	440	445		
Leu Arg Ser Arg Glu Ala	Glu Leu Lys Lys Val	Phe Glu Glu Arg Leu			
	450	455	460		
Ser Tyr Tyr Gly Lys Ser	Gly Glu Glu Ala Ser	Ala Pro Leu Asp Tyr			
465	470	475	480		
Glu Met Lys Ala His Val	Ser Tyr Leu Ser Met	Gly Glu Lys Arg Phe			
	485	490	495		
Val Tyr Asn Asn Gly Glu	Asn Pro Val Ser Thr	Gln Tyr Leu Thr Asp			
	500	505	510		
Pro Ile Leu Val Val Phe	Thr Pro Thr Ser Thr	Gly Asp Ser Phe Ile			
	515	520	525		
Ser Leu Ser Ser Trp Ser	Ile Asn Ala Gly Lys	Gln Leu Phe Ile Lys			
	530	535	540		
Gly Tyr Glu Ser Gly Leu	Glu Leu Leu Lys Lys	Ala Gly Ile Tyr Glu			
545	550	555	560		
Gln Val Ser Tyr Leu Lys	Glu Gly Arg Ser Val	Tyr Leu Thr Arg Tyr			
	565	570	575		
Asn Glu Val Gln Thr Glu	Thr Ala Thr Leu Ile	Leu Gly Ala Ile Val			
	580	585	590		
Gly Ile Ala Ser Ser Leu	Leu Leu Phe Tyr Ser	Val Asn Leu Leu Tyr			
	595	600	605		
Phe Glu Gln Phe Arg Arg	Asp Ile Leu Ile Lys	Arg Ile Ser Gly Leu			
	610	615	620		
Arg Phe Phe Glu Thr His	Ala Gln Tyr Met Val	Ser Gln Phe Ala Ser			
625	630	635	640		
Phe Val Phe Gly Ala Ser	Leu Phe Ile Leu Ser	Ser Arg Asp Leu Val			
	645	650	655		
Ile Gly Leu Leu Thr Leu	Leu Val Phe Leu Ala	Ser Ala Val Leu Thr			
	660	665	670		

Leu Tyr Arg Gln Ala Gln Lys Glu Ser Arg Val Ser Met Thr Ile Met
675 680 685
Lys Gly Lys
690

(2) INFORMATION FOR SEQ ID NO:3568:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 506 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...506

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3568:

Pro Leu Gln Asn Asp Pro Asn Ala Asn Gln Phe Trp Phe Gln Tyr Ala
1 5 10 15
Arg Tyr Pro Lys Trp Tyr Thr Glu Asn Phe Val Ser Ser Ser Asp Phe
20 25 30
Gly Cys Leu Tyr Arg Ala Pro Lys Arg Met Val Val Arg Arg Thr Arg
35 40 45
Phe Asp Lys Glu Lys Ala Glu Ala Arg Ala His Ile Leu Glu Gly Leu
50 55 60
Leu Ile Ala Leu Asp His Ile Asp Glu Val Ile Arg Ile Ile Arg Ala
65 70 75 80
Ser Glu Thr Asp Ala Glu Ala Gln Ala Glu Leu Met Ser Lys Phe Lys
85 90 95
Leu Ser Glu Arg Gln Ser Gln Ala Ile Leu Asp Met Arg Leu Arg Arg
100 105 110
Leu Thr Gly Leu Glu Arg Asp Lys Ile Gln Ser Glu Tyr Asp Asp Leu
115 120 125
Leu Ala Leu Ile Ala Asp Leu Ala Asp Ile Leu Ala Lys Pro Glu Arg
130 135 140
Val Ser Gln Ile Ile Lys Asp Glu Leu Asp Glu Val Lys Arg Lys Phe
145 150 155 160
Ser Asp Lys Arg Arg Thr Glu Leu Met Val Gly Gln Ile Leu Ser Leu
165 170 175
Glu Asp Glu Asp Leu Ile Glu Glu Ser Asp Val Leu Ile Thr Leu Ser
180 185 190
Asn Arg Gly Tyr Ile Lys Arg Leu Asp Gln Asp Glu Phe Thr Ala Gln
195 200 205
Lys Arg Gly Gly Arg Gly Val Gln Gly Thr Gly Val Lys Asp Asp Asp
210 215 220
Phe Val Arg Glu Leu Val Ser Thr Ser Thr His Asp His Leu Leu Phe
225 230 235 240
Phe Thr Asn Lys Gly Arg Val Tyr Arg Leu Lys Gly Tyr Glu Ile Pro

Asp	Lys	Ile	Cys	Pro	Phe	Ser	Ser	Leu	Ala	Phe	Leu	Gln	Pro	Thr	Thr
		20						25				30			
Val	Asp	Lys	Glu	Pro	Phe	Leu	Leu	Phe	Lys	Asn	Leu	Ile	Ser	Ser	Met
	35					40					45				
His	Pro	Arg	Arg	His	Pro	Leu	Lys	Glu	Leu	Arg	Gly	Arg	His	Val	Val
	50				55					60					
Ser	Ile	Gln	Phe	Phe	Val	Leu	Glu								
65					70										

(2) INFORMATION FOR SEQ ID NO:3570:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 78 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...78

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3570:

Lys	Leu	Gln	Lys	Thr	Asp	Phe	Tyr	Arg	Ser	Glu	His	Gln	Lys	Arg	Lys
1			5					10					15		
Asp	Glu	Ile	Cys	Pro	Phe	Ser	Ser	Leu	Ala	Asp	Phe	Asn	Pro	Leu	Gln
	20							25				30			
Leu	Thr	Lys	Ser	Gln	Lys	Ile	Leu	Phe	Ser	Tyr	Ser	Phe	Lys	Ile	Lys
	35				40						45				
Lys	Gly	Ile	Tyr	Arg	Phe	Thr	Asp	Met	Tyr	Ile	Thr	Asp	Phe	Tyr	Arg
	50				55					60					
Ser	Cys	Ile	Asp	Arg	Ile	Ser	Ser	Leu	Gly	Ser	Phe	Pro	Phe		
65					70				75						

(2) INFORMATION FOR SEQ ID NO:3571:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 129 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...129

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3571:

```
Gln Tyr Gln Asn Thr Val Ala Arg Ile Lys Thr Gly Thr Gln Ile Arg
1      5      10      15
Gly Gly Ile Leu Met Thr Asp Thr Asp Pro Ile Lys Arg Ala Gln Thr
20      25      30
Leu Ile Thr Asp Leu Asn Lys Ala Tyr Gln Ala Cys Lys Gln Ala Thr
35      40      45
Ala Asp Asp Val Arg Phe Gln Glu Gln Leu Asn Ser Ile Leu Gly Phe
50      55      60
Leu Ala Lys Ala Glu Thr Val Asp Asn Arg Phe Leu Ile Glu Leu Glu
65      70      75      80
Lys Phe Tyr Gln Thr Ser Ser Leu Leu Met Gly Leu Ser Ala Leu Asp
85      90      95
Pro Asp Ala Pro Thr Arg Ala Ala Trp Arg Ala Tyr Asp Arg Phe His
100     105     110
Phe Asp Gln Val Lys Thr Lys Leu Ile Leu Asn Glu Asn Gln Arg Ala
115     120     125
Asn
```

(2) INFORMATION FOR SEQ ID NO:3572:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...62

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3572:

```
Val Ser Gln Lys Glu Gly Ile Gln Ala Lys Gln Ile Val Ile Lys Ile
1      5      10      15
Thr Asp Gln Gly Tyr Val Thr Ser His Gly Asp His Tyr Arg Tyr Tyr
20      25      30
Asn Gly Lys Val Pro Phe Asp Ala Leu Phe Ser Glu Glu Leu Leu Met
35      40      45
Lys Ala Pro Asn Tyr Gln Pro Lys Asp Gln Asp Ile Val Ser
50      55      60
```

(2) INFORMATION FOR SEQ ID NO:3573:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...71
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3573:

```

Val Ile Gln Asn His Phe Ser Pro Asn Gly Phe Gly Asn Ile Phe Gln
1           5           10           15
Leu Asn His Lys Met Pro Pro Phe Asn Asn Ser Thr Arg Leu Leu Phe
          20           25           30
Ser Ile Leu Glu Ala Lys Pro Ser Thr Asn Ser Ile Ser Arg His Val
          35           40           45
Lys Pro Ala Asn Ser Arg Ser Gly Lys Asn Ala Trp Ala Lys Lys Ile
          50           55           60
Lys Thr Arg Arg Gly Lys Leu
65           70

```

(2) INFORMATION FOR SEQ ID NO:3574:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 468 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...468
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3574:

```

Leu Lys Gln Asn Leu Glu Arg Glu Ser Met Leu His Asn Ala Phe Ala
1           5           10           15
Tyr Val Thr Arg Lys Phe Phe Lys Ser Ile Val Ile Phe Leu Ile Ile
          20           25           30
Leu Leu Met Ala Ser Leu Ser Leu Val Gly Leu Ser Ile Lys Gly Ala
          35           40           45
Thr Ala Lys Ala Ser Gln Glu Thr Phe Lys Asn Ile Thr Asn Ser Phe
          50           55           60
Ser Met Gln Ile Asn Arg Arg Val Asn Gln Gly Thr Pro Arg Gly Ala
65           70           75           80
Gly Asn Ile Lys Gly Glu Asp Ile Lys Lys Ile Thr Glu Asn Lys Ala
          85           90           95

```

Ile	Glu	Ser	Tyr	Val	Lys	Arg	Ile	Asn	Ala	Ile	Gly	Asp	Leu	Thr	Gly		
			100					105					110				
Tyr	Asp	Leu	Ile	Glu	Thr	Pro	Glu	Thr	Lys	Lys	Asn	Leu	Thr	Ala	Asp		
		115					120					125					
Arg	Ala	Lys	Arg	Phe	Gly	Ser	Ser	Leu	Met	Ile	Thr	Gly	Val	Asn	Asp		
	130					135					140						
Ser	Ser	Lys	Glu	Asp	Lys	Phe	Val	Ser	Gly	Ser	Tyr	Lys	Leu	Val	Glu		
145					150					155					160		
Gly	Glu	His	Leu	Thr	Asn	Asp	Asp	Lys	Asp	Lys	Ile	Leu	Leu	His	Lys		
			165						170					175			
Asp	Leu	Ala	Ala	Lys	His	Gly	Trp	Lys	Val	Gly	Asp	Lys	Val	Lys	Leu		
			180					185					190				
Asp	Ser	Asn	Ile	Tyr	Asp	Ala	Asp	Asn	Glu	Lys	Gly	Ala	Lys	Glu	Thr		
		195					200					205					
Val	Glu	Val	Thr	Ile	Lys	Gly	Leu	Phe	Asp	Gly	His	Asn	Lys	Ser	Ala		
	210					215					220						
Val	Thr	Tyr	Ser	Gln	Glu	Leu	Tyr	Glu	Asn	Thr	Ala	Ile	Thr	Asp	Ile		
225					230					235					240		
His	Thr	Ala	Ala	Lys	Leu	Tyr	Gly	Tyr	Thr	Glu	Asp	Thr	Ala	Ile	Tyr		
				245					250					255			
Gly	Asp	Ala	Thr	Phe	Phe	Val	Thr	Ala	Asp	Lys	Asn	Leu	Asp	Asp	Val		
		260						265					270				
Met	Lys	Glu	Leu	Asn	Gly	Ile	Ser	Gly	Ile	Asn	Trp	Lys	Ser	Tyr	Thr		
	275					280					285						
Leu	Val	Lys	Ser	Ser	Ser	Asn	Tyr	Pro	Ala	Leu	Glu	Gln	Ser	Ile	Ser		
	290					295					300						
Gly	Met	Tyr	Lys	Met	Ala	Asn	Leu	Leu	Phe	Trp	Gly	Ser	Leu	Ser	Phe		
305					310				315						320		
Ser	Val	Leu	Leu	Leu	Ala	Leu	Leu	Leu	Ser	Leu	Trp	Ile	Asn	Ala	Arg		
				325					330					335			
Arg	Lys	Glu	Val	Gly	Ile	Leu	Leu	Ser	Ile	Gly	Leu	Lys	Gln	Ala	Ser		
		340						345					350				
Ile	Leu	Gly	Gln	Phe	Ile	Thr	Glu	Ser	Ile	Leu	Ile	Ala	Ile	Pro	Ala		
	355						360					365					
Leu	Val	Ser	Ala	Tyr	Phe	Leu	Ala	Asn	Tyr	Thr	Ala	Arg	Ala	Ile	Gly		
	370					375					380						
Asn	Thr	Val	Leu	Ala	Asn	Val	Thr	Ser	Gly	Val	Ala	Lys	Gln	Ala	Ser		
385					390					395					400		
Lys	Ala	Ala	Gln	Ala	Ser	Asn	Leu	Gly	Gly	Gly	Ala	Glu	Val	Asp	Gly		
			405					410						415			
Phe	Ser	Lys	Thr	Leu	Ser	Ser	Leu	Asp	Ile	Ser	Ile	Gln	Thr	Ser	Asp		
		420						425					430				
Phe	Ile	Ile	Ile	Phe	Val	Leu	Ala	Leu	Val	Leu	Val	Val	Leu	Val	Met		
	435					440						445					
Ala	Leu	Ala	Ser	Ser	Asn	Leu	Leu	Arg	Lys	Gln	Pro	Lys	Glu	Leu	Leu		
	450					455					460						
Leu	Asp	Gly	Glu														
465																	

(2) INFORMATION FOR SEQ ID NO:3575:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...267

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3575:

Lys	Lys	Gln	Lys	Gly	Glu	Ile	Leu	Met	Ala	Val	Ile	Ser	Met	Lys	Gln
1				5					10					15	
Leu	Leu	Glu	Ala	Gly	Val	His	Phe	Gly	His	Gln	Thr	Arg	Arg	Trp	Asn
			20					25					30		
Pro	Lys	Met	Ala	Lys	Tyr	Ile	Phe	Thr	Glu	Arg	Asn	Gly	Ile	His	Val
		35					40					45			
Ile	Asp	Leu	Gln	Gln	Thr	Val	Lys	Tyr	Ala	Asp	Gln	Ala	Tyr	Asp	Phe
50						55				60					
Met	Arg	Asp	Ala	Ala	Ala	Asn	Asp	Ala	Val	Val	Leu	Phe	Val	Gly	Thr
65					70					75				80	
Lys	Lys	Gln	Ala	Ala	Asp	Ala	Val	Ala	Glu	Glu	Ala	Val	Arg	Ser	Gly
				85					90					95	
Gln	Tyr	Phe	Ile	Asn	His	Arg	Trp	Leu	Gly	Gly	Thr	Leu	Thr	Asn	Trp
			100					105					110		
Gly	Thr	Ile	Gln	Lys	Arg	Ile	Ala	Arg	Leu	Lys	Glu	Ile	Lys	Arg	Met
			115				120					125			
Glu	Glu	Asp	Gly	Thr	Phe	Glu	Val	Leu	Pro	Lys	Lys	Glu	Val	Ala	Leu
130						135					140				
Leu	Asn	Lys	Gln	Arg	Ala	Arg	Leu	Glu	Lys	Phe	Leu	Gly	Gly	Ile	Glu
145					150					155				160	
Asp	Met	Pro	Arg	Ile	Pro	Asp	Val	Met	Tyr	Val	Val	Asp	Pro	His	Lys
				165				170						175	
Glu	Gln	Ile	Ala	Val	Lys	Glu	Ala	Lys	Lys	Leu	Gly	Ile	Pro	Val	Val
			180					185					190		
Ala	Met	Val	Asp	Thr	Asn	Thr	Asp	Pro	Asp	Asp	Ile	Asp	Val	Ile	Ile
		195					200					205			
Pro	Ala	Asn	Asp	Asp	Ala	Ile	Arg	Ala	Val	Lys	Leu	Ile	Thr	Ala	Lys
	210					215					220				
Leu	Ala	Asp	Ala	Ile	Ile	Glu	Gly	Arg	Gln	Gly	Glu	Asp	Ala	Val	Ala
225					230					235				240	
Val	Glu	Ala	Glu	Phe	Ala	Ala	Ser	Glu	Thr	Gln	Ala	Asp	Ser	Ile	Glu
				245					250					255	
Glu	Ile	Val	Glu	Val	Val	Glu	Gly	Asp	Asn	Ala					
			260				265								

(2) INFORMATION FOR SEQ ID NO:3576:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 132 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...132

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3576:

```
Leu Arg Gln Lys Asp Lys Arg Lys Glu Thr Lys Met Ser Trp Thr Phe
1          5          10          15
Asp Asn Lys Lys Pro Ile Tyr Leu Gln Ile Met Glu Lys Ile Lys Leu
20          25          30
Gln Ile Val Ser His Thr Leu Glu Pro Asn Gln Gln Leu Pro Thr Val
35          40          45
Arg Glu Leu Ala Ser Glu Ala Gly Val Asn Pro Asn Thr Ile Gln Arg
50          55          60
Ala Leu Ser Asp Leu Glu Arg Glu Gly Phe Val Tyr Ser Lys Arg Thr
65          70          75          80
Thr Gly Arg Phe Val Thr Lys Asp Lys Glu Leu Ile Ala Gln Ser Arg
85          90          95
Lys Gln Leu Ser Glu Glu Glu Leu Glu His Phe Val Ser Ser Met Thr
100         105         110
His Phe Gly Tyr Glu Lys Glu Glu Leu Pro Gly Val Val Ser Asp Tyr
115         120         125
Ile Lys Gly Val
130
```

(2) INFORMATION FOR SEQ ID NO:3577:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 209 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...209

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3577:

```
Lys Arg Gln Lys Trp Gln Lys Asn Leu Phe Ile Arg Arg Thr Thr Met
1          5          10          15
Asp Asn Lys Lys Leu Lys Val Lys Asp Leu Val Ser Ile Gly Val Phe
20          25          30
Gly Val Ile Tyr Phe Ala Phe Met Phe Gly Val Gly Met Met Gly Leu
35          40          45
Ile Pro Ile Leu Phe Leu Ile Tyr Pro Thr Val Leu Ala Ile Val Ala
50          55          60
```

Gly	Thr	Val	Val	Met	Leu	Phe	Met	Ala	Lys	Val	Gln	Lys	Pro	Trp	Ala
65					70					75					80
Leu	Phe	Ile	Phe	Gly	Met	Ile	Ser	Pro	Leu	Val	Met	Phe	Ala	Ala	Gly
				85					90						95
His	Thr	Tyr	Val	Val	Val	Leu	Ser	Leu	Ile	Val	Met	Ile	Ile	Ala	
			100					105					110		
Glu	Leu	Ile	Arg	Lys	Ile	Gly	Asn	Tyr	Asn	Ser	Phe	Lys	Tyr	Asn	Met
		115					120					125			
Leu	Ser	Tyr	Ala	Ile	Phe	Ser	Thr	Trp	Ile	Cys	Ser	Ser	Leu	Met	Gln
	130					135					140				
Met	Leu	Leu	Ala	Lys	Glu	Lys	Tyr	Met	Glu	Trp	Ser	Leu	Met	Thr	Met
145					150					155					160
Gly	Lys	Asp	Tyr	Val	Asp	Val	Leu	Glu	Lys	Leu	Ile	Thr	Tyr	Pro	His
			165						170						175
Met	Ala	Leu	Val	Ala	Leu	Gly	Ala	Phe	Leu	Gly	Gly	Ile	Leu	Gly	Ala
			180					185					190		
Tyr	Ile	Gly	Lys	Ala	Leu	Leu	Lys	Lys	His	Phe	Glu	Lys	Ala	Gly	Ile
		195					200					205			
Val															

(2) INFORMATION FOR SEQ ID NO:3578:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 218 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...218

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3578:

Leu	Met	Gln	Asn	Leu	Ile	Ile	Gly	Ile	Gln	Lys	Arg	Lys	Asn	Arg	Ile
1				5					10					15	
Thr	Leu	Phe	Ser	Ser	Leu	Phe	Leu	Leu	Ile	Ile	Ile	Ser	Leu	Ser	Phe
			20					25					30		
Phe	Ile	Leu	Leu	Ile	Gly	Asn	Glu	Ser	Tyr	Ser	Phe	Ser	Thr	Leu	Ile
		35					40					45			
Lys	Val	Leu	Asn	Ser	Glu	Thr	Val	Pro	Gly	Ala	Ser	Phe	Ser	Ile	Met
	50					55					60				
Glu	Ile	Arg	Leu	Pro	Lys	Leu	Leu	Ala	Gly	Ile	Ile	Ala	Gly	Trp	Ser
65					70					75					80
Phe	Gly	Leu	Ala	Gly	Phe	Ile	Phe	Gln	Thr	Met	Leu	Arg	Asn	Pro	Leu
			85						90					95	
Ala	Ser	Pro	Asp	Ile	Ile	Gly	Val	Thr	Ser	Ser	Ser	Ser	Ile	Ala	Ala
			100					105					110		
Val	Phe	Cys	Ile	Leu	Val	Leu	Lys	Thr	Asn	Ser	Leu	Thr	Thr	Gly	Ile
		115					120					125			


```

Ile Ser Ile Thr Cys Gly Leu Thr Ser Ser Leu Ile Leu Phe Leu Leu
130          135          140
Ala Lys Lys Asp Gly Phe Ser Ala Ala Arg Leu Ile Ile Leu Gly Ile
145          150          155          160
Gly Phe Gln Ala Val Thr Arg Ala Gly Thr Ser Phe Leu Leu Leu Lys
          165          170          175
Val Ala Arg Tyr Glu Leu Gln Glu Val Met Arg Trp Leu Ser Gly Ser
          180          185          190
Leu Ser Phe Thr Lys Leu Asp Asp Ile Pro Leu Val Leu Xaa Ser Lys
          195          200          205
Tyr Tyr Cys Tyr Tyr Ile Ser Phe Ile Phe
210          215

```

(2) INFORMATION FOR SEQ ID NO:3579:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 207 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...207
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3579:

```

Glu Met Gln Lys Thr Ala Phe Ile Trp Asp Leu Asp Gly Thr Leu Leu
1          5          10          15
Asp Ser Tyr Glu Ala Ile Leu Ser Gly Ile Glu Glu Thr Phe Ala Gln
          20          25          30
Phe Ser Ile Pro Tyr Asp Lys Glu Lys Val Arg Glu Phe Ile Phe Lys
          35          40          45
Tyr Ser Val Gln Asp Leu Leu Val Arg Val Ala Glu Asp Arg Asn Leu
          50          55          60
Asp Val Glu Val Leu Asn Gln Val Arg Ala Gln Ser Leu Ala Glu Lys
          65          70          75          80
Asn Ala Gln Val Val Leu Met Pro Gly Ala Arg Glu Val Leu Ala Trp
          85          90          95
Ala Asp Glu Ser Gly Ile Gln Gln Phe Ile Tyr Thr His Lys Gly Asn
          100          105          110
Asn Ala Phe Thr Ile Leu Lys Asp Leu Gly Val Glu Ser Tyr Phe Thr
          115          120          125
Glu Ile Leu Thr Ser Gln Ser Gly Phe Val Arg Lys Pro Ser Pro Glu
          130          135          140
Ala Ala Thr Tyr Leu Leu Asp Lys Tyr Gln Leu Asn Ser Asp Asn Thr
          145          150          155          160
Tyr Tyr Ile Gly Asp Arg Thr Leu Asp Val Glu Phe Ala Gln Asn Ser
          165          170          175
Gly Ile Gln Ser Ile Asn Phe Leu Glu Ser Thr Tyr Glu Gly Asn His
          180          185          190

```

Arg Ile Gln Ala Leu Ala Asp Ile Ser Arg Ile Phe Glu Thr Lys
 195 200 205

(2) INFORMATION FOR SEQ ID NO:3580:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...88

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3580:

Val	Tyr	Lys	Lys	Glu	Lys	Glu	Tyr	Leu	Ile	Met	Leu	Gln	Lys	Ile	Tyr
1				5				10						15	
Glu	Gln	Met	Thr	Asn	Phe	Tyr	Asp	Ser	Ile	Glu	Glu	Glu	Tyr	Gly	Pro
			20					25					30		
Thr	Phe	Gly	Asp	Asn	Phe	Asp	Trp	Glu	His	Val	His	Phe	Lys	Phe	Leu
		35					40					45			
Ile	Tyr	Tyr	Leu	Val	Arg	Tyr	Gly	Ile	Gly	Cys	Arg	Lys	Asp	Phe	Ile
	50					55				60					
Val	Tyr	His	Tyr	Arg	Val	Ala	Tyr	Arg	Leu	Tyr	Leu	Glu	Lys	Leu	Val
65					70				75						80
Met	Asn	Arg	Gly	Phe	Ile	Ser	Cys								
					85										

(2) INFORMATION FOR SEQ ID NO:3581:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...232

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3581:

Cys Tyr Lys Asn Lys Ile Gly Ala Asp Met Lys Thr Ile Gln Ile Ala

1				5					10					15				
Ile	Asp	Gly	Pro	Ala	Ser	Ser	Gly	Lys	Ser	Thr	Val	Ala	Lys	Ile	Ile			
			20					25					30					
Ala	Lys	Asp	Phe	Gly	Phe	Thr	Tyr	Leu	Asp	Thr	Gly	Ala	Met	Tyr	Arg			
		35					40					45						
Ala	Ala	Thr	Tyr	Met	Ala	Leu	Lys	Asn	Gln	Leu	Gly	Val	Glu	Glu	Val			
	50					55					60							
Glu	Ala	Leu	Leu	Ala	Leu	Leu	Asp	Gln	His	Pro	Ile	Ser	Phe	Gly	Arg			
65					70					75					80			
Ser	Glu	Thr	Gly	Asp	Gln	Leu	Val	Phe	Val	Gly	Asp	Val	Asp	Ile	Thr			
			85					90						95				
His	Pro	Ile	Arg	Glu	Asn	Glu	Val	Thr	Asn	His	Val	Ser	Ala	Ile	Ala			
		100						105					110					
Ala	Ile	Pro	Gln	Val	Arg	Glu	Lys	Leu	Val	Ser	Leu	Gln	Gln	Glu	Ile			
	115						120					125						
Ala	Gln	Gln	Gly	Gly	Ile	Val	Met	Asp	Gly	Arg	Asp	Ile	Gly	Thr	Val			
	130					135				140								
Val	Leu	Pro	Gln	Ala	Glu	Leu	Lys	Ile	Phe	Leu	Val	Ala	Ser	Val	Asp			
145				150				155						160				
Glu	Arg	Ala	Glu	Arg	Arg	Tyr	Lys	Glu	Asn	Ile	Ala	Lys	Gly	Ile	Glu			
			165					170					175					
Thr	Asp	Leu	Glu	Thr	Leu	Lys	Lys	Glu	Ile	Ala	Ala	Arg	Asp	Tyr	Lys			
		180					185						190					
Asp	Ser	His	Arg	Glu	Thr	Ser	Pro	Leu	Lys	Gln	Ala	Glu	Asp	Ala	Val			
	195					200						205						
Tyr	Leu	Asp	Thr	Thr	Gly	Leu	Asn	Ile	Gln	Glu	Val	Val	Glu	Lys	Ile			
	210					215					220							
Lys	Ala	Glu	Ala	Glu	Lys	Arg	Met											
225					230													

(2) INFORMATION FOR SEQ ID NO:3582:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...77

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3582:

Asn	Asn	Lys	Lys	Gly	Glu	Leu	Ile	Met	Lys	Lys	Met	Lys	Val	Trp	Ser			
1				5				10					15					
Thr	Val	Leu	Ala	Thr	Gly	Val	Ala	Leu	Thr	Thr	Leu	Ala	Ala	Cys	Ser			
		20					25					30						
Gly	Gly	Ser	Asn	Ser	Thr	Thr	Ala	Ser	Ser	Ser	Glu	Glu	Lys	Ala	Asp			
	35					40					45							
Lys	Ser	Gln	Glu	Leu	Val	Ile	Tyr	Ser	Asn	Ser	Val	Ser	Asn	Gly	Arg			

(2) INFORMATION FOR SEQ ID NO:3583:

(A) LENGTH: 149 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: YES

(A) ORGANISM: *Streptococcus pneumoniae*

(A) NAME/KEY: misc_feature
(B) LOCATION 1...149

(2) INFORMATION FOR SEQ ID NO:3584:

(A) LENGTH: 111 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...111

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3584:

```
Pro Arg Lys Lys Glu Lys Arg Met Gln Ile Pro Ser Arg Phe Thr Ile
1          5          10          15
Ala Thr His Met Leu Ile Ile Ile Ala Leu Glu Gly Lys Glu Ser Lys
          20          25          30
Val Thr Ser Asp Phe Leu Ala Ala Ser Val Gly Val Asn Pro Val Ile
          35          40          45
Ile Arg Lys Ile Leu Ser Gln Leu Lys Lys Ala Glu Leu Ile Ser Val
          50          55          60
Ala Arg Gly Thr Gly Gly Thr Glu Ile Val Lys Asp Leu Lys Asp Ile
65          70          75          80
Ser Leu Leu Asp Val Tyr Gln Gly Gly Ser Asn Val Leu Val Arg Gln
          85          90          95
Val Asn Ser Ser Val Ser Met Thr Ile Arg Ile Gln Ile Ala Leu
          100          105          110
```

(2) INFORMATION FOR SEQ ID NO:3585:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 190 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...190

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3585:

```
Arg Gly Lys Asn Met Ile Glu Ala Ser Lys Leu Lys Ala Gly Met Thr
1          5          10          15
Phe Glu Thr Ala Asp Gly Lys Leu Ile Arg Val Leu Glu Ala Ser His
          20          25          30
His Lys Pro Gly Lys Gly Asn Thr Ile Met Arg Met Lys Leu Arg Asp
          35          40          45
Val Arg Thr Gly Ser Thr Phe Asp Thr Ser Tyr Arg Pro Glu Glu Lys
          50          55          60
Phe Glu Gln Ala Ile Ile Glu Thr Val Pro Ala Gln Tyr Leu Tyr Lys
65          70          75          80
Met Asp Asp Thr Ala Tyr Phe Met Asn Thr Glu Thr Tyr Asp Gln Tyr
          85          90          95
Glu Ile Pro Val Val Asn Val Glu Asn Glu Leu Leu Tyr Ile Leu Glu
```

		100					105				110				
Asn	Ser	Asp	Val	Lys	Ile	Gln	Phe	Tyr	Gly	Thr	Glu	Val	Ile	Gly	Val
		115					120					125			
Thr	Val	Pro	Thr	Thr	Val	Glu	Leu	Thr	Val	Ala	Glu	Thr	Gln	Pro	Ser
		130					135					140			
Ile	Lys	Gly	Ala	Thr	Val	Thr	Gly	Ser	Gly	Lys	Pro	Ala	Thr	Met	Glu
145					150					155					160
Thr	Gly	Leu	Val	Val	Asn	Val	Pro	Asp	Phe	Ile	Glu	Ala	Gly	Gln	Lys
				165					170					175	
Leu	Val	Ile	Asn	Thr	Ala	Glu	Gly	Thr	Tyr	Val	Ser	Arg	Ala		
			180					185					190		

(2) INFORMATION FOR SEQ ID NO:3586:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 301 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...301
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3586:

Leu Val Lys Lys Leu Lys Arg Leu Gly Ile Glu Lys Gly Ile Ser Arg

1				5				10				15			
Pro	Asp	Phe	Cys	Gly	Asp	Glu	Gln	Glu	Leu	Thr	Val	Arg	Gln	Leu	Ser
			20					25				30			
Arg	Ile	Glu	Ser	Gly	Ala	Ser	Gln	Pro	Ser	Leu	Pro	Lys	Leu	Asp	Tyr
		35					40					45			
Ile	Ala	Arg	Arg	Leu	Gly	Val	Pro	Val	Tyr	Ser	Leu	Met	Pro	Asp	Phe
	50					55					60				
Ser	Ala	Leu	Pro	Ser	Ala	Tyr	Leu	Glu	Leu	Lys	Tyr	Gln	Ile	Leu	Arg
65					70					75					80
Glu	Pro	Ile	Tyr	Asp	Lys	Glu	Glu	Glu	Tyr	Asp	Lys	Lys	Glu	Ala	Cys
				85				90					95		
Leu	Glu	Glu	Ile	Glu	Asp	Leu	Phe	Tyr	Glu	Gln	Leu	Pro	Asn	Glu	Glu
			100					105				110			
Lys	Val	Trp	Phe	Glu	Ala	Thr	Arg	Ala	Thr	Ile	Asp	Val	Ile	Arg	Ser
		115					120					125			
Gly	Gln	Pro	Glu	Tyr	Gly	Glu	Thr	Val	Leu	Asp	Asp	Tyr	Phe	Lys	Thr
	130					135				140					
Ile	Tyr	Asp	Lys	Glu	Leu	Phe	Leu	Ile	Asn	Glu	Leu	Glu	Val	Ile	Asn
145					150					155					160
Leu	Tyr	Phe	Ala	Ile	Val	Leu	Thr	Lys	Ile	Lys	Gln	Gly	Gln	Asn	Gln
				165					170					175	
Ile	Glu	Glu	Ile	Asn	Arg	Ile	His	Ser	Phe	Leu	Val	Arg	Leu	Thr	Asn
			180					185					190		

His	Val	Glu	Leu	Ile	Ala	Pro	Glu	Tyr	Leu	Phe	Ala	Leu	Ser	Asn	Thr
		195					200					205			
Leu	Phe	Ser	Gly	Leu	Ala	Cys	Leu	Asp	Asn	Leu	Ser	Ser	Tyr	Asp	Ser
	210					215					220				
Leu	Gly	Ala	Tyr	Ile	Phe	Ser	Leu	Asn	His	Ile	Met	Glu	Lys	Thr	Gln
225					230					235					240
Asp	Phe	Gln	Lys	Lys	Pro	Ile	Ile	Leu	Met	Leu	Glu	Trp	Lys	Leu	Ser
			245						250					255	
Leu	Ile	Ile	Asn	Asp	Tyr	Val	Ser	Ala	Glu	Gln	Phe	Tyr	Gln	Lys	
			260				265						270		
Ser	Lys	Leu	Phe	Ala	Asp	Ile	Ile	Glu	Asn	Ser	Tyr	Leu	Val	Thr	Met
	275						280					285			
Leu	Glu	Lys	Gln	Trp	Gln	Glu	Asp	Leu	Lys	Lys	Tyr	Leu			
	290					295					300				

(2) INFORMATION FOR SEQ ID NO:3587:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 106 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...106
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3587:

Phe	Ser	Lys	Lys	Asn	Thr	Ile	Asn	Phe	Gln	Val	Ser	Gln	Arg	Gly	Arg
1				5					10					15	
His	Lys	Met	Ser	Asp	Ala	Phe	Thr	Asp	Val	Ala	Lys	Met	Lys	Lys	Ile
		20						25					30		
Lys	Glu	Glu	Ile	Lys	Ala	His	Glu	Gly	Gln	Val	Val	Glu	Met	Thr	Leu
	35					40					45				
Glu	Asn	Gly	Arg	Lys	Arg	Gln	Lys	Asn	Arg	Leu	Gly	Lys	Leu	Ile	Glu
	50					55				60					
Val	Tyr	Pro	Ser	Leu	Phe	Ile	Val	Glu	Phe	Gly	Asp	Val	Glu	Gly	Asp
65				70					75					80	
Lys	Gln	Val	Asn	Val	Tyr	Val	Glu	Ser	Phe	Thr	Tyr	Ser	Asp	Ile	Leu
			85						90					95	
Thr	Glu	Lys	Asn	Leu	Ile	His	Tyr	Leu	Asp						
		100						105							

(2) INFORMATION FOR SEQ ID NO:3588:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 108 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...108
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3588:

```

Thr Asn Lys Lys Thr Ser Asp Thr Ile Asn Leu Ala Gly Lys Gly Arg
1      5      10      15
Ala Leu Tyr Thr Ser Ile Tyr Phe Leu Leu Glu Glu Thr Asn Pro Ser
      20      25      30
His Phe His Arg Leu Thr Ala Asp Glu Ile Trp Tyr Phe His Ala Gly
      35      40      45
Ser Pro Leu Thr Val His Met Ile Thr Ala Asp Gly His Tyr Glu Ala
      50      55      60
Val Thr Leu Gly Leu Asp Ile Ser Lys Gly Gln Gln Leu His Tyr Cys
65      70      75      80
Val Pro Lys Gly Thr Ile Trp Gly Ser Thr Val Asp Lys Asp Tyr Ala
      85      90      95
Leu Val Ser Cys Leu Val Ala Pro Gly Phe Glu Cys
      100      105

```

(2) INFORMATION FOR SEQ ID NO:3589:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 101 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...101
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3589:

```

Ile Ile Lys Lys Phe Glu Phe Asp Met Met Glu Lys Val Ala Ser Leu
1      5      10      15
Gly Val Pro Met Cys Lys Pro Ile Ser Ile Glu Leu Cys Asp Asp Glu
      20      25      30
Val His Ser Leu His Glu Trp Ile Asp Gly Arg Asp Ala Ile Asp Ser
      35      40      45
Ile Leu Thr Tyr Ser Glu Asn Gln Gln Tyr Thr Tyr Gly Val Glu Ala

```


50		55		60											
Gly	Lys	Ile	Leu	Arg	Lys	Ile	His	Thr	Ile	Pro	Ala	Thr	Glu	Val	Cys
65		70		75		80									
Glu	Asp	Trp	Glu	Ile	Phe	Phe	Asn	Leu	Lys	Ile	Asp	Asp	Lys	Ile	Ser
		85		90		95									
Asn	Glu	Met	Ile	Trp											
		100													

(2) INFORMATION FOR SEQ ID NO:3590:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 amino acids
- (B) TYPE: amino acid.
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...386

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3590:

Asn	Ile	Lys	Asn	Leu	Glu	Leu	Tyr	Gln	Ile	Ser	Met	Leu	Val	Ser	Thr
1		5		10		15									
Val	Phe	Gln	Asn	Pro	Lys	Thr	Tyr	Phe	Phe	Asn	Val	Asn	Thr	Thr	Leu
		20		25		30									
Glu	Leu	Leu	Phe	Tyr	Leu	Glu	Asn	Ile	Gly	Leu	Ala	Arg	Glu	Glu	Met
		35		40		45									
Asp	Arg	Arg	Leu	Lys	Asp	Ile	Leu	Glu	Ile	Phe	Pro	Ile	Lys	Asn	Leu
		50		55		60									
Leu	Asn	Arg	Asn	Ile	Phe	Asn	Leu	Ser	Gly	Gly	Glu	Lys	Gln	Ile	Leu
65		70		75		80									
Cys	Ile	Ala	Ala	Ser	Tyr	Ile	Ala	Gly	Thr	Lys	Ile	Ile	Val	Met	Asp
		85		90		95									
Glu	Pro	Ser	Ser	Asn	Leu	Asp	Ile	Lys	Ser	Ile	Ser	Val	Leu	Ala	Lys
		100		105		110									
Met	Leu	Lys	Ile	Leu	Lys	Glu	Lys	Gly	Ile	Ser	Ile	Ile	Val	Ala	Glu
		115		120		125									
His	Arg	Ile	Tyr	Tyr	Leu	Met	Asp	Ile	Val	Asp	Arg	Val	Phe	Leu	Ile
		130		135		140									
Asp	Lys	Gly	Lys	Leu	Lys	Lys	Thr	Tyr	Thr	Arg	Ser	Glu	Phe	Leu	Lys
145		150		155		160									
Leu	Asp	Lys	Asn	Glu	Leu	Asn	Ala	Leu	Ser	Leu	Arg	Asp	Lys	Glu	Leu
		165		170		175									
Ser	Lys	Leu	Lys	Val	Pro	Tyr	Leu	Lys	Glu	Gly	Gly	Glu	Tyr	Gln	Ile
		180		185		190									
Lys	Asn	Leu	Ser	Tyr	Lys	Phe	Thr	Asp	Asp	Glu	Cys	Leu	Ser	Leu	Lys
		195		200		205									
Asp	Ile	Ser	Phe	Lys	Leu	Gly	Lys	Ile	Tyr	Gly	Ile	Ile	Gly	Ser	Asn
210		215		220											
Gly	Arg	Gly	Lys	Ser	Thr	Leu	Leu	Arg	Cys	Leu	Ile	Gly	Leu	Glu	Lys

225		230		235		240									
Lys	Ser	Lys	Glu	Glu	Ile	Tyr	Phe	Lys	Gly	Glu	Lys	Leu	Ser	Lys	Lys
		245							250					255	
Glu	Arg	Leu	Lys	Asn	Ser	Ser	Leu	Val	Met	Gln	Asp	Val	Asn	His	Gln
		260						265					270		
Leu	Phe	Thr	Asp	Glu	Val	Phe	Asn	Glu	Leu	Arg	Leu	Gly	Val	Lys	Asn
		275					280					285			
Phe	Asp	Glu	Glu	Lys	Ala	Lys	Ile	Ile	Leu	Lys	Asp	Leu	Cys	Leu	Asp
	290					295					300				
Glu	Phe	Ile	Glu	Arg	His	Pro	Met	Ser	Leu	Ser	Gly	Gly	Arg	Lys	Gln
305					310					315					320
Arg	Leu	Ala	Ile	Ala	Ser	Val	Met	Cys	Lys	Asn	Ser	Pro	Phe	Val	Phe
				325					330					335	
Phe	Asp	Glu	Pro	Ser	Ser	Gly	Met	Asp	Tyr	Ser	Asn	Met	Ile	Lys	Ile
		340					345					350			
Ser	Glu	Leu	Ile	Asn	Lys	Tyr	Lys	Thr	Met	Asp	Lys	Ile	Ile	Phe	Ile
		355					360					365			
Val	Ser	His	Asp	Ile	Glu	Phe	Leu	Asn	Glu	Val	Ala	Asp	Glu	Ile	Phe
	370					375					380				
Glu	Leu														
385															

(2) INFORMATION FOR SEQ ID NO:3591:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...99

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3591:

Asn	Ser	Lys	Asn	Ala	Ser	Tyr	Gln	Val	Tyr	Met	Asn	Tyr	Thr	Pro	Lys
1			5					10					15		
Val	Arg	Gln	Lys	Lys	Ser	Asn	Phe	Trp	Gly	Val	Phe	Ile	Met	Lys	Leu
		20					25					30			
Thr	Tyr	Asp	Asp	Lys	Val	Gln	Ile	Tyr	Glu	Leu	Arg	Lys	Gln	Gly	Tyr
		35				40					45				
Ser	Leu	Glu	Lys	Leu	Ser	Asn	Lys	Phe	Gly	Ile	Asn	Asn	Ser	Asn	Ile
	50					55			60						
Arg	Tyr	Met	Ile	Lys	Leu	Ile	Asp	Arg	Tyr	Gly	Ile	Glu	Phe	Val	Lys
65				70					75					80	
Lys	Gly	Lys	Asn	Arg	Tyr	Tyr	Ser	Pro	Asp	Leu	Lys	Gln	Glu	Met	Ile
			85					90					95		
Asn	Lys	Val													

(2) INFORMATION FOR SEQ ID NO:3592:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 226 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...226
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3592:

```
Lys Ser Lys Lys Gly Glu Val Val Val Ile Leu Gly Ala Ser Gly Cys
1      5      10
Gly Lys Ser Thr Leu Leu Arg Cys Leu Asn Gly Leu Glu Ser Ile Gln
20      25      30
Gly Gly Asp Ile Leu Leu Asp Gly Gln Ser Ile Val Glu Asn Lys Lys
35      40      45
Asp Phe His Leu Val Arg Gln Lys Ile Gly Met Val Phe Gln Ser Tyr
50      55      60
Glu Leu Phe Pro His Leu Asp Val Leu Gln Asn Leu Ile Leu Gly Pro
65      70      75      80
Ile Lys Ala Gln Gly Arg Asp Lys Lys Glu Val Thr Glu Glu Ala Leu
85      90      95
Gln Leu Leu Glu Arg Val Gly Leu Leu Asp Lys Gln His Ser Phe Ala
100     105     110
Arg Gln Leu Ser Gly Gly Gln Lys Gln Arg Val Ala Ile Val Arg Ala
115     120     125
Leu Leu Met His Pro Glu Ile Ile Leu Phe Asp Glu Val Thr Ala Ser
130     135     140
Leu Asp Pro Glu Met Val Arg Glu Val Leu Glu Leu Ile Asn Asp Leu
145     150     155     160
Thr Gln Glu Gly Arg Thr Met Ile Leu Val Thr His Glu Met Gln Phe
165     170     175
Ala Gln Ala Ile Thr Asp Arg Ile Ile Phe Leu Asp Gln Gly Lys Ile
180     185     190
Ala Glu Glu Gly Thr Ala Gln Ala Phe Phe Thr Asn Pro Gln Thr Lys
195     200     205
Arg Ala Gln Glu Phe Leu Asn Val Phe Asp Phe Ser Gln Phe Gly Ser
210     215     220
Tyr Leu
225
```

(2) INFORMATION FOR SEQ ID NO:3593:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 156 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...156
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3593:

```

Lys Ala Lys Asn Asn Leu Leu Trp Gln Tyr Gly Leu Gly Met Thr Ile
 1             5             10             15
Leu Phe Val Val Ile Ser Ala Ser Phe Leu Tyr Met Val Ser Leu Ser
      20             25             30
Met Lys Pro Tyr Gln Thr Ala Lys Ser Glu Gly Glu Lys Leu Ala Gln
      35             40             45
Gln Tyr Ala Gly Leu Glu Gln Ala Asp Gln Val Asp Leu Tyr Asn Gly
 50             55             60
Leu Glu Ser Tyr Tyr Ser Val Leu Gly Arg Asn Lys Gln Gln Glu Ala
 65             70             75             80
Leu Ala Val Leu Ile Gly Lys Asp Asp His Lys Ile Tyr Val Tyr Gln
      85             90             95
Leu Asn Gln Gly Val Ser Gln Glu Lys Ala Glu Thr Val Ser Lys Glu
      100            105            110
Lys Gly Ala Gly Glu Ile Asp Lys Ile Ile Phe Gly Arg Tyr Gln Asp
      115            120            125
Lys Pro Ile Trp Glu Val Lys Ser Gly Ser Asp Phe Tyr Leu Val Asp
      130            135            140
Phe Glu Thr Gly Ala Leu Val Asn Lys Glu Gly Leu
145            150            155

```

(2) INFORMATION FOR SEQ ID NO:3594:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 69 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...69
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3594:

```

Thr Arg Lys Lys Glu Glu Ser Ser Met Thr Asn Phe Asp Ile Leu Asp
 1             5             10             15

```

```

Asn Gln Phe Leu Ser Leu Ser Glu Asn Glu Leu Ser Asp Ile Asp Gly
      20              25              30
Gly Leu Ala Pro Leu Val Ile Phe Gly Val Ala Val Ser Trp Lys Ala
      35              40              45
Ile Ala Gly Gly Thr Ala Leu Ile Gly Ser Gly Leu Ala Ala Gly Tyr
      50              55              60
Phe Leu Gly Gly Asp
65

```

(2) INFORMATION FOR SEQ ID NO:3595:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 83 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...83
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3595:

```

Arg Arg Lys Asn Met Ala Gln Gln Arg Arg Gly Gly Phe Lys Arg Arg
1      5      10      15
Lys Lys Val Asp Tyr Ile Ala Ala Asn Lys Ile Glu Tyr Val Asp Tyr
      20      25      30
Lys Asp Thr Glu Leu Leu Ser Arg Phe Val Ser Glu Arg Gly Lys Ile
      35      40      45
Leu Pro Arg Arg Val Thr Gly Thr Ser Ala Lys Asn Gln Arg Lys Val
      50      55      60
Thr Thr Ala Ile Lys Arg Ala Arg Val Met Ala Leu Met Pro Phe Val
65      70      75      80
Asn Glu Asp

```

(2) INFORMATION FOR SEQ ID NO:3596:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 182 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...182

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3596:

```

Asp Gly Lys Lys Glu Ile Thr Gly Asp Lys Met Asn Tyr Phe Asn Val
1      5      10      15
Gly Lys Ile Val Asn Thr Gln Gly Leu Gln Gly Glu Met Arg Val Leu
      20      25      30
Ser Val Thr Asp Phe Ala Glu Glu Arg Phe Lys Lys Gly Ala Glu Leu
      35      40      45
Ala Leu Phe Asp Glu Lys Asp Gln Phe Val Gln Thr Val Thr Ile Ala
      50      55      60
Ser His Arg Lys Gln Lys Asn Phe Asp Ile Ile Lys Phe Lys Asp Met
65      70      75      80
Tyr His Ile Asn Thr Ile Glu Lys Tyr Lys Gly Tyr Ser Leu Lys Val
      85      90      95
Ala Glu Glu Asp Leu Asn Asp Leu Asp Asp Gly Glu Phe Tyr Tyr His
      100     105     110
Glu Ile Ile Gly Leu Glu Val Tyr Glu Gly Asp Ser Leu Val Gly Thr
      115     120     125
Ile Lys Glu Ile Leu Gln Pro Gly Ala Asn Asp Val Trp Val Val Lys
      130     135     140
Arg Lys Gly Lys Arg Asp Leu Leu Leu Pro Tyr Ile Pro Pro Val Val
145     150     155     160
Leu Asn Val Asp Ile Pro Asn Lys Arg Val Asp Val Glu Ile Leu Glu
      165     170     175
Gly Leu Asp Asp Glu Asp
      180

```

(2) INFORMATION FOR SEQ ID NO:3597:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 345 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3597:

```

Ile Met Lys Lys Ser Asp Val Leu Asp Leu Ile Lys Tyr His Tyr Glu
1      5      10      15
Gly Arg Glu Thr Glu Phe Arg Asn Gln Ser Ile Ala Ile Ala Arg Asn
      20      25      30
Phe Asn Lys His Gly Asp Thr Gln Ile Ala Gln Tyr Ile Met Gly Leu
      35      40      45
Met Ser Gln Ser Asp Arg Phe Met Pro Gln Ile Glu Asn Pro Ser Glu

```

50		55		60											
Tyr	Leu	Thr	Pro	Ala	Lys	Leu	Asp	Ile	Gly	Pro	Leu	Pro	Leu	Pro	Leu
65					70					75					80
Ser	Ile	Met	Asn	Asp	Leu	Lys	Gly	Ile	Ile	Asn	Ala	Val	Asn	His	His
				85						90					95
Ile	Gly	Ile	Asn	Lys	Phe	Leu	Phe	Val	Gly	Ser	Thr	Gly	Thr	Gly	Lys
			100					105					110		
Thr	Glu	Ser	Val	Lys	Gln	Val	Ala	Arg	Leu	Ile	Gly	Lys	Glu	Leu	Leu
		115						120					125		
Val	Val	Asp	Phe	Ser	His	Leu	Val	Asp	Ser	Lys	Leu	Gly	Gln	Thr	Val
	130							135					140		
Lys	Asn	Leu	Ala	Thr	Leu	Phe	Asn	Glu	Ile	Asn	Asn	Leu	Pro	Phe	Lys
145					150					155					160
Gln	Asn	Tyr	Ile	Ile	Leu	Phe	Asp	Glu	Ile	Asp	Ser	Ile	Val	Leu	Asp
			165						170					175	
Arg	Val	Asn	Gln	Asn	Asp	Leu	Arg	Glu	Met	Gly	Arg	Val	Thr	Ser	Ala
		180						185					190		
Phe	Leu	Lys	Glu	Leu	Asp	Arg	Leu	Ser	Pro	Glu	Ile	Val	Leu	Ile	Ala
	195						200					205			
Thr	Thr	Asn	Leu	Phe	Glu	Asn	Leu	Asp	Lys	Ala	Val	Thr	Arg	Arg	Phe
	210					215					220				
Asp	Ala	Ile	Ile	Asp	Phe	Asp	Arg	Tyr	Thr	Asp	Glu	Asp	Lys	Val	Glu
225					230					235					240
Val	Ala	Thr	Ile	Ile	Leu	Asn	Glu	Leu	Leu	Lys	Gln	Phe	Lys	Asn	Val
			245						250					255	
Ala	Arg	Asp	Leu	Lys	Leu	Phe	Lys	Lys	Ile	Ile	Asn	Ser	Ala	Asn	Val
	260							265					270		
Ile	Pro	Asn	Pro	Gly	Asp	Leu	Arg	Asn	Ser	Ile	Arg	Thr	Ser	Leu	Ala
	275						280					285			
Phe	Ser	Asp	Pro	Ser	Asp	Pro	His	Asp	Tyr	Gln	Lys	Arg	Leu	Leu	Arg
	290					295					300				
Ser	Leu	His	Asn	Gly	Arg	Asn	Leu	Ser	Ile	Ser	Lys	Leu	Ser	Lys	Leu
305					310					315					320
Gly	Phe	Thr	Val	Arg	Glu	Ile	Glu	Ile	Leu	Thr	Gly	Val	Ser	Lys	Ser
			325						330					335	
Ser	Val	Ser	Arg	Glu	Leu	Ser	Glu	Asp							
			340					345							

(2) INFORMATION FOR SEQ ID NO:3598:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...348

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3598:

Lys	Met	Lys	Asn	Glu	Met	Leu	Ala	Leu	Ile	Leu	Ala	Gly	Gly	Gln	Gly
1			5						10					15	
Thr	Arg	Leu	Gly	Lys	Leu	Thr	Gln	Ser	Ile	Ala	Lys	Pro	Ala	Val	Gln
		20						25					30		
Phe	Gly	Gly	Arg	Tyr	Arg	Ile	Ile	Asp	Phe	Ala	Leu	Ser	Asn	Cys	Ala
		35					40					45			
Asn	Ser	Gly	Ile	His	Asn	Val	Gly	Val	Val	Thr	Gln	Tyr	Gln	Pro	Leu
	50					55					60				
Ala	Leu	Asn	Asn	His	Ile	Gly	Asn	Gly	Ser	Ser	Trp	Gly	Leu	Asp	Gly
65					70					75					80
Ile	Asn	Ser	Gly	Val	Ser	Ile	Leu	Gln	Pro	Tyr	Ser	Ala	Ser	Glu	Gly
			85						90					95	
Asn	Arg	Trp	Phe	Glu	Gly	Thr	Ser	His	Ala	Ile	Tyr	Gln	Asn	Ile	Asp
			100					105					110		
Tyr	Ile	Asp	Ser	Val	Asn	Pro	Glu	Tyr	Val	Leu	Ile	Leu	Ser	Gly	Asp
		115					120					125			
His	Ile	Tyr	Lys	Met	Asp	Tyr	Asp	Asp	Met	Leu	Gln	Ser	His	Lys	Asp
	130					135					140				
Asn	Asn	Ala	Ser	Leu	Thr	Val	Ala	Val	Leu	Asp	Val	Pro	Leu	Lys	Glu
145					150					155					160
Ala	Ser	Arg	Phe	Gly	Ile	Met	Asn	Thr	Asp	Ala	Asn	Asn	Arg	Ile	Val
			165						170					175	
Glu	Phe	Glu	Glu	Lys	Pro	Ala	Gln	Pro	Lys	Ser	Thr	Lys	Ala	Ser	Met
		180						185					190		
Gly	Ile	Tyr	Ile	Phe	Asp	Trp	Gln	Arg	Leu	Arg	Asn	Met	Leu	Val	Ala
		195					200					205			
Ala	Glu	Lys	Ser	Lys	Val	Gly	Met	Ser	Asp	Phe	Gly	Lys	Asn	Val	Ile
	210					215					220				
Pro	Asn	Tyr	Leu	Glu	Ser	Gly	Glu	Ser	Val	Tyr	Ala	Tyr	Glu	Phe	Ser
225					230					235					240
Gly	Tyr	Trp	Lys	Asp	Val	Gly	Thr	Ile	Glu	Ser	Leu	Trp	Glu	Ala	Asn
			245						250					255	
Met	Glu	Tyr	Ile	Ser	Pro	Glu	Asn	Ala	Leu	Asp	Ser	Arg	Asn	Arg	Gln
			260						265				270		
Trp	Lys	Ile	Tyr	Ser	Arg	Asn	Leu	Ile	Ser	Pro	Pro	Asn	Phe	Leu	Gly
		275					280					285			
Ala	Asn	Ala	His	Val	Glu	Asp	Ser	Leu	Val	Val	Asp	Gly	Cys	Phe	Val
	290					295					300				
Asp	Gly	Thr	Val	Lys	His	Ser	Ile	Leu	Ser	Thr	Gly	Ala	Gln	Val	Arg
305					310					315					320
Glu	Gly	Ala	Glu	Val	Leu	Asp	Ser	Val	Ile	Met	Ser	Gly	Ala	Ile	Ile
			325						330					335	
Gly	Gln	Gly	Ala	Lys	Ile	Lys	Arg	Ala	Ile	Ile	Glu				
			340					345							

(2) INFORMATION FOR SEQ ID NO:3599:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...239

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3599:

Arg	Met	Lys	Lys	Tyr	Phe	Ile	Gly	Gly	Leu	Gly	Ser	Asn	Ala	Tyr	His
1				5					10					15	
Ser	Lys	Asp	Phe	Leu	Gln	Glu	Leu	Asp	Ser	Gln	Val	Tyr	Phe	Leu	Asn
			20					25					30		
Pro	Tyr	Glu	Lys	His	Leu	Arg	Asp	Glu	Thr	Glu	Leu	Lys	Ser	Trp	Phe
			35				40					45			
Lys	Asn	Glu	Ile	Val	Glu	Glu	Glu	Phe	Ile	Cys	Leu	Ile	Gly	His	Ser
	50					55				60					
Leu	Gly	Gly	Asp	Leu	Ala	Arg	Tyr	Leu	Ala	Ser	Glu	Phe	Glu	Glu	Val
65				70					75					80	
Lys	Lys	Leu	Ile	Leu	Leu	Asp	Gly	Gly	Tyr	Leu	Asp	Leu	Asp	Lys	Ile
			85					90					95		
Leu	Pro	Leu	Asp	Thr	Glu	Leu	Glu	Glu	Thr	Lys	Asn	Tyr	Ile	Lys	Ser
		100					105					110			
Gln	Ile	Val	Leu	Asp	Leu	Asp	Val	Leu	Thr	Ser	Lys	Glu	Lys	Ser	Glu
		115				120						125			
Ala	Lys	His	Trp	Ser	Glu	Asn	Met	Glu	Lys	Ala	Val	Arg	Gln	Ser	Tyr
	130					135				140					
His	Trp	Asn	Val	Glu	Tyr	Asn	Arg	Tyr	Glu	Leu	Ala	Ile	Asn	Tyr	Glu
145				150					155					160	
Asn	Ile	Glu	Ala	Ile	Leu	Arg	Leu	Arg	Arg	Lys	Ile	Gln	Ala	Phe	Lys
			165				170					175			
Arg	Glu	Val	Gly	Asp	Thr	Leu	Phe	Ile	Ser	Pro	Arg	Tyr	Pro	Asn	Glu
		180				185						190			
Ala	Thr	Trp	Arg	Glu	Glu	Ala	Leu	Lys	Glu	Leu	Pro	Asp	Tyr	Phe	Asp
		195				200					205				
Thr	Ile	Phe	Leu	Glu	Asn	Phe	Gly	His	Glu	Leu	Tyr	Thr	Gln	Ala	Pro
	210				215				220						
Lys	Glu	Ile	Ala	Ser	Leu	Met	Asn	Glu	Trp	Leu	Ala	Tyr	Phe	Leu	
225				230					235						

(2) INFORMATION FOR SEQ ID NO:3600:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 332 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...332

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3600:

Arg	Met	Lys	Lys	Gln	Ala	Tyr	Val	Ile	Ile	Ala	Leu	Thr	Ser	Phe	Leu	1	5	10	15
Phe	Val	Phe	Phe	Phe	Ser	His	Ser	Leu	Leu	Glu	Ile	Leu	Asp	Phe	Asp	20	25	30	
Trp	Ser	Ile	Phe	Leu	His	Asp	Val	Glu	Lys	Thr	Glu	Lys	Phe	Val	Phe	35	40	45	
Leu	Leu	Leu	Val	Phe	Ser	Met	Ser	Ile	Thr	Cys	Leu	Leu	Ala	Leu	Phe	50	55	60	
Trp	Arg	Gly	Ile	Glu	Glu	Leu	Ser	Leu	Arg	Lys	Met	Gln	Ala	Asn	Leu	65	70	75	80
Lys	Arg	Leu	Leu	Ala	Gly	Gln	Glu	Val	Val	Gln	Val	Ala	Asp	Pro	Asp	85	90	95	
Leu	Asp	Ala	Ser	Phe	Lys	Ser	Leu	Ser	Gly	Lys	Leu	Asn	Leu	Leu	Thr	100	105	110	
Glu	Ala	Leu	Gln	Lys	Ala	Glu	Asn	His	Ser	Leu	Ala	Gln	Glu	Glu	Glu	115	120	125	
Ile	Ile	Glu	Lys	Glu	Arg	Lys	Arg	Ile	Ala	Arg	Asp	Leu	His	Asp	Thr	130	135	140	
Val	Ser	Gln	Glu	Leu	Phe	Ala	Ala	His	Met	Ile	Leu	Ser	Gly	Ile	Ser	145	150	155	160
Gln	Gln	Ala	Leu	Lys	Leu	Asp	Arg	Glu	Lys	Met	Gln	Ile	Gln	Leu	Gln	165	170	175	
Ser	Val	Thr	Ala	Ile	Leu	Glu	Thr	Ala	Gln	Lys	Asp	Leu	Arg	Val	Leu	180	185	190	
Leu	Leu	His	Leu	Arg	Pro	Val	Glu	Leu	Glu	Gln	Lys	Ser	Leu	Ile	Glu	195	200	205	
Gly	Ile	Gln	Ile	Leu	Leu	Lys	Glu	Leu	Glu	Asp	Lys	Ser	Asp	Leu	Arg	210	215	220	
Val	Ser	Leu	Lys	Gln	Asn	Met	Thr	Lys	Leu	Pro	Lys	Lys	Ile	Glu	Glu	225	230	235	240
His	Ile	Phe	Arg	Ile	Leu	Gln	Glu	Leu	Ile	Ser	Asn	Thr	Leu	Arg	His	245	250	255	
Ala	Gln	Ala	Ser	Cys	Leu	Asp	Val	Tyr	Leu	Tyr	Gln	Thr	Asp	Val	Glu	260	265	270	
Leu	Gln	Leu	Lys	Val	Val	Asp	Asn	Gly	Ile	Gly	Phe	Arg	Leu	Gly	Ser	275	280	285	
Leu	Asp	Asp	Leu	Ser	Tyr	Gly	Leu	Arg	Asn	Ile	Lys	Glu	Arg	Val	Glu	290	295	300	
Asp	Met	Ala	Gly	Thr	Val	Gln	Leu	Leu	Thr	Ala	Pro	Lys	Gln	Gly	Leu	305	310	315	320
Ala	Val	Asp	Ile	Arg	Ile	Pro	Leu	Leu	Asp	Lys	Glu					325	330		

(2) INFORMATION FOR SEQ ID NO:3601:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...69

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3601:

```
Lys Gln Lys Lys Glu Trp Gly Gly Asp Val Leu His Ser Leu Leu Phe
1          5          10          15
Pro Phe Cys Tyr Ser Ser Lys Ile Ser Ser Asn His Val Ser Val Ala
          20          25          30
Leu Pro Tyr Val Trp Leu Leu Thr Ser Ser Val Ser Ser Thr Thr Ser
          35          40          45
Lys Gln Cys Phe Glu Gln Pro Ala Ala Ser Phe Leu Val Phe Ser Leu
          50          55          60
Ile Phe Ile Glu Tyr
65
```

(2) INFORMATION FOR SEQ ID NO:3602:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1120 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3602:

```
Ser Glu Lys Lys Met Gly Asn Phe Ser Phe Leu Leu Lys Asn Asp Glu
1          5          10          15
Tyr Glu Ser Phe Ser Lys Pro Cys Ile Glu Ala Glu Asn Met Ile Ala
          20          25          30
Thr Ser Thr Val Ala Thr Ala Phe Met Ala Arg Arg Ala Leu Glu Gln
          35          40          45
Ala Val His Trp Ile Tyr Ser His Asp Ser Tyr Leu Glu Ala Pro Tyr
          50          55          60
Arg Ala Thr Leu Ser Ser Leu Val Trp Asp Asp Asp Phe Arg Asp Ile
65          70          75          80
Val Asp Ser Glu Leu His Lys Gln Ile Val Leu Leu Ile Arg Trp Gly
          85          90          95
Asn His Ala Ala His Gly Gly Glu Ile Lys Glu Arg Glu Ala Ile Leu
          100          105          110
Ala Leu His His Leu Tyr Gln Phe Val Asn Phe Ile Asp Tyr Cys Tyr
```

2557

Ser	Cys	Glu	Lys	Asp	Ile	Asp	Gly	Ser	Val	Phe	Asn	Ser	Phe	Val	Phe		
			580					585					590				
Asn	Lys	Ser	Thr	Val	Glu	Ile	Val	Leu	Asn	Glu	Leu	Met	Thr	Arg	Gly		
		595					600					605					
Ile	Gln	Thr	Ala	Ser	Gly	Asp	Glu	Ile	Gly	Lys	Thr	Ile	Ile	Phe	Ala		
	610				615						620						
Lys	Asn	His	Asp	His	Ala	Glu	Tyr	Ile	Arg	Gly	Ile	Phe	Asn	Asn	Arg		
625				630						635					640		
Tyr	Pro	Glu	Lys	Gly	Ser	Asp	Tyr	Ala	Gln	Val	Ile	Asp	Tyr	Ser	Ile		
			645						650					655			
Lys	His	Tyr	Gln	Thr	Leu	Ile	Asp	Asp	Phe	Lys	Ile	Lys	Glu	Lys	Tyr		
		660					665						670				
Pro	Gln	Ile	Ala	Ile	Ser	Val	Asp	Met	Leu	Asp	Thr	Gly	Ile	Asp	Val		
	675						680					685					
Pro	Glu	Val	Val	Asn	Leu	Val	Phe	Phe	Lys	Lys	Val	Arg	Ser	Lys	Thr		
	690					695					700						
Lys	Phe	Trp	Gln	Met	Ile	Gly	Arg	Gly	Thr	Arg	Leu	Cys	Lys	Asp	Leu		
705				710						715					720		
Phe	Gly	Pro	Glu	Gln	Asp	Lys	Glu	Asn	Phe	Leu	Val	Phe	Asp	Tyr	Gly		
			725						730					735			
Asp	Asn	Phe	Asp	Tyr	Phe	Arg	Ala	Asp	Pro	Arg	Asp	Gly	Glu	Gly	Arg		
		740					745						750				
His	Ile	Val	Ser	Leu	Thr	Gln	Arg	Leu	Phe	Asn	Ile	Lys	Val	Asp	Leu		
	755					760						765					
Ile	Arg	Glu	Leu	Gln	Gly	Leu	Gln	Tyr	Gln	Glu	Asp	Gln	Phe	Ala	Arg		
	770				775						780						
Ala	Tyr	Arg	Gln	Gln	Leu	Val	Ser	Glu	Leu	Gln	Gly	Arg	Ile	Glu	Ser		
785				790						795					800		
Leu	Asn	Glu	Leu	Asp	Phe	Arg	Val	Arg	Met	Val	Leu	Asp	Thr	Val	Tyr		
			805						810					815			
Ser	Tyr	Arg	Lys	Leu	Glu	Ser	Trp	Gln	Asn	Leu	Thr	Ala	Val	Thr	Ser		
		820						825					830				
Glu	Thr	Ile	Gln	Lys	Asn	Leu	Ser	Pro	Leu	Leu	Phe	Asp	Glu	Asp	Lys		
	835					840						845					
Glu	Asp	Glu	Met	Ala	Arg	Arg	Phe	Asp	Leu	Trp	Leu	Leu	His	Ile	Gln		
	850				855						860						
Leu	Gly	Gln	Leu	Thr	Ala	Lys	Ser	Ser	Thr	Val	His	Ile	Ser	Gln	Val		
865				870						875					880		
Met	Lys	Thr	Ala	Arg	Ala	Leu	Ser	Ala	Ile	Gly	Asn	Ile	Pro	Gln	Val		
			885						890					895			
Phe	Glu	Gln	Ala	Glu	Ile	Ile	Arg	Lys	Val	Gln	Glu	Pro	Glu	Phe	Trp		
	900							905					910				
Lys	Glu	Val	Asn	Leu	Ser	Asp	Leu	Glu	Lys	Ile	Arg	Leu	Ala	Ile	Arg		
	915						920						925				
Asp	Leu	Gln	Phe	Leu	Asp	Lys	Thr	Asp	Arg	Lys	Pro	Tyr	Tyr	Val			
	930				935					940							
Asn	Phe	Glu	Asp	Arg	Ile	Leu	Ser	Thr	Val	His	Glu	Thr	Thr	Ala	Phe		
945				950						955					960		
Leu	Gln	Val	Asn	Asp	Leu	Arg	Ser	Tyr	Asn	Glu	Lys	Val	Glu	His	Tyr		
			965						970					975			
Leu	Lys	Thr	His	Leu	Asp	Glu	Glu	Ser	Ile	Ser	Lys	Leu	Tyr	His	Asn		
	980						985						990				
Lys	Lys	Leu	Thr	Ser	Asp	Asp	Met	Leu	Ala	Leu	Glu	Lys	Leu	Leu	Trp		
	995					1000							1005				
Glu	Lys	Leu	Gly	Ser	Lys	Ala	Asp	Tyr	Gln	Ser	His	Tyr	Glu	Asn	Lys		
	1010					1015					1020						
Ala	Ile	Pro	Arg	Leu	Val	Arg	Glu	Ile	Ile	Gly	Leu	Asp	Arg	Glu	Ser		

1025		1030		1035		1040
Ala Asn Arg Ile	Phe Ser Lys Phe Leu Ser Asp Glu Asn Leu Asn Ala					
	1045		1050		1055	
Arg Gln Ile Ser Phe Val Lys Leu Ile Val Asp Tyr Ile Val Glu Asn						
	1060		1065		1070	
Gly Phe Leu Glu Thr Lys Val Leu Thr Gln Glu Pro Phe Lys Ser Tyr						
	1075		1080		1085	
Gly Ser Val Gln Leu Leu Phe Gln His Gln Leu Pro Val Leu Arg Asn						
	1090		1095		1100	
Ile Val Gln Ile Ile Glu Leu Ile Asn Asn Arg Ala Gly Glu Ala Ala						
1105	1110		1115		1120	

(2) INFORMATION FOR SEQ ID NO:3603:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3603:

Gly	Glu	Lys	Lys	Met	Lys	Lys	Lys	Phe	Ala	Leu	Ser	Phe	Val	Ala	Leu
1				5				10						15	
Ala	Ser	Val	Ala	Leu	Leu	Ala	Ala	Cys	Gly	Glu	Val	Lys	Ser	Gly	Ala
			20					25						30	
Val	Asn	Thr	Ala	Gly	Asn	Ser	Val	Glu	Glu	Lys	Thr	Ile	Lys	Ile	Gly
			35				40						45		
Phe	Asn	Phe	Glu	Glu	Thr	Gly	Ser	Leu	Thr	Ala	Tyr	Gly	Thr	Ala	Glu
	50					55					60				
Gln	Lys	Gly	Ala	Gln	Leu	Ala	Val	Asp	Glu	Ile	Asn	Ala	Ala	Gly	Gly
65				70					75					80	
Ile	Asp	Gly	Lys	Gln	Ile	Glu	Val	Ile	Asp	Lys	Asp	Asn	Lys	Ser	Glu
			85					90						95	
Thr	Ala	Glu	Ala	Ala	Ser	Val	Thr	Thr	Asn	Leu	Val	Thr	Gln	Ser	Lys
			100					105					110		
Val	Ser	Ala	Val	Val	Gly	Pro	Ala	Thr	Ser	Gly	Ala	Thr	Ala	Ala	Ala
			115				120						125		
Val	Ala	Asn	Ala	Thr	Lys	Ala	Gly	Val	Pro	Leu	Ile	Ser	Pro	Ser	Ala
	130					135					140				
Thr	Gln	Asp	Gly	Leu	Thr	Lys	Gly	Gln	Asp	Tyr	Leu	Phe	Ile	Gly	Thr
145				150						155				160	
Phe	Gln	Asp	Ser	Phe	Gln	Gly	Lys	Ile	Ile	Ser	Asn	Tyr	Val	Ser	Glu
			165					170						175	
Lys	Leu	Asn	Ala	Lys	Lys	Val	Val	Leu	Tyr	Thr	Asp	Asn	Ala	Ser	Asp
			180					185					190		
Tyr	Ala	Lys	Gly	Ile	Ala	Lys	Ser	Phe	Arg	Glu	Ser	Tyr	Lys	Gly	Glu

	195		200		205										
Ile	Val	Ala	Asp	Glu	Thr	Phe	Val	Ala	Gly	Asp	Thr	Asp	Phe	Gln	Ala
	210					215					220				
Ala	Leu	Thr	Lys	Met	Lys	Gly	Lys	Asp	Phe	Asp	Ala	Ile	Val	Val	Pro
225					230					235					240
Gly	Tyr	Tyr	Asn	Glu	Ala	Gly	Lys	Ile	Val	Asn	Gln	Ala	Arg	Gly	Met
			245						250					255	
Gly	Ile	Asp	Lys	Pro	Ile	Val	Gly	Gly	Asp	Gly	Phe	Asn	Gly	Glu	Glu
		260					265						270		
Phe	Val	Gln	Gln	Ala	Thr	Ala	Glu	Lys	Ala	Ser	Asn	Ile	Tyr	Phe	Ile
	275					280						285			
Ser	Gly	Phe	Ser	Thr	Thr	Val	Glu	Val	Ser	Ala	Lys	Ala	Lys	Ala	Phe
	290				295				300						
Leu	Asp	Ala	Tyr	Arg	Ala	Lys	Tyr	Asn	Glu	Glu	Pro	Ser	Thr	Phe	Ala
305					310				315						320
Ala	Leu	Ala	Tyr	Asp	Ser	Val	His	Leu	Val	Ala	Asn	Ala	Ala	Lys	Gly
			325					330					335		
Ala	Lys	Asn	Ser	Gly	Glu	Ile	Lys	Asn	Asn	Leu	Ala	Lys	Thr	Lys	Asp
		340					345					350			
Phe	Glu	Gly	Val	Thr	Gly	Gln	Thr	Ser	Phe	Asp	Ala	Asp	His	Asn	Thr
	355				360					365					
Val	Lys	Thr	Ala	Tyr	Met	Met	Thr	Met	Asn	Asn	Gly	Lys	Val	Glu	Ala
	370				375				380						
Ala	Glu	Val	Val	Lys	Pro										
385				390											

(2) INFORMATION FOR SEQ ID NO:3604:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...137

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3604:

Glu	Glu	Lys	Asn	Lys	Met	Val	Met	Thr	Asp	Pro	Ile	Ala	Asp	Phe	Leu
1			5					10					15		
Thr	Arg	Ile	Arg	Asn	Ala	Asn	Gln	Ala	Lys	His	Glu	Val	Leu	Glu	Val
		20					25					30			
Pro	Ala	Ser	Asn	Ile	Lys	Lys	Gly	Ile	Ala	Glu	Ile	Leu	Lys	Arg	Glu
	35					40					45				
Gly	Phe	Val	Lys	Asn	Val	Glu	Ile	Ile	Glu	Asp	Asp	Lys	Gln	Gly	Val
	50				55				60						
Ile	Arg	Val	Phe	Leu	Lys	Tyr	Gly	Pro	Asn	Gly	Glu	Lys	Val	Ile	Thr
65				70				75					80		
Asn	Leu	Lys	Arg	Val	Ser	Lys	Pro	Gly	Leu	Arg	Val	Tyr	Lys	Lys	Arg

				85				90					95				
Glu	Asp	Leu	Pro	Lys	Val	Leu	Asn	Gly	Leu	Gly	Ile	Ala	Ile	Leu	Ser		
			100					105					110				
Thr	Ser	Glu	Gly	Leu	Leu	Thr	Asp	Lys	Glu	Ala	Arg	Gln	Lys	Asn	Val		
		115					120					125					
Gly	Gly	Glu	Val	Ile	Ala	Tyr	Val	Trp									
		130					135										

(2) INFORMATION FOR SEQ ID NO:3605:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3605:

Glu	Arg	Lys	Lys	Met	Ser	Asn	Ile	Ser	Thr	Asp	Leu	Gln	Asp	Val	Glu		
1				5					10					15			
Lys	Ile	Ile	Val	Leu	Asp	Tyr	Gly	Ser	Gln	Tyr	Asn	Gln	Leu	Ile	Ser		
			20					25					30				
Arg	Arg	Ile	Arg	Glu	Ile	Gly	Val	Phe	Ser	Glu	Leu	Lys	Ser	His	Lys		
		35				40						45					
Ile	Ser	Ala	Ala	Glu	Val	Arg	Glu	Val	Asn	Pro	Val	Gly	Ile	Ile	Leu		
	50					55					60						
Ser	Gly	Gly	Pro	Asn	Ser	Val	Tyr	Glu	Asp	Gly	Ser	Phe	Asp	Ile	Asp		
65				70					75					80			
Pro	Glu	Ile	Phe	Glu	Leu	Gly	Ile	Pro	Ile	Leu	Gly	Ile	Cys	Tyr	Gly		
			85					90					95				
Met	Gln	Leu	Leu	Thr	His	Lys	Leu	Gly	Gly	Lys	Val	Val	Pro	Ala	Gly		
		100						105					110				
Asp	Ala	Gly	Asn	Arg	Glu	Tyr	Gly	Gln	Ser	Thr	Leu	Thr	His	Thr	Pro		
		115					120					125					
Ser	Ala	Leu	Phe	Glu	Ser	Thr	Pro	Asp	Glu	Gln	Thr	Val	Leu	Met	Ser		
		130				135					140						
His	Gly	Asp	Ala	Val	Thr	Glu	Ile	Pro	Ala	Asp	Phe	Val	Arg	Thr	Gly		
145					150					155					160		
Thr	Ser	Ala	Asp	Cys	Pro	Tyr	Ala	Ala	Ile	Glu	Asn	Pro	Asp	Lys	His		
			165					170						175			
Ile	Tyr	Gly	Ile	Gln	Phe	His	Pro	Glu	Val	Arg	His	Ser	Val	Tyr	Gly		
		180						185					190				
Asn	Asp	Ile	Leu	Arg	Asn	Phe	Ala	Leu	Asn	Ile	Cys	Lys	Ala	Lys	Gly		
		195					200					205					
Asp	Trp	Ser	Met	Asp	Asn	Phe	Ile	Asp	Met	Gln	Ile	Lys	Lys	Ile	Arg		
	210					215					220						
Glu	Thr	Val	Gly	Asp	Lys	Arg	Val	Leu	Leu	Gly	Leu	Ser	Gly	Gly	Val		

225					230					235					240	
Asp	Ser	Ser	Val	Val	Gly	Val	Leu	Leu	Gln	Lys	Ala	Ile	Gly	Asp	Gln	
				245					250					255		
Leu	Ile	Cys	Ile	Phe	Val	Asn	His	Gly	Leu	Leu	Arg	Lys	Gly	Glu	Ala	
				260					265					270		
Asp	Gln	Val	Met	Asp	Met	Leu	Gly	Gly	Asn	Leu	Gly	Leu	Asn	Ile	Val	
				275					280					285		
Lys	Ala	Asp	Ala	Ala	Lys	Arg	Phe	Pro								
				290					295							

(2) INFORMATION FOR SEQ ID NO:3606:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3606:

Glu	Phe	Glu	Lys	Met	Ile	Asp	Gln	Leu	Ser	Lys	Tyr	Tyr	Ser	Cys	Arg
1				5					10					15	
Ile	Leu	Thr	Glu	Lys	Asp	Ile	Pro	Ser	Ile	Leu	Ser	Leu	Tyr	Glu	Ser
			20					25					30		
Asn	Pro	Leu	Tyr	Phe	Gln	His	Cys	Pro	Pro	Glu	Pro	Asn	Phe	Ala	Thr
		35					40					45			
Val	Lys	Glu	Asp	Met	Leu	Cys	Leu	Pro	Glu	Gly	Lys	Ala	Lys	Ala	Asp
	50					55					60				
Lys	Phe	Phe	Val	Gly	Phe	Trp	Asn	Gly	Ser	Asp	Leu	Val	Ala	Val	Met
65					70					75				80	
Asp	Phe	Val	Tyr	Ala	Tyr	Pro	Asp	Glu	Glu	Thr	Val	Phe	Ile	Gly	Leu
				85					90					95	
Phe	Met	Val	Asp	Gln	Ala	Tyr	Gln	Arg	Lys	Gly	Ile	Gly	Ser	His	Ile
			100					105					110		
Val	Thr	Glu	Ala	Leu	Ala	Tyr	Phe	Ala	Lys	Asn	Phe	Arg	Lys	Ala	Arg
		115						120					125		
Leu	Ala	Tyr	Val	Lys	Gly	Asn	Pro	Gln	Ser	Gln	His	Phe	Trp	Glu	Lys
	130					135					140				
Gln	Gly	Phe	Lys	Ser	Ile	Gly	Cys	Glu	Val	Lys	Gln	Glu	Leu	Tyr	Thr
145					150					155					160
Val	Val	Ile	Val	Glu	Gln	Ser	Leu	Asp	Asp						
				165					170						

(2) INFORMATION FOR SEQ ID NO:3607:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 838 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...838

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3607:

Lys	Leu	Glu	Asn	Phe	Tyr	Lys	Asn	Arg	Tyr	Tyr	Ile	Phe	Glu	Arg	Asn	1	5	10	15
Lys	Asn	Ile	Phe	Glu	Arg	Lys	Val	Leu	Thr	Met	Val	Asn	Thr	Glu	Val	20	25	30	
Ala	Arg	Thr	Thr	Ile	Lys	Thr	Glu	Tyr	Phe	Gly	Ser	Leu	Thr	Glu	Arg	35	40	45	
Met	Asn	Lys	Tyr	Arg	Glu	Asp	Val	Leu	Asn	Lys	Lys	Pro	Tyr	Ile	Asp	50	55	60	
Ala	Glu	Arg	Ala	Val	Leu	Ala	Thr	Arg	Ala	Tyr	Glu	Arg	Tyr	Lys	Glu	65	70	75	80
Gln	Pro	Asn	Val	Leu	Lys	Arg	Ala	Tyr	Met	Leu	Lys	Glu	Ile	Leu	Glu	85	90	95	
Asn	Met	Thr	Ile	Tyr	Ile	Glu	Glu	Glu	Ser	Met	Ile	Ala	Gly	Asn	Gln	100	105	110	
Ala	Ser	Ser	Asn	Lys	Asp	Ala	Pro	Ile	Phe	Pro	Glu	Tyr	Thr	Leu	Glu	115	120	125	
Phe	Val	Leu	Asn	Glu	Leu	Asp	Leu	Phe	Glu	Lys	Arg	Asp	Gly	Asp	Val	130	135	140	
Phe	Tyr	Ile	Thr	Glu	Glu	Thr	Lys	Glu	Gln	Leu	Arg	Ser	Ile	Ala	Pro	145	150	155	160
Phe	Trp	Glu	Asn	Asn	Asn	Leu	Arg	Ala	Arg	Ala	Gly	Ala	Leu	Leu	Pro	165	170	175	
Glu	Glu	Val	Ser	Val	Tyr	Met	Glu	Thr	Gly	Phe	Phe	Gly	Met	Glu	Gly	180	185	190	
Lys	Met	Asn	Ser	Gly	Asp	Ala	His	Leu	Ala	Val	Asn	Tyr	Gln	Lys	Leu	195	200	205	
Leu	Gln	Phe	Gly	Leu	Arg	Gly	Phe	Glu	Glu	Arg	Ala	Arg	Lys	Ala	Lys	210	215	220	
Val	Ala	Leu	Asp	Leu	Thr	Asp	Pro	Ala	Ser	Ile	Asp	Lys	Tyr	His	Phe	225	230	235	240
Tyr	Asp	Ser	Ile	Phe	Ile	Val	Ile	Asp	Ala	Ile	Lys	Val	Tyr	Ala	Lys	245	250	255	
Arg	Phe	Val	Ala	Leu	Ala	Lys	Ser	Leu	Ala	Glu	Asn	Ala	Asn	Pro	Lys	260	265	270	
Arg	Lys	Lys	Glu	Leu	Leu	Glu	Ile	Ala	Asp	Ile	Cys	Ser	Arg	Val	Pro	275	280	285	
Tyr	Glu	Pro	Ala	Thr	Thr	Phe	Ala	Glu	Ala	Ile	Gln	Ser	Val	Trp	Phe	290	295	300	
Ile	Gln	Cys	Ile	Leu	Gln	Ile	Glu	Ser	Asn	Gly	His	Ser	Leu	Ser	Tyr	305	310	315	320
Gly	Arg	Phe	Asp	Gln	Tyr	Met	Tyr	Pro	Tyr	Met	Lys	Ala	Asp	Leu	Glu				

				325				330					335				
Ser	Gly	Lys	Glu	Thr	Glu	Asp	Ser	Ile	Val	Glu	Arg	Leu	Thr	Asn	Leu		
			340					345					350				
Trp	Ile	Lys	Thr	Ile	Thr	Ile	Asn	Lys	Val	Arg	Ser	Gln	Ser	His	Thr		
		355					360					365					
Phe	Ser	Ser	Ala	Gly	Ser	Pro	Leu	Tyr	Gln	Asn	Val	Thr	Ile	Gly	Gly		
	370					375					380						
Gln	Thr	Arg	Asp	Lys	Lys	Asp	Ala	Val	Asn	Pro	Leu	Ser	Tyr	Leu	Val		
385				390						395					400		
Leu	Lys	Ser	Val	Ala	Gln	Thr	His	Leu	Pro	Gln	Pro	Asn	Leu	Thr	Val		
			405					410						415			
Arg	Tyr	His	Ala	Gly	Leu	Asp	Ala	Arg	Phe	Met	Asn	Glu	Cys	Ile	Glu		
		420					425					430					
Val	Met	Lys	Leu	Gly	Phe	Gly	Met	Pro	Ala	Phe	Asn	Asn	Asp	Glu	Ile		
	435					440					445						
Ile	Ile	Pro	Ser	Phe	Ile	Ala	Lys	Gly	Val	Leu	Glu	Asp	Asp	Ala	Tyr		
	450				455					460							
Asp	Tyr	Ser	Ala	Ile	Gly	Cys	Val	Glu	Thr	Ala	Val	Pro	Gly	Lys	Trp		
465				470				475						480			
Gly	Tyr	Arg	Cys	Thr	Gly	Met	Ser	Tyr	Met	Asn	Phe	Pro	Lys	Val	Leu		
		485				490							495				
Leu	Ile	Thr	Met	Asn	Asp	Gly	Ile	Asp	Pro	Ala	Ser	Gly	Lys	Arg	Phe		
	500					505						510					
Ala	Pro	Ser	Phe	Gly	His	Phe	Lys	Asp	Met	Lys	Asn	Phe	Ser	Glu	Leu		
	515					520					525						
Glu	Asn	Ala	Trp	Asp	Lys	Thr	Leu	Arg	Tyr	Leu	Thr	Arg	Met	Ser	Val		
	530			535						540							
Ile	Val	Glu	Asn	Ser	Ile	Asp	Leu	Ser	Leu	Glu	Arg	Glu	Val	Pro	Asp		
545				550					555					560			
Ile	Leu	Cys	Ser	Ala	Leu	Thr	Asp	Asp	Cys	Ile	Gly	Arg	Gly	Lys	His		
		565				570							575				
Leu	Lys	Glu	Gly	Gly	Ala	Val	Tyr	Asp	Tyr	Ile	Ser	Gly	Leu	Gln	Val		
	580					585						590					
Gly	Ile	Ala	Asn	Leu	Ser	Asp	Ser	Leu	Ala	Ala	Ile	Lys	Lys	Leu	Val		
	595				600						605						
Phe	Glu	Glu	Glu	Arg	Ile	Ser	Pro	Ser	Gln	Leu	Trp	His	Ala	Leu	Glu		
	610				615					620							
Thr	Asp	Tyr	Ala	Gly	Glu	Glu	Gly	Lys	Val	Ile	Gln	Glu	Met	Leu	Ile		
625				630					635					640			
His	Asp	Ala	Pro	Lys	Tyr	Gly	Asn	Asp	Asp	Asp	Tyr	Ala	Asp	Lys	Leu		
		645				650						655					
Val	Thr	Ala	Ala	Tyr	Asp	Ile	Tyr	Val	Asp	Glu	Ile	Ala	Lys	Tyr	Pro		
	660					665						670					
Asn	Thr	Arg	Tyr	Gly	Arg	Gly	Pro	Ile	Gly	Gly	Ile	Arg	Tyr	Ser	Gly		
	675					680					685						
Thr	Ser	Ser	Ile	Ser	Ala	Asn	Val	Gly	Gln	Gly	Arg	Gly	Thr	Leu	Ala		
	690				695						700						
Thr	Pro	Asp	Gly	Arg	Asn	Ala	Gly	Thr	Pro	Leu	Ala	Glu	Gly	Cys	Ser		
705				710					715					720			
Pro	Ser	His	Asn	Met	Asp	Gln	His	Gly	Pro	Thr	Ser	Val	Leu	Lys	Ser		
		725				730						735					
Val	Ser	Lys	Leu	Pro	Thr	Asp	Glu	Ile	Val	Gly	Gly	Val	Leu	Leu	Asn		
	740					745						750					
Gln	Lys	Val	Asn	Pro	Gln	Thr	Leu	Ala	Lys	Glu	Glu	Asp	Lys	Leu	Lys		
	755				760						765						
Leu	Ile	Ala	Leu	Leu	Arg	Thr	Phe	Phe	Asn	Arg	Leu	His	Gly	Tyr	His		
	770				775						780						

(2) INFORMATION FOR SEQ ID NO:3608:

- | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Pro | Glu | Lys | Glu | Gly | Ser | Arg | Ile | Glu | Gly | Leu | Tyr | Met | Lys | Ser |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Glu | Leu | Arg | Lys | Gln | Val | Leu | His | Glu | Met | Lys | Ala | Leu | Ser | Gln | Glu |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Gln | Lys | Gln | Ala | Ile | Asp | Gln | Ala | Leu | Thr | Glu | Arg | Ile | Leu | Gln | His |
| | | | 35 | | | | 40 | | | | | 45 | | | |
| Pro | Phe | Tyr | Gln | Glu | Ala | Lys | Val | Ile | Ala | Thr | Tyr | Leu | Ser | Phe | Ser |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| His | Glu | Phe | Gln | Thr | Arg | Glu | Leu | Ile | Glu | Gln | Ala | Leu | Lys | Asp | Gly |
| 65 | | | | | 70 | | | | | 75 | | | | 80 | |
| Lys | Lys | Val | Leu | Ile | Pro | Lys | Thr | Tyr | Pro | Lys | Gly | Arg | Met | Asp | Phe |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Val | Val | Tyr | Asp | Pro | Gln | Gln | Leu | Val | Lys | Thr | Ala | Phe | Ala | Leu | Leu |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Glu | Pro | Gln | Gly | Asp | Leu | Glu | Val | Val | Asp | Val | Ser | Gln | Ile | Asp | Leu |
| | | | 115 | | | | 120 | | | | | 125 | | | |
| Ile | His | Val | Pro | Gly | Leu | Ala | Phe | Thr | Thr | Asp | Gly | Tyr | Arg | Ile | Gly |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Tyr | Gly | Gly | Gly | Tyr | Tyr | Asp | Arg | Tyr | Leu | Glu | His | Phe | Ser | Gly | His |
| 145 | | | | | 150 | | | | | 155 | | | | 160 | |
| Thr | Leu | Ser | Thr | Val | His | Pro | Cys | Gln | Ile | Gln | Asp | Phe | Ile | Pro | Glu |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| Asn | His | Asp | Ile | Pro | Val | Gln | Glu | Val | Leu | Ile | Asp | Glu | Gly | Asn | Leu |
| | | | 180 | | | | | 185 | | | | | 190 | | |

- 2565

(A) LENGTH: 101 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3609:

```
Gln Tyr Glu Asn Cys Cys Phe Leu Val Tyr Pro Met Ile Gly Thr Phe
1          5          10          15
Ala Ala Ala Leu Val Ala Val Leu Ala Ser Phe Ile Val Pro Ile Glu
20          25          30
Ile Thr Leu Asn Ser Ala Asn Thr Glu Ile Ala Pro Pro Asp Gly Ile
35          40          45
Gly Gln Val Leu Ser Asn Leu Leu Lys Leu Val Asp Ser Pro Val
50          55          60
Asn Ala Leu Leu Thr Ala Asn Tyr Ile Gly Ile Leu Ser Trp Ala Val
65          70          75          80
Ile Phe Asp Ile Ala Met Arg Glu Ala Arg Lys Asn Ser Lys Glu Leu
85          90          95
Ala Lys Asn Tyr Arg
100
```

(2) INFORMATION FOR SEQ ID NO:3610:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 763 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...763

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3610:

```
Lys Asn Glu Lys Ile Gly Pro Phe Gly Ala Val Phe Phe Ser Ser Arg
1          5          10          15
Asn Ala Cys Glu Ile Trp Tyr Asn Arg Arg Met Ala Asn Lys Asn Thr
20          25          30
Ser Thr Thr Arg Arg Arg Pro Ser Lys Ala Glu Leu Glu Arg Lys Glu
```

		35				40				45					
Ala	Ile	Gln	Arg	Met	Leu	Ile	Ser	Leu	Gly	Ile	Ala	Ile	Leu	Leu	Ile
50						55				60					
Phe	Ala	Ala	Phe	Lys	Leu	Gly	Ala	Ala	Gly	Ile	Thr	Leu	Tyr	Asn	Leu
65					70					75					80
Ile	Arg	Leu	Leu	Val	Gly	Ser	Leu	Ala	Tyr	Leu	Ala	Ile	Phe	Gly	Leu
				85					90					95	
Leu	Ile	Tyr	Leu	Phe	Phe	Phe	Lys	Trp	Ile	Arg	Lys	Gln	Glu	Gly	Leu
			100					105					110		
Leu	Ser	Gly	Phe	Phe	Thr	Ile	Phe	Ala	Gly	Leu	Leu	Leu	Ile	Phe	Glu
		115					120					125			
Ala	Tyr	Leu	Val	Trp	Lys	Tyr	Gly	Leu	Asp	Lys	Ser	Val	Leu	Lys	Gly
130						135					140				
Thr	Met	Ala	Gln	Val	Val	Thr	Asp	Leu	Thr	Gly	Phe	Arg	Thr	Thr	Ser
145					150					155					160
Phe	Ala	Gly	Gly	Gly	Leu	Ile	Gly	Val	Ala	Leu	Tyr	Ile	Pro	Thr	Ala
				165					170					175	
Phe	Leu	Phe	Ser	Asn	Ile	Gly	Thr	Tyr	Phe	Ile	Gly	Ser	Ile	Leu	Ile
			180					185					190		
Leu	Val	Gly	Ser	Leu	Leu	Val	Ser	Pro	Trp	Ser	Val	Tyr	Asp	Ile	Ala
		195					200					205			
Glu	Phe	Phe	Ser	Arg	Gly	Phe	Ala	Lys	Trp	Trp	Glu	Gly	His	Glu	Arg
210						215					220				
Arg	Lys	Glu	Glu	Arg	Phe	Val	Lys	Gln	Glu	Glu	Lys	Ala	Arg	Gln	Lys
225					230					235					240
Ala	Glu	Lys	Glu	Ala	Arg	Leu	Glu	Gln	Glu	Thr	Glu	Lys	Ala	Leu	
				245					250					255	
Leu	Asp	Leu	Pro	Pro	Ala	Asp	Met	Glu	Thr	Gly	Glu	Ile	Leu	Thr	Glu
			260					265					270		
Glu	Ala	Val	Gln	Asn	Leu	Pro	Pro	Ile	Pro	Glu	Glu	Lys	Trp	Val	Glu
		275					280					285			
Pro	Glu	Ile	Ile	Leu	Pro	Gln	Ala	Glu	Leu	Lys	Phe	Pro	Glu	Gln	Glu
290						295					300				
Asp	Asp	Ser	Asp	Asp	Gln	Asp	Val	Gln	Val	Asp	Phe	Ser	Ala	Lys	Glu
305					310					315					320
Ala	Leu	Glu	Tyr	Lys	Leu	Pro	Ser	Leu	Gln	Leu	Phe	Ala	Pro	Asp	Lys
				325					330					335	
Pro	Lys	Asp	Gln	Ser	Lys	Glu	Lys	Lys	Ile	Val	Arg	Glu	Asn	Ile	Lys
			340					345					350		
Ile	Leu	Glu	Ala	Thr	Phe	Ala	Ser	Phe	Gly	Ile	Lys	Val	Thr	Val	Glu
		355					360					365			
Arg	Ala	Glu	Ile	Gly	Pro	Ser	Val	Thr	Lys	Tyr	Glu	Val	Lys	Pro	Ala
370						375					380				
Val	Gly	Val	Arg	Val	Asn	Arg	Ile	Ser	Asn	Leu	Ser	Asp	Asp	Leu	Ala
385					390					395					400
Leu	Ala	Leu	Ala	Ala	Lys	Asp	Val	Arg	Ile	Glu	Ala	Pro	Ile	Pro	Gly
				405					410					415	
Lys	Ser	Leu	Ile	Gly	Ile	Glu	Val	Pro	Asn	Ser	Asp	Ile	Ala	Thr	Val
			420					425					430		
Ser	Phe	Arg	Glu	Leu	Trp	Glu	Gln	Ser	Gln	Thr	Lys	Ala	Glu	Asn	Phe
		435					440					445			
Leu	Glu	Ile	Pro	Leu	Gly	Lys	Ala	Val	Asn	Gly	Thr	Ala	Arg	Ala	Phe
450						455					460				
Asp	Leu	Ser	Lys	Met	Pro	His	Leu	Leu	Val	Ala	Gly	Ser	Thr	Gly	Ser
465					470					475					480
Gly	Lys	Ser	Val	Ala	Val	Asn	Gly	Ile	Ile	Ala	Ser	Ile	Leu	Met	Lys
				485					490					495	

Ala	Arg	Pro	Asp	Gln	Val	Lys	Phe	Met	Met	Val	Asp	Pro	Lys	Met	Val
			500					505					510		
Glu	Leu	Ser	Val	Tyr	Asn	Asp	Ile	Pro	His	Leu	Leu	Ile	Pro	Val	Val
		515					520					525			
Thr	Asn	Pro	Arg	Lys	Ala	Ser	Lys	Ala	Leu	Gln	Lys	Val	Val	Asp	Glu
	530					535					540				
Met	Glu	Asn	Arg	Tyr	Glu	Leu	Phe	Ala	Lys	Val	Gly	Val	Arg	Asn	Ile
545					550					555					560
Ala	Gly	Phe	Asn	Ala	Lys	Val	Glu	Glu	Phe	Asn	Ser	Gln	Ser	Glu	Tyr
			565						570						575
Lys	Gln	Ile	Pro	Leu	Pro	Phe	Ile	Val	Val	Ile	Val	Asp	Glu	Leu	Ala
			580					585					590		
Asp	Leu	Met	Met	Val	Ala	Ser	Lys	Glu	Val	Glu	Asp	Ala	Ile	Ile	Arg
		595					600					605			
Leu	Gly	Gln	Lys	Ala	Arg	Ala	Ala	Gly	Ile	His	Met	Ile	Leu	Ala	Thr
	610					615					620				
Gln	Arg	Pro	Ser	Val	Asp	Val	Ile	Ser	Gly	Leu	Ile	Lys	Ala	Asn	Val
625					630					635					640
Pro	Ser	Arg	Val	Ala	Phe	Ala	Val	Ser	Ser	Gly	Thr	Asp	Ser	Arg	Thr
			645						650					655	
Ile	Leu	Asp	Glu	Asn	Gly	Ala	Glu	Lys	Leu	Leu	Gly	Arg	Gly	Asp	Met
		660						665					670		
Leu	Phe	Lys	Pro	Ile	Asn	Glu	Asn	His	Pro	Val	Arg	Leu	Gln	Gly	Ser
		675					680					685			
Phe	Ile	Ser	Asp	Asp	Asp	Val	Glu	Arg	Ile	Val	Asn	Phe	Ile	Lys	Thr
	690					695					700				
Gln	Ala	Asp	Ala	Asp	Tyr	Asp	Glu	Ser	Phe	Asp	Pro	Gly	Glu	Val	Ser
705					710					715					720
Glu	Asn	Glu	Gly	Glu	Phe	Ser	Asp	Gly	Asp	Ala	Gly	Gly	Asp	Pro	Leu
			725						730					735	
Phe	Glu	Glu	Ala	Lys	Ser	Leu	Val	Ile	Glu	Ile	Gln	Lys	Ala	Val	Gly
			740					745					750		
Ile	His	Asp	Ser	Ala	Ser	Phe	Val	Ser	Trp	Ile					
		755					760								

(2) INFORMATION FOR SEQ ID NO:3611:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 201 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...201
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3611:

Thr	Ser	Glu	Asn	Gln	Ala	Leu	Ile	Gly	Trp	Lys	Ser	Met	Glu	Ser	Ile
1				5				10					15		

Phe	Val	Lys	Leu	Ala	Gln	Tyr	Pro	Ser	Ile	Glu	Thr	Glu	Arg	Leu	Leu
		20						25					30		
Leu	Arg	Pro	Val	Thr	Leu	Asp	Asp	Ala	Glu	Ala	Met	Phe	Asp	Tyr	Ala
		35					40					45			
Ser	Asp	Lys	Gly	Asn	Thr	Arg	Tyr	Thr	Phe	Pro	Thr	Asn	Gln	Ser	Leu
	50					55					60				
Glu	Glu	Thr	Lys	Asn	Asn	Ile	Ala	Gln	Phe	Tyr	Leu	Ala	Asn	Pro	Leu
65					70					75					80
Gly	Arg	Trp	Gly	Ile	Glu	Leu	Lys	Ser	Asn	Gly	Gln	Phe	Ile	Gly	Thr
			85						90					95	
Ile	Asp	Leu	His	Lys	Ile	Asp	Ser	Val	Leu	Lys	Lys	Ala	Ala	Ile	Gly
		100						105					110		
Tyr	Ile	Ile	Asn	Lys	Lys	Tyr	Trp	Asn	Gln	Gly	Leu	Thr	Thr	Glu	Ala
	115						120					125			
Asn	Arg	Ala	Val	Ile	Glu	Leu	Ala	Phe	Glu	Lys	Ile	Gly	Met	Asn	Lys
	130					135						140			
Leu	Thr	Ala	Leu	His	Asp	Lys	Asp	Asn	Pro	Ala	Ser	Gly	Lys	Val	Met
145					150					155					160
Glu	Lys	Ser	Gly	Met	Arg	Phe	Ser	His	Ala	Glu	Pro	Tyr	Ala	Cys	Met
			165						170					175	
Asp	Gln	His	Glu	Lys	Gly	Arg	Ile	Val	Thr	Arg	Val	His	Tyr	Val	Leu
		180						185					190		
Thr	Lys	Glu	Asp	Tyr	Phe	Ala	Asn	Lys							
		195					200								

(2) INFORMATION FOR SEQ ID NO:3612:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...117

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3612:

Met	Asn	Glu	Lys	Glu	Leu	Leu	Glu	Leu	Val	Val	Lys	Ala	Ala	Asp	Glu
1				5					10					15	
Lys	Arg	Ala	Glu	Asp	Ile	Leu	Ala	Leu	Asp	Val	Gln	Asp	Leu	Thr	Ser
		20						25					30		
Val	Thr	Asp	Tyr	Phe	Val	Ile	Thr	Ser	Ser	Met	Asn	Ser	Arg	Gln	Leu
	35						40					45			
Asp	Ala	Ile	Ala	Ala	Asn	Ile	Arg	Glu	Lys	Val	Ala	Gln	Ala	Gly	Phe
	50					55					60				
Lys	Gly	Ser	His	Val	Glu	Gly	Asp	Ala	Ala	Gly	Gly	Trp	Val	Leu	Leu
65					70					75					80
Asp	Leu	Gly	Ala	Val	Val	Val	His	Ile	Phe	Ser	Glu	Glu	Met	Arg	Ala
			85						90					95	

His Tyr Asn Leu Glu Lys Leu Trp His Glu Ala Asn Ser Val Asp Ile
100 105 110
Ser Glu Ala Leu Ala
115

(2) INFORMATION FOR SEQ ID NO:3613:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 263 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3613:

Met Asp Glu Lys Lys Arg Met Gln Ile Ile Ala Glu Asn Ile Thr His
1 5 10 15
Phe Arg Lys Gln Arg Gly Ile Thr Gln Lys Asp Leu Ala Lys Glu Val
20 25 30
Gly Ile Thr Ala Ser Thr Met Thr Asp Tyr Met Lys Leu Arg Ser Ala
35 40 45
Pro Ser Phe Gly Val Ile Gln Lys Leu Ala Asp Tyr Phe Gly Val Lys
50 55 60
Lys Ser Asp Ile Asp Thr Thr Phe Lys Glu Glu Ser Thr Asn Ser Leu
65 70 75 80
Pro Asp Ala Pro Asp Ser Leu Thr Gln Gln Ile Met Asp Lys Val Val
85 90 95
Gln Leu Thr Pro Pro Asn Gln Lys Ile Val Leu Arg Thr Ser Glu Glu
100 105 110
Leu Leu Glu Ser Gln Asn Glu Glu Glu Thr Lys Ile Asn Glu Val Ser
115 120 125
Glu Val Ile Ser Leu Tyr Gln Val Glu Val Val Ser Glu Thr Ala Ala
130 135 140
Ala Ser Gly Phe Asn Tyr Gly Phe Gly Tyr Asp Asp Thr Asp Arg Glu
145 150 155 160
Thr Ile Glu Val Asp Glu Arg Pro Pro Arg His Asp Ile Ala Thr Lys
165 170 175
Val Ser Gly Asp Ser Met Gln Pro Asp Tyr Gln Asp Gly Asp Ile Leu
180 185 190
Tyr Leu Val Asp Lys Gly Leu Thr Thr Tyr Asn Gly Asp Leu Ala Ile
195 200 205
Ile Ala Tyr Gly Asp Arg Ser Tyr Phe Lys Lys Ile Tyr Thr Glu Asn
210 215 220
Gly Arg Leu Arg Leu Val Ser Leu Asn Asp Lys Tyr Glu Asp Ile Ile
225 230 235 240
Leu Asp Phe Pro Pro Ala Glu Asp Thr His Ile Lys Ile Tyr Ala Val
245 250 255

Val Gly Val Tyr Arg Gly Glu
260

(2) INFORMATION FOR SEQ ID NO:3614:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3614:

Asn	Leu	Glu	Asn	Arg	Tyr	Lys	Gln	Met	Met	Leu	Lys	Pro	Ser	Ile	Asp
1			5					10						15	
Thr	Leu	Leu	Asp	Lys	Val	Pro	Ser	Lys	Tyr	Ser	Leu	Val	Ile	Leu	Glu
			20					25					30		
Ala	Lys	Arg	Ala	His	Glu	Leu	Glu	Ala	Gly	Ala	Pro	Ala	Thr	Gln	Gly
			35					40					45		
Phe	Lys	Ser	Glu	Lys	Ser	Thr	Leu	Arg	Ala	Leu	Glu	Glu	Ile	Glu	Ser
			50					55					60		
Gly	Asn	Val	Thr	Ile	His	Pro	Asp	Pro	Glu	Gly	Lys	Arg	Glu	Ala	Val
65					70					75				80	
Arg	Arg	Arg	Ile	Glu	Glu	Glu	Lys	Arg	Arg	Lys	Glu	Glu	Glu	Glu	Lys
			85					90						95	
Lys	Ile	Lys	Glu	Gln	Ile	Ala	Lys	Glu	Lys	Glu	Asp	Gly	Glu	Lys	Ile
			100					105						110	

(2) INFORMATION FOR SEQ ID NO:3615:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...82

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3615:

```
Ser Leu Glu Lys Gly Asn Asn Met Ile Phe Lys Ala Phe Lys Thr Lys
1      5      10      15
Lys Gln Arg Lys Arg Gln Val Glu Leu Leu Thr Val Phe Phe Asp
20      25      30
Ser Phe Leu Ile Asp Leu Phe Leu His Leu Phe Gly Ile Val Pro Phe
35      40      45
Lys Leu Asp Lys Ile Leu Ile Val Ser Leu Ile Ile Phe Pro Ile Ile
50      55      60
Ser Thr Ser Ile Tyr Ala Tyr Glu Lys Leu Phe Glu Lys Val Phe Asp
65      70      75      80
Lys Asp
```

(2) INFORMATION FOR SEQ ID NO:3616:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...470

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3616:

```
Lys Glu Glu Lys Met Thr Ala Ile Asp Phe Thr Ala Glu Val Glu Lys
1      5      10      15
Arg Lys Glu Asp Leu Leu Ala Asp Leu Phe Ser Leu Leu Glu Ile Asn
20      25      30
Ser Glu Arg Asp Asp Ser Lys Ala Asp Ala Gln His Pro Phe Gly Pro
35      40      45
Gly Pro Val Lys Ala Leu Glu Lys Phe Leu Glu Ile Ala Asp Arg Asp
50      55      60
Gly Tyr Pro Thr Lys Asn Val Asp Asn Tyr Ala Gly His Phe Glu Phe
65      70      75      80
Gly Asp Gly Glu Glu Val Leu Gly Ile Phe Ala His Met Asp Val Val
85      90      95
Pro Ala Gly Ser Gly Trp Asp Thr Asp Pro Tyr Thr Pro Thr Ile Lys
100      105      110
Asp Gly Arg Leu Tyr Ala Arg Gly Ala Ser Asp Asp Lys Gly Pro Thr
115      120      125
Thr Ala Cys Tyr Tyr Gly Leu Lys Ile Ile Lys Glu Leu Gly Leu Pro
130      135      140
Thr Ser Lys Lys Val Arg Phe Ile Val Gly Thr Asp Glu Glu Ser Gly
145      150      155      160
Trp Ala Asp Met Asp Tyr Tyr Phe Glu His Val Gly Leu Ala Lys Pro
165      170      175
```

Asp	Phe	Gly	Phe	Ser	Pro	Asp	Ala	Glu	Phe	Pro	Ile	Ile	Asn	Gly	Glu
			180					185					190		
Lys	Gly	Asn	Ile	Thr	Glu	Tyr	Leu	His	Phe	Ala	Gly	Glu	Asn	Thr	Gly
		195					200					205			
Val	Ala	Arg	Leu	His	Ser	Phe	Thr	Gly	Gly	Leu	Arg	Glu	Asn	Met	Val
	210					215					220				
Pro	Glu	Ser	Ala	Thr	Ala	Val	Val	Ser	Gly	Asp	Leu	Ala	Asp	Leu	Gln
225					230					235					240
Ala	Lys	Leu	Asp	Ala	Phe	Val	Ala	Glu	His	Lys	Leu	Arg	Gly	Glu	Leu
			245						250					255	
Gln	Glu	Glu	Ala	Gly	Lys	Tyr	Lys	Val	Thr	Ile	Ile	Gly	Lys	Ser	Ala
			260					265					270		
His	Gly	Ala	Met	Pro	Ala	Ser	Gly	Val	Asn	Gly	Ala	Thr	Tyr	Leu	Ala
	275						280					285			
Leu	Phe	Leu	Ser	Gln	Phe	Gly	Phe	Ala	Gly	Pro	Ala	Lys	Asp	Tyr	Leu
	290					295					300				
Asp	Ile	Ala	Gly	Lys	Ile	Leu	Leu	Asn	Asp	His	Glu	Gly	Glu	Asn	Leu
305					310					315					320
Lys	Ile	Ala	His	Val	Asp	Glu	Lys	Met	Gly	Ala	Leu	Ser	Met	Asn	Ala
			325						330					335	
Gly	Val	Phe	His	Phe	Asp	Glu	Thr	Ser	Ala	Asp	Asn	Thr	Ile	Ala	Leu
		340						345					350		
Asn	Ile	Arg	Tyr	Pro	Lys	Gly	Thr	Ser	Pro	Glu	Gln	Ile	Lys	Ser	Ile
	355					360					365				
Leu	Glu	Asn	Leu	Pro	Val	Val	Ser	Val	Ser	Leu	Ser	Glu	His	Gly	His
	370				375					380					
Thr	Pro	His	Tyr	Val	Pro	Met	Glu	Asp	Pro	Leu	Val	Gln	Thr	Leu	Leu
385					390					395					400
Asn	Ile	Tyr	Glu	Lys	Gln	Thr	Gly	Phe	Lys	Gly	His	Glu	Gln	Val	Ile
				405				410						415	
Gly	Gly	Gly	Thr	Phe	Gly	Arg	Leu	Leu	Glu	Arg	Gly	Val	Ala	Tyr	Gly
			420				425						430		
Ala	Met	Phe	Pro	Asp	Ser	Ile	Asp	Thr	Met	His	Gln	Ala	Asn	Glu	Phe
	435						440					445			
Ile	Ala	Leu	Asp	Asp	Leu	Phe	Arg	Ala	Ala	Ala	Ile	Tyr	Ala	Glu	Ala
	450					455					460				
Ile	Tyr	Glu	Leu	Ile	Lys										
465					470										

(2) INFORMATION FOR SEQ ID NO:3617:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 135 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3617:

Glu	Glu	Glu	Asn	Met	Tyr	Asn	Lys	Val	Ile	Met	Ile	Gly	Arg	Leu	Thr	
1				5					10					15		
Ser	Thr	Pro	Glu	Leu	His	Lys	Thr	Asn	Asp	Lys	Ser	Val	Ala	Arg		
			20					25				30				
Ala	Thr	Ile	Ala	Val	Asn	Arg	Arg	Tyr	Lys	Asp	Gln	Asn	Gly	Glu	Arg	
			35				40					45				
Glu	Ala	Asp	Phe	Val	Asn	Met	Val	Leu	Trp	Gly	Arg	Leu	Ala	Glu	Thr	
	50					55					60					
Leu	Ala	Thr	Tyr	Ala	Thr	Lys	Gly	Ser	Leu	Ile	Ser	Val	Asp	Gly	Glu	
65					70					75					80	
Leu	Arg	Thr	Arg	Arg	Phe	Glu	Lys	Asn	Gly	Gln	Met	Asn	Tyr	Val	Thr	
			85					90					95			
Glu	Val	Leu	Val	Thr	Gly	Phe	Gln	Leu	Leu	Glu	Ser	Arg	Ala	Gln	Arg	
			100					105					110			
Ala	Met	Arg	Glu	Asn	Asn	Ala	Gly	Gln	Asp	Leu	Ala	Asp	Leu	Val	Leu	
		115				120						125				
Glu	Glu	Glu	Glu	Leu	Pro	Phe										
	130					135										

(2) INFORMATION FOR SEQ ID NO:3618:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 112 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3618:

Leu	Arg	Glu	Asn	Arg	Arg	Thr	Asn	Arg	Met	Glu	Leu	Lys	Asp	Phe	Thr	
1				5					10					15		
Glu	Lys	Glu	Gln	Glu	Met	Ile	Lys	Lys	Arg	Leu	Thr	Met	Ser	Asn	Ile	
			20					25				30				
Ser	Asp	Lys	Glu	Thr	Thr	Glu	Lys	Ile	Leu	Ala	Leu	Val	Pro	Gln	Asp	
		35					40					45				
Leu	Ile	Lys	Arg	Ile	Pro	Phe	Phe	Val	Arg	Lys	His	Ala	Thr	Thr	Arg	
	50					55					60					
Thr	Ile	Lys	Arg	Ile	Ser	Ile	Glu	His	Pro	Glu	Leu	Tyr	Ala	Val	Ala	
65				70						75					80	
Gln	Thr	Ser	Gly	Glu	Ile	Pro	Glu	Lys	Glu	Cys	Glu	Glu	Leu	Arg	Gln	
			85					90					95			
Ile	Ile	Thr	Thr	Ile	Phe	Glu	Gln	Lys	Met	Asn	Lys	His	Ser	Ile	Lys	
			100					105					110			

(2) INFORMATION FOR SEQ ID NO:3619:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 418 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...418
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3619:

```

Lys Arg Glu Asn Arg Met Val Leu Pro Asn Phe Lys Glu Asn Leu Glu
1      5      10      15
Lys Tyr Ala Lys Leu Leu Val Ala Asn Gly Ile Asn Val Gln Pro Gly
20      25      30
His Thr Leu Ala Leu Ser Ile Asp Val Glu Gln Arg Glu Leu Ala His
35      40      45
Leu Ile Val Lys Glu Ala Tyr Ala Leu Gly Ala His Glu Val Ile Val
50      55      60
Gln Trp Thr Asp Asp Val Ile Asn Arg Glu Lys Phe Leu His Ala Pro
65      70      75      80
Met Glu Arg Leu Asp Asn Val Pro Glu Tyr Lys Ile Ala Glu Met Asn
85      90      95
Tyr Leu Leu Glu Asn Lys Ala Ser Arg Leu Gly Val Arg Ser Ser Asp
100     105     110
Pro Gly Ala Leu Asn Gly Val Asp Ala Asp Lys Leu Ser Ala Ser Ala
115     120     125
Lys Ala Met Gly Leu Ala Met Lys Pro Met Arg Ile Ala Thr Gln Ser
130     135     140
Asn Lys Val Ser Trp Thr Val Ala Ala Ala Gly Leu Glu Trp Ala
145     150     155     160
Lys Lys Val Phe Pro Asn Ala Ala Ser Asp Glu Glu Ala Val Asp Phe
165     170     175
Leu Trp Asp Gln Ile Phe Lys Thr Cys Arg Val Tyr Glu Ala Asp Pro
180     185     190
Val Lys Ala Trp Glu Glu His Ala Ala Ile Leu Lys Ser Lys Ala Asp
195     200     205
Met Leu Asn Lys Glu Gln Phe Ser Ala Leu His Tyr Thr Ala Pro Gly
210     215     220
Thr Asp Leu Thr Leu Gly Leu Pro Lys Asn His Val Trp Glu Ser Ala
225     230     235     240
Gly Ala Val Asn Ala Gln Gly Glu Glu Phe Leu Pro Asn Met Pro Thr
245     250     255
Glu Glu Val Phe Thr Ala Pro Asp Phe Arg Arg Ala Asp Gly Tyr Val
260     265     270
Thr Ser Thr Lys Pro Leu Ser Tyr Asn Gly Asn Ile Ile Glu Gly Ile
275     280     285
Lys Val Thr Phe Lys Asp Gly Gln Ile Val Asp Ile Thr Ala Glu Lys
290     295     300

```

Gly	Asp	Gln	Val	Met	Lys	Asp	Leu	Val	Phe	Glu	Asn	Ala	Gly	Ala	Arg
305					310					315					320
Ala	Leu	Gly	Glu	Cys	Ala	Leu	Val	Pro	Asp	Pro	Ser	Pro	Ile	Ser	Gln
				325					330					335	
Ser	Gly	Ile	Thr	Phe	Phe	Asn	Thr	Leu	Phe	Asp	Glu	Asn	Ala	Ser	Asn
			340					345					350		
His	Leu	Ala	Ile	Gly	Ala	Ala	Tyr	Ala	Thr	Ser	Val	Val	Asp	Gly	Ala
		355					360					365			
Glu	Met	Ser	Glu	Glu	Glu	Leu	Glu	Ala	Ala	Gly	Leu	Asn	Arg	Ser	Asp
	370					375					380				
Val	His	Val	Asp	Phe	Met	Ile	Gly	Ser	Asn	Gln	Met	Asp	Ile	Asp	Gly
385					390					395					400
Ile	Arg	Glu	Asp	Gly	Thr	Arg	Val	Pro	Leu	Phe	Arg	Asn	Gly	Asn	Trp
				405					410					415	
Ala	Asn														

(2) INFORMATION FOR SEQ ID NO:3620:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...228

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3620:

Asp	Gly	Glu	Lys	Lys	Ser	Ser	Arg	Val	Ile	Glu	Arg	Gly	His	Leu	Met
1			5					10						15	
Ile	Glu	Leu	Lys	Asn	Ile	Thr	Lys	Thr	Ile	Gly	Gly	Lys	Val	Ile	Leu
		20					25					30			
Asp	Asn	Leu	Ser	Leu	Arg	Ile	Asp	Gln	Gly	Asp	Leu	Val	Ala	Ile	Val
		35				40					45				
Gly	Lys	Ser	Gly	Ser	Gly	Lys	Ser	Thr	Leu	Leu	Asn	Leu	Leu	Gly	Leu
	50					55				60					
Ile	Asp	Gly	Asp	Tyr	Ser	Gly	Arg	Tyr	Glu	Ile	Phe	Gly	Gln	Thr	Asn
65				70				75						80	
Leu	Ala	Val	Asn	Ser	Ala	Lys	Ser	Gln	Thr	Ile	Ile	Arg	Glu	His	Ile
			85				90					95			
Ser	Tyr	Leu	Phe	Gln	Asn	Phe	Ala	Leu	Ile	Asp	Asp	Glu	Thr	Val	Glu
		100					105					110			
Tyr	Asn	Leu	Met	Leu	Ala	Leu	Lys	Tyr	Val	Lys	Leu	Pro	Lys	Lys	Asp
	115					120					125				
Lys	Leu	Lys	Lys	Val	Glu	Glu	Ile	Leu	Glu	Arg	Val	Gly	Leu	Ser	Ala
130					135				140						
Thr	Leu	His	Gln	Arg	Val	Ser	Glu	Leu	Ser	Gly	Gly	Glu	Gln	Gln	Arg

145		150		155		160
Ile	Ala	Val	Ala	Arg	Ala	Ile
			165			170
Asp	Glu	Pro	Thr	Gly	Ser	Leu
			180			185
Lys	Phe	Leu	Glu	Met	Asn	Arg
			195			200
Thr	His	Asp	Ala	Tyr	Val	Ala
			210			215
Gly	Glu	Gly	Lys			
225						

(2) INFORMATION FOR SEQ ID NO:3621:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 612 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...612

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3621:

Gln	Gly	Glu	Lys	His	Met	Ser	Lys	Ile	Ile	Gly	Ile	Asp	Leu	Gly	Thr
1				5				10						15	
Thr	Asn	Ser	Ala	Val	Ala	Val	Leu	Glu	Gly	Thr	Glu	Ser	Lys	Ile	Ile
			20					25					30		
Ala	Asn	Pro	Glu	Gly	Asn	Arg	Thr	Thr	Pro	Ser	Val	Val	Ser	Phe	Lys
			35				40					45			
Asn	Gly	Glu	Ile	Ile	Val	Gly	Asp	Ala	Ala	Lys	Arg	Gln	Ala	Val	Thr
			50			55					60				
Asn	Pro	Asp	Thr	Val	Ile	Ser	Ile	Lys	Ser	Lys	Met	Gly	Thr	Ser	Glu
65				70						75				80	
Lys	Val	Ser	Ala	Asn	Gly	Lys	Glu	Tyr	Thr	Pro	Gln	Glu	Ile	Ser	Ala
				85				90						95	
Met	Ile	Leu	Gln	Tyr	Leu	Lys	Gly	Tyr	Ala	Glu	Asp	Tyr	Leu	Gly	Glu
			100					105					110		
Lys	Val	Thr	Lys	Ala	Val	Ile	Thr	Val	Pro	Ala	Tyr	Phe	Asn	Asp	Ala
			115				120					125			
Gln	Arg	Gln	Ala	Thr	Lys	Asp	Ala	Gly	Lys	Ile	Ala	Gly	Leu	Glu	Val
			130			135					140				
Glu	Arg	Ile	Val	Asn	Glu	Pro	Thr	Ala	Ala	Ala	Leu	Ala	Tyr	Gly	Leu
145				150						155				160	
Asp	Lys	Thr	Asp	Lys	Glu	Glu	Lys	Ile	Leu	Val	Phe	Asp	Leu	Gly	Gly
			165					170						175	
Gly	Thr	Phe	Asp	Val	Ser	Ile	Leu	Glu	Leu	Gly	Asp	Gly	Val	Phe	Asp
			180					185					190		
Val	Leu	Ser	Thr	Ala	Gly	Asp	Asn	Lys	Leu	Gly	Gly	Asp	Asp	Phe	Asp

	195					200				205					
Gln	Lys	Ile	Ile	Asp	His	Leu	Val	Ala	Glu	Phe	Lys	Lys	Glu	Asn	Gly
	210					215					220				
Ile	Asp	Leu	Ser	Thr	Asp	Lys	Met	Ala	Met	Gln	Arg	Leu	Lys	Asp	Ala
225					230					235					240
Ala	Glu	Lys	Ala	Lys	Lys	Asp	Leu	Ser	Gly	Val	Thr	Ser	Thr	Gln	Ile
				245					250					255	
Ser	Leu	Pro	Phe	Ile	Thr	Ala	Gly	Glu	Ala	Gly	Pro	Leu	His	Leu	Glu
			260					265					270		
Met	Thr	Leu	Thr	Arg	Ala	Lys	Phe	Asp	Asp	Leu	Thr	Arg	Asp	Leu	Val
			275				280					285			
Glu	Arg	Thr	Lys	Val	Pro	Val	Arg	Gln	Ala	Leu	Ser	Asp	Ala	Gly	Leu
	290					295					300				
Ser	Leu	Ser	Glu	Ile	Asp	Glu	Val	Ile	Leu	Val	Gly	Gly	Ser	Thr	Arg
305					310					315					320
Ile	Pro	Ala	Val	Val	Glu	Ala	Val	Lys	Ala	Glu	Thr	Gly	Lys	Glu	Pro
				325					330					335	
Asn	Lys	Ser	Val	Asn	Pro	Asp	Glu	Val	Val	Ala	Met	Gly	Ala	Ala	Ile
			340				345					350			
Gln	Gly	Gly	Val	Ile	Thr	Gly	Asp	Val	Lys	Asp	Val	Val	Leu	Leu	Asp
	355					360					365				
Val	Thr	Pro	Leu	Ser	Leu	Gly	Ile	Glu	Thr	Met	Gly	Gly	Val	Phe	Thr
	370					375				380					
Lys	Leu	Ile	Asp	Arg	Asn	Thr	Thr	Ile	Pro	Thr	Ser	Lys	Ser	Gln	Val
385					390					395					400
Phe	Ser	Thr	Ala	Ala	Asp	Asn	Gln	Pro	Ala	Val	Asp	Ile	His	Val	Leu
				405					410					415	
Gln	Gly	Glu	Arg	Pro	Met	Ala	Ala	Asp	Asn	Lys	Thr	Leu	Gly	Arg	Phe
			420					425				430			
Gln	Leu	Thr	Asp	Ile	Pro	Ala	Ala	Pro	Arg	Gly	Ile	Pro	Gln	Ile	Glu
	435					440					445				
Val	Thr	Phe	Asp	Ile	Asp	Lys	Asn	Gly	Ile	Val	Ser	Val	Lys	Ala	Lys
	450					455				460					
Asp	Leu	Gly	Thr	Gln	Lys	Glu	Gln	Thr	Ile	Val	Ile	Gln	Ser	Asn	Ser
465					470					475					480
Gly	Leu	Thr	Asp	Glu	Glu	Ile	Asp	Arg	Met	Met	Lys	Asp	Ala	Glu	Ala
				485					490					495	
Asn	Ala	Glu	Ser	Asp	Lys	Lys	Arg	Lys	Glu	Glu	Val	Asp	Leu	Arg	Asn
			500					505				510			
Glu	Val	Asp	Gln	Ala	Ile	Phe	Ala	Thr	Glu	Lys	Thr	Ile	Lys	Glu	Thr
	515						520					525			
Glu	Gly	Lys	Gly	Phe	Asp	Ala	Glu	Arg	Asp	Ala	Ala	Gln	Ala	Ala	Leu
	530					535				540					
Asp	Asp	Leu	Lys	Lys	Ala	Gln	Glu	Asp	Asn	Asn	Leu	Asp	Asp	Met	Lys
545					550					555					560
Ala	Lys	Leu	Glu	Ala	Leu	Asn	Glu	Lys	Ala	Gln	Gly	Leu	Ala	Val	Lys
				565					570					575	
Leu	Tyr	Glu	Gln	Ala	Ala	Ala	Ala	Gln	Gln	Ala	Gln	Glu	Gly	Ala	Glu
			580					585				590			
Gly	Ala	Gln	Ala	Thr	Gly	Asn	Ala	Gly	Asp	Asp	Val	Val	Asp	Gly	Glu
	595					600						605			
Phe	Thr	Glu	Lys												
	610														

(2) INFORMATION FOR SEQ ID NO:3622:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 195 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...195

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3622:

Lys	Gly	Glu	Lys	Phe	Met	Asn	Lys	Leu	Met	Lys	Phe	Ile	Ser	Val	Phe	1	5	10	15
Leu	Thr	Ser	Ile	Val	Leu	Ile	Val	Ser	Ala	Ile	Pro	Ser	Val	Ser	Ala	20	25	30	
Val	Tyr	Ala	Ser	Glu	Gln	Val	Ser	Gln	Ile	Glu	Thr	Asn	Met	Glu	Leu	35	40	45	
Gln	Pro	Val	Thr	Ser	Leu	Thr	Glu	Glu	Gln	Ile	Asn	Thr	Leu	Ala	Asn	50	55	60	
Glu	Ile	Gln	Ser	Phe	His	Pro	Asp	Val	Ser	Gln	Gln	Trp	Ile	Lys	Glu	65	70	75	80
Val	Ile	Asn	Arg	Gln	Leu	Gln	Gly	Asp	Tyr	Thr	Ile	Pro	Pro	Thr	Tyr	85	90	95	
Ser	Pro	Phe	Arg	Ala	Ala	Trp	Gln	Gly	Ile	Thr	Val	Asn	Gln	Met	Gly	100	105	110	
Ala	Leu	Leu	Asp	Thr	Ala	Ile	Ala	Leu	Ala	Leu	Gly	Gly	Thr	Thr	Ala	115	120	125	
Gly	Leu	Ala	Asn	Leu	Ile	Lys	Val	Lys	Gly	Lys	His	Ala	Ala	Lys	Ser	130	135	140	
Ala	Ile	Arg	Ser	Ala	Ile	Ser	Arg	Tyr	Leu	Gly	Ser	Trp	Phe	Val	Asn	145	150	155	160
Asp	Val	Ala	Leu	Glu	Phe	Ala	Met	Asn	Leu	Leu	Ser	Pro	Gly	Thr	Tyr	165	170	175	
Leu	Ala	Gln	Leu	Trp	Asp	Lys	Asn	Asp	Ala	Ile	Pro	Asn	Asn	Arg	Arg	180	185	190	
Ile	Asn	Phe														195			

(2) INFORMATION FOR SEQ ID NO:3623:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 87 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...87

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3623:

```
Ser Leu Glu Lys Arg Asn Gly Asn Lys Gln Glu Asn Glu Val Ser Arg
1      5      10      15
Met Asn Leu Leu Ser Arg Ile Lys Asn Tyr Phe Ser Glu Glu Val Lys
      20      25      30
Glu Thr Asn Leu Asp Trp Lys Glu Val Ala Leu Asp Leu Asn Gln Ser
      35      40      45
Leu Ile Glu Thr Gln Glu Lys Leu Gln Glu Ala Asn Gln Glu Ile Ala
      50      55      60
Asp Leu Lys Lys Ile Val Ala Ile Tyr Lys Glu Lys Glu Lys Glu Lys
65      70      75      80
Arg Trp Asn Ile Phe Thr Trp
      85
```

(2) INFORMATION FOR SEQ ID NO:3624:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 101 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3624:

```
Glu Met Glu Lys Leu Asn Ala Leu Arg Lys Gln Lys Ile Arg Ala Val
1      5      10      15
Ile Leu Leu Glu Ala Val Val Ala Leu Ala Ile Phe Ala Ser Ile Ala
      20      25      30
Thr Leu Leu Leu Gly Gln Ile Gln Lys Asn Arg Gln Glu Glu Ala Lys
      35      40      45
Ile Leu Gln Lys Glu Glu Val Leu Arg Val Ala Lys Met Ala Leu Gln
      50      55      60
Thr Gly Gln Asn Gln Val Ser Ile Asn Gly Val Glu Ile Gln Val Phe
65      70      75      80
Ser Ser Glu Lys Gly Leu Glu Val Tyr His Gly Ser Glu Gln Leu Leu
      85      90      95
Ala Ile Lys Glu Pro
      100
```

(2) INFORMATION FOR SEQ ID NO:3625:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 118 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...118
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3625:

```

Met Lys Glu Lys Glu Phe Arg Arg Asn Met Ala Val Phe Pro Ile Gly
1      5      10      15
Ser Val Met Lys Leu Thr Asp Leu Ser Ala Arg Gln Ile Arg Tyr Tyr
      20      25      30
Glu Asp Gln Glu Leu Ile Lys Pro Asp Arg Asn Glu Gly Asn Arg Arg
      35      40      45
Met Tyr Ser Leu Asn Asp Met Asp Arg Leu Leu Glu Ile Lys Asp Tyr
      50      55      60
Ile Ser Glu Gly Tyr Asn Ile Ala Ala Ile Lys Lys Lys Tyr Ala Glu
65      70      75      80
Arg Glu Ala Lys Ser Lys Lys Ala Val Ser Gln Thr Glu Val Arg Arg
      85      90      95
Ala Leu His Asn Glu Leu Leu Gln Gln Gly Arg Phe Ala Ser Val Gln
      100      105      110
Ser Pro Phe Gly Arg Gly
      115

```

(2) INFORMATION FOR SEQ ID NO:3626:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 742 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...742
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3626:

```

Lys Glu Glu Asn Lys Leu Lys Ile Phe Lys Gly Glu Phe Tyr Arg Ile
1      5      10      15

```


450		455		460	
Met	Lys	Lys	Tyr	Leu	Arg
465		470		475	
Thr	Met	Asn	Val	Lys	Thr
		485		490	
Ile	Tyr	Tyr	Phe	Tyr	Pro
		500		505	
Gln	Tyr	Phe	Gly	Thr	Glu
		515		520	
Met	Asp	Leu	Thr	Phe	Gln
		530		535	
Gly	Glu	Trp	Tyr	Asp	Phe
545				550	
Lys	Leu	Ser	Val	Tyr	Arg
				565	
Ser	Gly	Ala	Ile	Ile	Pro
				580	
Asp	Leu	Pro	Glu	Val	Val
				595	
Ser	Phe	Glu	Met	Leu	Glu
				610	
Leu	Ser	Ile	Asp	Trp	Glu
625				630	
Asp	Ser	Ser	Ile	Val	Pro
				645	
Gly	Thr	Asn	Val	Ser	Ile
				660	
Lys	Phe	Glu	Trp	Lys	Asp
				675	
Phe	Arg	Leu	Leu	Lys	Thr
				690	
Leu	Leu	Asn	Gln	Phe	Ile
705				710	
Ile	Leu	His	His	Gln	Asp
				725	
Ile	Phe	Thr	Ser	Gln	Asn
				740	

(2) INFORMATION FOR SEQ ID NO:3627:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...94

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3627:

```

Leu Trp Glu Asn Ser Tyr Lys Glu Ile Val Gly Glu Ile Asp Asp Glu
1          5          10          15
Thr Asp Lys Ala Ala Ile Asp Val His Gln Ile Gly Glu Asp Thr Tyr
          20          25          30
Ile Val Gln Arg Thr Met Thr Leu Asn Asp Phe Asn Asn Tyr Phe Asp
          35          40          45
Val Glu Leu Xaa Ser Asp Asp Val Asp Thr Ile Ala Gly Tyr Tyr Leu
          50          55          60
Thr Gly Val Gly Thr Ile Pro Thr Thr Glu Lys Leu Ser Tyr Glu Leu
65          70          75          80
Val Ser Gln Asn Lys Gln Phe Ile Leu Thr Asn Asp Lys Val
          85          90

```

(2) INFORMATION FOR SEQ ID NO:3628:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 83 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...83
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3628:

```

Lys Gln Pro Leu Tyr Asn Thr Phe Leu Gly Glu Lys Leu Thr Gly Phe
1          5          10          15
Gly Phe Ile Pro Asp Gly Leu Ser Val Lys Arg Thr Arg Asn Val Phe
          20          25          30
Thr Val Asp Thr Asn Leu Asn Leu Arg Val Phe Arg Ser Asp Phe Pro
          35          40          45
Asn Tyr Trp Cys Leu Ile Gly Ala Leu Ser Ser Ile Trp Trp Cys Glu
          50          55          60
Gly Asp Ile Ser Phe Phe Leu Arg Pro Ile Gly Val Ile Phe Ile Phe
65          70          75          80
Phe Leu Pro

```

(2) INFORMATION FOR SEQ ID NO:3629:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 76 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...76

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3629:

Met	Val	Arg	Asn	Lys	Ile	Gly	Asp	Leu	Thr	Asn	Thr	Leu	Phe	Ala	Gln
1				5					10					15	
Leu	Glu	Thr	Leu	Asp	Asp	Arg	Asp	Leu	Thr	Ala	Asp	Glu	Leu	Lys	Val
			20					25					30		
Glu	Leu	Gln	Arg	Ser	Lys	Gln	Met	Val	Ala	Ile	Ser	Gly	Gln	Ile	Leu
		35				40						45			
Gln	Ala	Gly	Gln	Leu	Ala	Leu	Asp	Ala	Glu	Lys	Phe	Lys	Asp	Lys	Val
	50					55					60				
Gly	Glu	Val	Asn	Ala	Pro	Ile	Ala	Leu	Leu	Glu	Gly				
65					70					75					

(2) INFORMATION FOR SEQ ID NO:3630:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 480 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...480

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3630:

Ile	Ile	Arg	Asn	Glu	Glu	Arg	Lys	Asp	Thr	Met	Ala	Glu	Glu	Arg	Val
1				5					10					15	
Glu	Pro	Lys	Pro	Ile	Asp	Leu	Gly	Glu	Tyr	Lys	Phe	Gly	Phe	His	Asp
			20					25					30		
Asp	Val	Glu	Pro	Val	Leu	Ser	Thr	Gly	Lys	Gly	Leu	Asn	Glu	Gly	Val
		35				40						45			
Ile	Arg	Glu	Leu	Ser	Ala	Ala	Lys	Gly	Glu	Pro	Glu	Trp	Met	Leu	Glu
	50					55					60				
Phe	Arg	Leu	Lys	Ser	Tyr	Glu	Thr	Phe	Lys	Lys	Met	Pro	Met	Gln	Thr
65					70				75					80	
Trp	Gly	Ala	Asp	Leu	Ser	Glu	Ile	Asp	Phe	Asp	Asp	Leu	Ile	Tyr	Tyr
			85					90						95	
Gln	Lys	Pro	Ser	Asp	Lys	Pro	Ala	Arg	Ser	Trp	Asp	Asp	Val	Pro	Glu
		100					105						110		
Lys	Ile	Lys	Glu	Thr	Phe	Glu	Arg	Ile	Gly	Ile	Pro	Glu	Ala	Glu	Arg
		115					120						125		

Ala	Tyr	Leu	Ala	Gly	Ala	Ser	Ala	Gln	Tyr	Glu	Ser	Glu	Val	Val	Tyr	130	135	140
His	Asn	Met	Lys	Glu	Glu	Phe	Gln	Lys	Leu	Gly	Ile	Ile	Phe	Thr	Asp	145	150	155
Thr	Asp	Ser	Ala	Leu	Lys	Glu	Tyr	Pro	Asp	Leu	Phe	Lys	Gln	Tyr	Phe	165	170	175
Ala	Lys	Leu	Val	Pro	Pro	Thr	Asp	Asn	Lys	Leu	Ala	Ala	Leu	Asn	Ser	180	185	190
Ala	Val	Trp	Ser	Gly	Gly	Thr	Phe	Ile	Tyr	Val	Pro	Lys	Gly	Val	Lys	195	200	205
Val	Asp	Ile	Pro	Leu	Gln	Thr	Tyr	Phe	Arg	Ile	Asn	Asn	Glu	Asn	Ile	210	215	220
Gly	Gln	Phe	Glu	Arg	Thr	Leu	Ile	Ile	Val	Asp	Glu	Gly	Ala	Ser	Val	225	230	235
His	Tyr	Val	Glu	Gly	Cys	Thr	Ala	Pro	Thr	Tyr	Ser	Ser	Asn	Ser	Leu	245	250	255
His	Ala	Ala	Ile	Val	Glu	Ile	Phe	Ala	Leu	Asp	Gly	Ala	Tyr	Met	Arg	260	265	270
Tyr	Thr	Thr	Ile	Gln	Asn	Trp	Ser	Asp	Asn	Val	Tyr	Asn	Leu	Val	Thr	275	280	285
Lys	Arg	Ala	Lys	Ala	Gln	Lys	Asp	Ala	Thr	Val	Glu	Trp	Ile	Asp	Gly	290	295	300
Asn	Leu	Gly	Ala	Lys	Thr	Thr	Met	Lys	Tyr	Pro	Ser	Val	Tyr	Leu	Asp	305	310	315
Gly	Glu	Gly	Ala	Arg	Gly	Thr	Met	Leu	Ser	Ile	Ala	Phe	Ala	Asn	Ala	325	330	335
Gly	Gln	His	Gln	Asp	Thr	Gly	Ala	Lys	Met	Ile	His	Asn	Ala	Pro	His	340	345	350
Thr	Ser	Ser	Ser	Ile	Val	Ser	Lys	Ser	Ile	Ala	Lys	Gly	Gly	Gly	Lys	355	360	365
Val	Asp	Tyr	Arg	Gly	Gln	Val	Thr	Phe	Asn	Lys	Asn	Ser	Lys	Lys	Ser	370	375	380
Val	Ser	His	Ile	Glu	Cys	Asp	Thr	Ile	Ile	Met	Asp	Asp	Leu	Ser	Ala	385	390	395
Ser	Asp	Thr	Ile	Pro	Phe	Asn	Glu	Ile	His	Asn	Ser	Gln	Val	Ala	Leu	405	410	415
Glu	His	Glu	Ala	Lys	Val	Ser	Lys	Ile	Ser	Glu	Glu	Gln	Leu	Tyr	Tyr	420	425	430
Leu	Met	Ser	Arg	Gly	Leu	Ser	Glu	Ser	Glu	Ala	Thr	Glu	Met	Ile	Val	435	440	445
Met	Gly	Phe	Val	Glu	Pro	Phe	Thr	Lys	Glu	Leu	Pro	Met	Glu	Tyr	Ala	450	455	460
Val	Glu	Leu	Asn	Arg	Leu	Ile	Ser	Tyr	Glu	Met	Glu	Gly	Ser	Val	Gly	465	470	475
																		480

(2) INFORMATION FOR SEQ ID NO:3631:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3631:

Leu	Ile	Arg	Lys	Tyr	Arg	Met	Asp	Ile	Gln	Phe	Leu	Gly	Thr	Gly	Ala	
1				5					10					15		
Gly	Gln	Pro	Ser	Lys	Ala	Arg	Asn	Val	Ser	Ser	Leu	Ala	Leu	Lys	Leu	
			20					25					30			
Leu	Asp	Glu	Ile	Asn	Glu	Val	Trp	Leu	Phe	Asp	Cys	Gly	Glu	Gly	Thr	
		35					40					45				
Gln	Asn	Arg	Ile	Leu	Glu	Thr	Thr	Ile	Arg	Pro	Arg	Lys	Val	Ser	Lys	
		50					55				60					
Ile	Phe	Ile	Thr	His	Leu	His	Gly	Asp	His	Ile	Phe	Gly	Leu	Pro	Gly	
65					70					75					80	
Phe	Leu	Ser	Ser	Arg	Ala	Phe	Gln	Ala	Asn	Glu	Glu	Gln	Thr	Asp	Leu	
				85					90					95		
Glu	Ile	Tyr	Gly	Pro	Gln	Gly	Ile	Lys	Ser	Phe	Val	Leu	Thr	Ser	Leu	
				100					105					110		
Arg	Val	Ser	Gly	Ser	Arg	Leu	Pro	Tyr	Arg	Ile	His	Phe	His	Glu	Phe	
		115					120					125				
Asp	Gln	Asp	Ser	Leu	Gly	Lys	Ile	Leu	Glu	Ile	Asp	Lys	Phe	Thr	Val	
		130				135					140					
Tyr	Ala	Glu	Glu	Leu	Asp	His	Thr	Ile	Phe	Cys	Val	Gly	Tyr	Arg	Val	
145					150					155					160	
Met	Gln	Lys	Asp	Leu	Glu	Gly	Thr	Leu	Asp	Ala	Glu	Lys	Leu	Lys	Ala	
				165					170					175		
Ala	Gly	Val	Pro	Phe	Gly	Pro	Leu	Phe	Gly	Lys	Ile	Lys	Asn	Gly	Gln	
			180					185					190			
Asp	Leu	Val	Leu	Glu	Asp	Gly	Thr	Glu	Ile	Lys	Ala	Ala	Asp	Tyr	Ile	
		195					200					205				
Ser	Ala	Pro	Arg	Pro	Gly	Lys	Ile	Ile	Thr	Ile	Leu	Gly	Asp	Thr	Arg	
	210				215						220					
Lys	Thr	Asp	Ala	Ser	Val	Arg	Leu	Ala	Val	Asn	Ala	Asp	Val	Leu	Val	
225					230					235					240	
His	Glu	Ser	Thr	Tyr	Gly	Lys	Gly	Asp	Glu	Lys	Ile	Ala	Arg	Asn	His	
				245					250					255		
Gly	His	Ser	Thr	Asn	Met	Gln	Ala	Ala	Gln	Val	Ala	Val	Glu	Ala	Gly	
			260					265					270			
Ala	Lys	Arg	Leu	Leu	Leu	Asn	His	Ile	Ser	Ala	Arg	Phe	Leu	Ser	Lys	
		275					280					285				
Asp	Ile	Ser	Lys	Leu	Lys	Lys	Asp	Ala	Ala	Thr	Ile	Phe	Glu	Asn	Val	
	290					295					300					
His	Val	Val	Lys	Asp	Leu	Glu	Glu	Val	Glu	Ile						
305					310					315						

(2) INFORMATION FOR SEQ ID NO:3632:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 262 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...262
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3632:

```

Pro Thr Arg Asn Thr Ala Arg Gly Gln Arg Val Leu Tyr Glu Leu Arg
1      5      10      15
Asp Arg Leu Lys Arg Asn Gln Phe Ile Leu Asn Asp Thr Asn Pro Asp
      20      25      30
Ile Val Ile Ser Ile Gly Gly Asp Gly Met Leu Leu Ser Ala Phe His
      35      40      45
Lys Tyr Glu Asn Gln Leu Asp Lys Val Arg Phe Ile Gly Leu His Thr
      50      55      60
Gly His Leu Gly Phe Tyr Thr Asp Tyr Arg Asp Phe Glu Leu Asp Lys
      65      70      75      80
Leu Val Thr Asn Leu Gln Leu Asp Thr Gly Ala Arg Val Ser Tyr Pro
      85      90      95
Val Leu Asn Val Lys Val Phe Leu Glu Asn Gly Glu Val Lys Ile Phe
      100     105     110
Arg Ala Leu Asn Glu Ala Ser Ile Arg Arg Ser Asp Arg Thr Met Val
      115     120     125
Ala Asp Ile Val Ile Asn Gly Val Pro Phe Glu Arg Phe Arg Gly Asp
      130     135     140
Gly Leu Thr Val Ser Thr Pro Thr Gly Ser Thr Ala Tyr Asn Lys Ser
      145     150     155     160
Leu Gly Gly Ala Val Leu His Pro Thr Ile Glu Ala Leu Gln Leu Thr
      165     170     175
Glu Ile Ala Ser Leu Asn Asn Arg Val Tyr Arg Thr Leu Gly Ser Ser
      180     185     190
Ile Ile Val Pro Lys Lys Asp Lys Ile Glu Leu Ile Pro Thr Arg Asn
      195     200     205
Asp Tyr His Thr Ile Ser Val Asp Asn Ser Val Tyr Ser Phe Arg Asn
      210     215     220
Ile Glu Arg Ile Glu Tyr Gln Ile Asp His His Lys Ile His Phe Val
      225     230     235     240
Ala Thr Pro Ser His Thr Ser Phe Trp Asn Arg Val Lys Asp Ala Phe
      245     250     255
Ile Gly Glu Val Asp Glu
      260

```

(2) INFORMATION FOR SEQ ID NO:3633:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 196 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...196

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3633:

Phe	Tyr	Arg	Lys	Leu	Glu	Glu	Pro	Val	Met	Thr	Asn	Thr	Arg	Arg	Leu
1				5					10					15	
Ser	Thr	Ile	Ala	Ile	Leu	Ser	Ala	Ile	Ser	Phe	Val	Leu	Met	Tyr	Phe
			20					25					30		
Asp	Phe	Pro	Leu	Leu	Pro	Ala	Ala	Ser	Phe	Leu	Lys	Ile	Glu	Phe	Ser
		35				40						45			
Ile	Leu	Pro	Val	Leu	Val	Gly	Leu	Val	Val	Met	Asp	Leu	Pro	Ala	Ala
50						55					60				
Leu	Gly	Val	Leu	Leu	Leu	Arg	Ser	Leu	Leu	Lys	Leu	Leu	Leu	Asn	Ser
65					70					75				80	
Gln	Gly	Val	Asn	Thr	Tyr	Ile	Gly	Leu	Pro	Met	Asn	Ile	Val	Ala	Leu
			85						90					95	
Gly	Val	Phe	Val	Ile	Val	Phe	Ala	Leu	Ile	Trp	Lys	Lys	Glu	Arg	Thr
			100					105					110		
Thr	Leu	Arg	Phe	Leu	Leu	Gly	Ser	Leu	Ala	Gly	Thr	Val	Gly	Leu	Thr
		115				120						125			
Leu	Ala	Met	Leu	Val	Leu	Asn	Tyr	Val	Tyr	Ala	Val	Pro	Leu	Tyr	Ala
130						135					140				
Lys	Phe	Ala	Asn	Phe	Asp	Ile	Gly	Lys	Ile	Leu	Gly	Leu	Ser	Asn	Tyr
145				150						155				160	
Leu	Met	Thr	Met	Val	Leu	Pro	Phe	Asn	Leu	Ile	Glu	Gly	Val	Ile	Phe
			165					170						175	
Ser	Val	Ser	Phe	Trp	Leu	Leu	Tyr	Val	Leu	Leu	Lys	Pro	Thr	Leu	Lys
			180				185						190		
His	Tyr	Glu	Arg												
			195												

(2) INFORMATION FOR SEQ ID NO:3634:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 460 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...460

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3634:

Arg	Tyr	Arg	Lys	Arg	Phe	Val	Ile	Ala	Lys	Lys	Lys	Ala	Thr	Phe	Val
1				5					10					15	
Cys	Gln	Asn	Cys	Gly	Tyr	Asn	Ser	Pro	Lys	Tyr	Leu	Gly	Arg	Cys	Pro
			20					25					30		
Asn	Cys	Gly	Ser	Trp	Ser	Ser	Phe	Val	Glu	Glu	Val	Glu	Val	Ala	Glu
		35					40					45			
Val	Lys	Asn	Ala	Arg	Val	Ser	Leu	Thr	Gly	Glu	Lys	Thr	Lys	Pro	Met
	50					55					60				
Lys	Leu	Ala	Glu	Val	Thr	Ser	Ile	Asn	Val	Asn	Arg	Thr	Lys	Thr	Glu
65					70					75					80
Met	Glu	Glu	Phe	Asn	Arg	Val	Leu	Gly	Gly	Gly	Val	Val	Pro	Gly	Ser
				85				90						95	
Leu	Val	Leu	Ile	Gly	Gly	Asp	Pro	Gly	Ile	Gly	Lys	Ser	Thr	Leu	Leu
			100					105					110		
Leu	Gln	Val	Ser	Thr	Gln	Leu	Ser	Gln	Val	Gly	Thr	Val	Leu	Tyr	Val
		115					120					125			
Ser	Gly	Glu	Glu	Ser	Ala	Gln	Gln	Ile	Lys	Leu	Arg	Ala	Glu	Arg	Leu
	130					135					140				
Gly	Asp	Ile	Asp	Ser	Glu	Phe	Tyr	Leu	Tyr	Ala	Glu	Thr	Asn	Met	Gln
145					150					155					160
Ser	Val	Arg	Ala	Glu	Val	Glu	Arg	Ile	Gln	Pro	Asp	Phe	Leu	Ile	Ile
				165					170					175	
Asp	Ser	Ile	Gln	Thr	Ile	Met	Ser	Pro	Glu	Ile	Ser	Gly	Val	Gln	Gly
			180					185					190		
Ser	Val	Ser	Gln	Val	Arg	Glu	Val	Thr	Ala	Glu	Leu	Met	Gln	Leu	Ala
		195				200						205			
Lys	Thr	Asn	Asn	Ile	Ala	Ile	Phe	Ile	Val	Gly	His	Val	Thr	Lys	Glu
	210					215					220				
Gly	Thr	Leu	Ala	Gly	Pro	Arg	Met	Leu	Glu	His	Met	Val	Asp	Thr	Val
225					230					235					240
Leu	Tyr	Phe	Glu	Gly	Glu	Arg	His	His	Thr	Phe	Arg	Ile	Leu	Arg	Ala
				245					250					255	
Val	Lys	Asn	Arg	Phe	Gly	Ser	Thr	Asn	Glu	Ile	Gly	Ile	Phe	Glu	Met
			260					265					270		
Gln	Ser	Gly	Gly	Leu	Val	Glu	Val	Leu	Asn	Pro	Ser	Gln	Val	Phe	Leu
		275					280					285			
Glu	Glu	Arg	Leu	Asp	Gly	Ala	Thr	Gly	Ser	Ser	Ile	Val	Val	Thr	Met
	290				295						300				
Glu	Gly	Thr	Arg	Pro	Ile	Leu	Ala	Glu	Val	Gln	Ala	Leu	Val	Thr	Pro
305					310					315					320
Thr	Met	Phe	Gly	Asn	Ala	Lys	Arg	Thr	Thr	Thr	Gly	Leu	Asp	Phe	Asn
				325					330					335	
Arg	Ala	Ser	Leu	Ile	Met	Ala	Val	Leu	Glu	Lys	Arg	Ala	Gly	Leu	Leu
			340					345					350		
Leu	Gln	Asn	Gln	Asp	Ala	Tyr	Leu	Lys	Ser	Ala	Gly	Gly	Val	Lys	Leu
		355					360					365			
Asp	Glu	Pro	Ala	Ile	Asp	Leu	Ala	Val	Ala	Val	Ala	Ile	Ala	Ser	Ser
	370				375						380				
Tyr	Lys	Asp	Lys	Pro	Thr	Asn	Pro	Gln	Glu	Cys	Phe	Val	Gly	Glu	Leu
385					390					395					400
Gly	Leu	Thr	Gly	Glu	Ile	Arg	Arg	Val	Asn	Arg	Ile	Glu	Gln	Arg	Ile
				405					410					415	
Asn	Glu	Ala	Ala	Lys	Leu	Gly	Phe	Thr	Lys	Ile	Tyr	Val	Pro	Gln	Asn
			420				425						430		
Ser	Leu	Thr	Gly	Ile	Thr	Leu	Pro	Lys	Glu	Ile	Gln	Val	Ile	Gly	Val
		435					440					445			

Thr Thr Ile Gln Glu Val Leu Lys Lys Val Phe Ala
 450 455 460

(2) INFORMATION FOR SEQ ID NO:3635:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 776 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...776

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3635:

Tyr	Asn	Arg	Asn	Ile	Asp	Phe	Lys	Ser	Lys	Glu	Glu	Lys	Met	Asn	Ala	1	5	10	15
Leu	Leu	Asn	Gly	Met	Asn	Asp	Arg	Gln	Ala	Glu	Ala	Val	Gln	Thr	Thr	20	25	30	
Glu	Gly	Pro	Leu	Leu	Ile	Met	Ala	Gly	Ala	Gly	Ser	Gly	Lys	Thr	Arg	35	40	45	
Val	Leu	Thr	His	Arg	Ile	Ala	Tyr	Leu	Ile	Asp	Glu	Lys	Leu	Val	Asn	50	55	60	
Pro	Trp	Asn	Ile	Leu	Ala	Ile	Thr	Phe	Thr	Asn	Lys	Ala	Ala	Arg	Glu	65	70	75	80
Met	Lys	Glu	Arg	Ala	Tyr	Ser	Leu	Asn	Pro	Ala	Thr	Gln	Asp	Cys	Leu	85	90	95	
Ile	Ala	Thr	Phe	His	Ser	Met	Cys	Val	Arg	Ile	Leu	Arg	Arg	Asp	Ala	100	105	110	
Asp	His	Ile	Gly	Tyr	Asn	Arg	Asn	Phe	Thr	Ile	Val	Asp	Pro	Gly	Glu	115	120	125	
Gln	Arg	Thr	Leu	Met	Lys	Arg	Ile	Leu	Lys	Gln	Leu	Asn	Leu	Asp	Pro	130	135	140	
Lys	Lys	Trp	Asn	Glu	Arg	Thr	Ile	Leu	Gly	Thr	Ile	Ser	Asn	Ala	Lys	145	150	155	160
Asn	Asn	Leu	Ile	Asp	Asp	Val	Ala	Tyr	Ala	Ala	Gln	Ala	Gly	Asp	Met	165	170	175	
Tyr	Thr	Gln	Ile	Val	Val	Gln	Cys	Tyr	Thr	Ala	Tyr	Gln	Lys	Glu	Leu	180	185	190	
Arg	Gln	Ser	Glu	Ser	Val	Asp	Phe	Asp	Asp	Leu	Ile	Met	Leu	Thr	Leu	195	200	205	
Arg	Leu	Phe	Asp	Gln	Asn	Pro	Asp	Val	Leu	Thr	Tyr	Tyr	Gln	Gln	Lys	210	215	220	
Phe	Gln	Tyr	Ile	His	Val	Asp	Glu	Tyr	Gln	Asp	Thr	Asn	His	Ala	Gln	225	230	235	240
Tyr	Gln	Leu	Val	Lys	Leu	Leu	Ala	Ser	Arg	Phe	Lys	Asn	Ile	Cys	Val	245	250	255	
Val	Gly	Asp	Ala	Asp	Gln	Ser	Ile	Tyr	Gly	Trp	Arg	Gly	Ala	Asp	Met	260	265	270	

Gln	Asn	Ile	Leu	Asp	Phe	Glu	Lys	Asp	Tyr	Pro	Lys	Ala	Lys	Val	Val
		275					280					285			
Leu	Leu	Glu	Glu	Asn	Tyr	Arg	Ser	Thr	Lys	Thr	Ile	Leu	Gln	Ala	Ala
	290					295					300				
Asn	Glu	Val	Ile	Lys	Asn	Asn	Lys	Asn	Arg	Arg	Pro	Lys	Asn	Leu	Trp
305					310					315					320
Thr	Gln	Asn	Ala	Asp	Gly	Glu	Gln	Ile	Val	Tyr	Tyr	Arg	Ala	Asp	Asp
				325					330					335	
Glu	Leu	Asp	Glu	Ala	Val	Phe	Val	Ala	Arg	Thr	Ile	Asp	Glu	Leu	Ser
		340						345				350			
Arg	Ser	Gln	Asn	Phe	Leu	His	Lys	Asp	Phe	Ala	Val	Leu	Tyr	Arg	Thr
	355						360					365			
Asn	Ala	Gln	Ser	Arg	Thr	Ile	Glu	Glu	Ala	Leu	Leu	Lys	Ser	Asn	Ile
	370					375					380				
Pro	Tyr	Thr	Met	Val	Gly	Gly	Thr	Lys	Phe	Tyr	Ser	Arg	Lys	Glu	Ile
385					390					395					400
Arg	Asp	Ile	Ile	Ala	Tyr	Leu	Asn	Leu	Ile	Ala	Asn	Leu	Ser	Asp	Asn
				405					410					415	
Ile	Ser	Phe	Glu	Arg	Ile	Ile	Asn	Glu	Pro	Lys	Arg	Gly	Ile	Gly	Pro
		420						425				430			
Gly	Thr	Val	Glu	Lys	Ile	Arg	Asp	Phe	Ala	Asn	Leu	Gln	Asn	Met	Ser
	435						440					445			
Met	Leu	Asp	Ala	Ser	Ala	Asn	Ile	Met	Leu	Ser	Gly	Ile	Lys	Gly	Lys
	450					455					460				
Ala	Ala	Gln	Ser	Ile	Trp	Asp	Phe	Ala	Asn	Met	Met	Leu	Asp	Leu	Arg
465					470					475					480
Glu	Gln	Leu	Asp	His	Leu	Ser	Ile	Thr	Glu	Leu	Val	Glu	Ser	Val	Leu
			485						490					495	
Glu	Lys	Thr	Gly	Tyr	Val	Asp	Ile	Leu	Asn	Ala	Gln	Ala	Thr	Leu	Glu
		500						505				510			
Ser	Lys	Ala	Arg	Val	Glu	Asn	Ile	Glu	Glu	Phe	Leu	Ser	Val	Thr	Lys
	515					520						525			
Asn	Phe	Asp	Asp	Thr	Thr	Asp	Val	Thr	Glu	Glu	Glu	Thr	Gly	Leu	Asp
	530					535					540				
Lys	Leu	Ser	Arg	Phe	Leu	Asn	Asp	Leu	Ala	Leu	Ile	Ala	Asp	Thr	Asp
545					550					555					560
Ser	Gly	Ser	Gln	Glu	Thr	Ser	Glu	Val	Thr	Leu	Met	Thr	Leu	His	Ala
			565						570					575	
Ala	Lys	Gly	Leu	Glu	Phe	Pro	Val	Val	Phe	Leu	Ile	Gly	Met	Glu	Glu
		580						585				590			
Asn	Val	Phe	Pro	Leu	Ser	Arg	Ala	Thr	Glu	Asp	Pro	Asp	Glu	Leu	Glu
	595						600					605			
Glu	Glu	Arg	Arg	Leu	Ala	Tyr	Val	Gly	Ile	Thr	Arg	Ala	Glu	Lys	Ile
	610					615					620				
Leu	Tyr	Leu	Thr	Asn	Ala	Asn	Ser	Arg	Leu	Leu	Phe	Gly	Arg	Thr	Asn
625				630						635					640
Tyr	Asn	Arg	Pro	Thr	Arg	Phe	Ile	Asn	Glu	Ile	Ser	Ser	Asp	Leu	Leu
			645						650					655	
Glu	Tyr	Gln	Gly	Leu	Ala	Arg	Pro	Ala	Asn	Thr	Ser	Phe	Lys	Ala	Ser
		660						665				670			
Tyr	Ser	Ser	Gly	Ser	Ile	Ser	Phe	Gly	Gln	Gly	Met	Ser	Leu	Ala	Gln
	675						680					685			
Ala	Leu	Gln	Asp	Arg	Lys	Arg	Gly	Ala	Ala	Pro	Lys	Ser	Ile	Gln	Ser
	690					695					700				
Ser	Gly	Leu	Pro	Phe	Gly	Gln	Phe	Thr	Ala	Gly	Ala	Lys	Pro	Ala	Ser
705					710				715						720
Ser	Glu	Ala	Asn	Trp	Ser	Ile	Gly	Asp	Ile	Ala	Leu	His	Lys	Lys	Trp

				725					730					735			
Gly	Glu	Gly	Thr	Val	Leu	Glu	Val	Ser	Gly	Ser	Gly	Ala	Arg	Gln	Glu		
			740					745					750				
Leu	Lys	Ile	Asn	Phe	Pro	Glu	Val	Gly	Leu	Lys	Lys	Leu	Leu	Ala	Ser		
		755					760					765					
Val	Ala	Pro	Ile	Glu	Lys	Lys	Ile										
	770					775											

(2) INFORMATION FOR SEQ ID NO:3636:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...451

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3636:

Tyr	Asn	Arg	Asn	Met	Asn	Leu	Lys	Thr	Thr	Leu	Gly	Leu	Leu	Ala	Gly		
1				5					10					15			
Arg	Ser	Ser	His	Phe	Val	Leu	Ser	Arg	Leu	Gly	Arg	Gly	Ser	Thr	Leu		
			20					25					30				
Pro	Gly	Lys	Val	Ala	Leu	Gln	Phe	Asp	Lys	Asp	Ile	Leu	Gln	Asn	Leu		
		35				40						45					
Ala	Lys	Asn	Tyr	Glu	Ile	Val	Val	Val	Thr	Gly	Thr	Asn	Gly	Lys	Thr		
	50				55					60							
Leu	Thr	Thr	Ala	Leu	Thr	Val	Gly	Ile	Leu	Lys	Glu	Val	Tyr	Gly	Gln		
65					70				75					80			
Val	Leu	Thr	Asn	Pro	Ser	Gly	Ala	Asn	Met	Ile	Thr	Gly	Ile	Ala	Thr		
			85					90					95				
Thr	Phe	Leu	Thr	Ala	Lys	Ser	Ser	Lys	Thr	Gly	Lys	Asn	Ile	Ala	Val		
		100						105					110				
Leu	Glu	Ile	Asp	Glu	Ala	Ser	Leu	Ser	Arg	Ile	Cys	Asp	Tyr	Ile	Gln		
	115					120				125							
Pro	Ser	Leu	Phe	Val	Ile	Thr	Asn	Ile	Phe	Arg	Asp	Gln	Met	Asp	Arg		
	130				135					140							
Phe	Gly	Glu	Ile	Tyr	Thr	Thr	Tyr	Asn	Met	Ile	Leu	Asp	Ala	Ile	Arg		
145				150					155					160			
Lys	Val	Pro	Thr	Ala	Thr	Val	Leu	Leu	Asn	Gly	Asp	Ser	Pro	Leu	Phe		
		165						170					175				
Tyr	Lys	Pro	Thr	Ile	Pro	Asn	Pro	Ile	Glu	Tyr	Phe	Gly	Phe	Asp	Leu		
		180				185						190					
Glu	Lys	Gly	Pro	Ala	Gln	Leu	Ala	His	Tyr	Asn	Thr	Glu	Gly	Ile	Leu		
	195				200						205						
Cys	Pro	Asp	Cys	Gln	Gly	Ile	Leu	Lys	Tyr	Glu	His	Asn	Thr	Tyr	Ala		
	210				215					220							
Asn	Leu	Gly	Ala	Tyr	Ile	Cys	Glu	Gly	Cys	Gly	Cys	Lys	Arg	Pro	Asp		

225		230		235		240
Leu	Asp	Tyr	Arg	Leu	Thr	Lys
		245		250		255
Arg	Phe	Val	Ile	Asp	Gly	Gln
		260		265		270
Tyr	Asn	Ile	Tyr	Asn	Ala	Leu
		275		280		285
Gly	Ala	Asp	Ser	Gln	Leu	Ile
		290		295		300
Val	Phe	Gly	Arg	Gln	Glu	Thr
305				310		315
Leu	Val	Leu	Ile	Lys	Asn	Pro
				325		330
Ile	Lys	Leu	Ala	Pro	Tyr	Pro
				340		345
Asn	Tyr	Ala	Asp	Gly	Ile	Asp
		355		360		365
Glu	Gln	Ile	Thr	Asp	Met	Asp
370				375		380
Arg	His	Ser	Glu	Ile	Ala	Arg
385				390		395
Glu	Lys	Ile	Thr	Glu	Thr	Ser
				405		410
Glu	Asn	Gln	Asp	Cys	Lys	His
				420		425
Met	Leu	Glu	Phe	Arg	Glu	Leu
				435		440
Glu	Met	Asn				
450						

(2) INFORMATION FOR SEQ ID NO:3637:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 233 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...233

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3637:

Asn	Cys	Arg	Asn	His	Leu	Leu	Asn	Gly	Gly	Lys	Thr	Glu	Met	Lys	Leu
1				5				10						15	
Asn	Lys	Tyr	Ile	Asp	His	Thr	Leu	Gly	Lys	Gln	Asp	Ala	Gln	Lys	Lys
			20					25					30		
Gln	Ile	Asp	Ser	Leu	Leu	Ser	Glu	Ala	Arg	Glu	Tyr	Asp	Phe	Ala	Ser
		35					40					45			
Val	Cys	Val	Asn	Pro	Thr	Trp	Val	Glu	His	Ala	Lys	Lys	Gly	Leu	Glu

50		55		60
Gly Thr Asp Val Lys Val Cys Thr Val Val Gly Phe Pro Leu Gly Ala				
65		70		80
Thr Thr Ser Ala Val Lys Ala Phe Glu Thr Lys Glu Ala Ile Gln Asn				
	85		90	95
Gly Ala Asp Glu Ile Asp Met Val Ile Asn Val Gly Ala Leu Lys Ser				
	100		105	110
Gly Asn Leu Ala Leu Val Glu Ser Asp Ile Arg Ala Val Val Glu Ala				
	115		120	125
Ser Gly Asp Lys Leu Val Lys Val Ile Ile Glu Ala Cys Leu Leu Thr				
	130		135	140
Asp Gln Glu Lys Ile Val Val Cys Gln Leu Ala Gln Lys Ala Gly Ala				
145		150		160
Asp Phe Val Lys Thr Ser Thr Gly Phe Ser Thr Gly Gly Ala Thr Ile				
	165		170	175
Ala Asp Val Arg Leu Met Arg Glu Thr Val Gly Ser Asp Met Gly Val				
	180		185	190
Lys Ala Ala Gly Gly Ala Arg Ser Tyr Ala Asp Ala Leu Ala Phe Val				
	195		200	205
Glu Ala Gly Ala Thr Arg Ile Gly Thr Ser Ala Gly Val Ala Ile Leu				
210		215		220
Lys Gly Glu Leu Ala Asp Gly Asp Tyr				
225		230		

(2) INFORMATION FOR SEQ ID NO:3638:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...342

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3638:

Val Ser Arg Asn Met Val Lys Lys Ile Ile Gly Met Val Leu Ala Leu
1 5 10 15
Leu Ser Val Thr Val Val Gly Val Gly Val Phe Ala Tyr Thr Ile Tyr
20 25 30
Gln Gln Gly Thr Glu Thr Leu Ala Lys Thr Tyr Lys Lys Ile Gly Glu
35 40 45
Glu Thr Lys Val Ile Glu Ala Thr Glu Pro Leu Thr Ile Leu Leu Met
50 55 60
Gly Val Asp Thr Gly Asn Val Glu Arg Thr Glu Thr Trp Val Gly Arg
65 70 75 80
Ser Asp Ser Met Ile Leu Met Thr Val Asn Pro Lys Thr Lys Lys Thr
85 90 95
Thr Met Met Ser Leu Glu Arg Asp Ile Leu Thr Arg Ile Glu Ser Gly

			100					105				110					
Asn	Gly	Gln	Ala	His	Glu	Ala	Lys	Leu	Asn	Ser	Ala	Tyr	Ala	Asp	Gly		
			115					120					125				
Gly	Ala	Glu	Leu	Ala	Ile	Glu	Thr	Ile	Gln	Lys	Met	Met	Asn	Ile	His		
			130					135				140					
Ile	Asp	Arg	Tyr	Val	Met	Val	Asn	Met	Arg	Gly	Leu	Gln	Lys	Leu	Val		
					150					155					160		
Asp	Ala	Val	Gly	Gly	Ile	Thr	Val	Asn	Asn	Ile	Leu	Gly	Phe	Pro	Ile		
				165					170					175			
Ser	Ile	Ser	Asp	Gln	Glu	Glu	Phe	Asn	Thr	Ile	Ser	Ile	Gly	Val	Gly		
			180					185					190				
Glu	Gln	His	Ile	Gly	Gly	Glu	Glu	Ala	Leu	Val	Tyr	Ala	Arg	Met	Arg		
		195						200				205					
Tyr	Gln	Asp	Pro	Glu	Gly	Asp	Tyr	Gly	Arg	Gln	Lys	Arg	Gln	Arg	Glu		
		210				215					220						
Val	Ile	Gln	Lys	Val	Met	Glu	Lys	Ala	Leu	Ser	Leu	Asn	Ser	Val	Gly		
					230				235					240			
His	Tyr	Gln	Glu	Ile	Leu	Lys	Ala	Leu	Ser	Asp	Asn	Met	Gln	Thr	Asn		
				245				250					255				
Ile	Asp	Leu	Ser	Ala	Lys	Ser	Ile	Pro	Asn	Leu	Leu	Gly	Tyr	Lys	Asp		
		260						265				270					
Ser	Phe	Lys	Thr	Ile	Glu	Thr	Gln	Gln	Leu	Gln	Gly	Glu	Gly	Glu	Ile		
		275					280				285						
Leu	Gln	Gly	Val	Ser	Tyr	Gln	Ile	Val	Ser	Arg	Ala	His	Met	Leu	Glu		
		290				295				300							
Met	Gln	Asn	Ile	Leu	Arg	Ser	Leu	Gly	Gln	Glu	Glu	Val	Thr	Gln			
				310				315					320				
Leu	Glu	Thr	Asn	Ala	Val	Leu	Phe	Glu	Asp	Leu	Phe	Gly	Arg	Ala	Pro		
			325					330					335				
Val	Gly	Asp	Glu	Asp	Asn												
			340														

(2) INFORMATION FOR SEQ ID NO:3639:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...245

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3639:

Ile	Phe	Arg	Lys	Glu	Asn	Leu	Lys	Leu	Phe	Tyr	Lys	Phe	Leu	Leu	Phe		
1				5				10					15				
Asp	Leu	Asp	His	Thr	Leu	Leu	Asp	Phe	Asp	Ala	Ala	Glu	Asn	Val	Ala		
			20					25				30					
Leu	Thr	Gln	Leu	Leu	Lys	Glu	Glu	Gly	Val	Ala	Asp	Ile	Gln	Ala	Tyr		

35					40					45					
Lys	Asp	Tyr	Tyr	Val	Pro	Met	Asn	Lys	Ala	Leu	Trp	Lys	Asp	Leu	Glu
50					55					60					
Leu	Lys	Lys	Ile	Ser	Lys	Gln	Glu	Leu	Val	Asn	Thr	Arg	Phe	Ser	Arg
65					70					75					80
Leu	Phe	Ala	His	Phe	Gly	Gln	Glu	Lys	Asp	Gly	Ser	Phe	Leu	Ala	Gln
			85						90					95	
Arg	Tyr	Gln	Phe	Tyr	Leu	Ala	Gln	Gln	Gly	Gln	Thr	Leu	Ser	Gly	Ala
			100						105					110	
His	Asp	Leu	Leu	Asp	Ser	Leu	Ile	Glu	Arg	Asp	Tyr	Asn	Leu	Tyr	Ala
	115						120					125			
Ala	Thr	Asn	Gly	Ile	Thr	Ala	Ile	Gln	Thr	Gly	Arg	Leu	Ala	Gln	Ser
	130						135					140			
Gly	Leu	Ala	Pro	Tyr	Phe	Asn	Gln	Val	Phe	Ile	Ser	Glu	Gln	Leu	Gln
145					150					155					160
Thr	Gln	Lys	Pro	Asp	Ala	Leu	Phe	Tyr	Glu	Lys	Ile	Gly	Gln	Gln	Ile
			165						170					175	
Ala	Gly	Phe	Ser	Lys	Glu	Lys	Thr	Leu	Met	Ile	Gly	Asp	Ser	Leu	Thr
			180					185					190		
Ala	Asp	Ile	Gln	Gly	Gly	Asn	Asn	Ala	Gly	Ile	Asp	Thr	Ile	Trp	Tyr
	195						200					205			
Asn	Pro	His	His	Leu	Glu	Asn	His	Thr	Gln	Ala	Gln	Pro	Thr	Tyr	Glu
	210					215					220				
Val	Tyr	Ser	Tyr	Gln	Asp	Leu	Leu	Asp	Cys	Leu	Asp	Lys	Asn	Ile	Leu
225					230					235					240
Glu	Lys	Ile	Thr	Phe											
				245											

(2) INFORMATION FOR SEQ ID NO:3640:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 219 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...219
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3640:

Ser	Val	Arg	Asn	Ile	Gln	Arg	Lys	Cys	Lys	Phe	Asp	Tyr	Leu	Ile	Arg
1			5					10						15	
Arg	Glu	Thr	Lys	Met	Lys	Val	Leu	Val	Ala	Glu	Asp	Gln	Ser	Met	Leu
			20					25					30		
Arg	Asp	Ala	Met	Cys	Gln	Leu	Leu	Thr	Leu	Gln	Pro	Asp	Val	Glu	Ser
		35					40					45			
Val	Leu	Gln	Ala	Lys	Asn	Gly	Gln	Glu	Ala	Ile	Gln	Leu	Leu	Glu	Lys
	50					55					60				

Glu	Ser	Val	Asp	Ile	Ala	Ile	Leu	Asp	Val	Glu	Met	Pro	Val	Lys	Thr
65					70					75					80
Gly	Leu	Glu	Val	Leu	Glu	Trp	Ile	Arg	Ser	Glu	Lys	Leu	Glu	Thr	Lys
				85					90					95	
Val	Val	Val	Val	Thr	Thr	Phe	Lys	Arg	Ala	Gly	Tyr	Phe	Glu	Arg	Ala
				100				105					110		
Val	Lys	Ala	Gly	Val	Asp	Ala	Tyr	Val	Leu	Lys	Glu	Arg	Ser	Ile	Ala
		115					120					125			
Asp	Leu	Met	Gln	Thr	Leu	His	Thr	Val	Leu	Glu	Gly	Arg	Lys	Glu	Tyr
		130				135						140			
Ser	Pro	Glu	Leu	Met	Glu	Met	Val	Met	Thr	Arg	Pro	Asn	Pro	Leu	Thr
145					150					155					160
Glu	Gln	Glu	Ile	Ala	Val	Leu	Lys	Gly	Ile	Ala	Arg	Gly	Leu	Ser	Asn
				165					170					175	
Gln	Glu	Ile	Ala	Asp	Gln	Leu	Tyr	Leu	Ser	Asn	Gly	Thr	Ile	Arg	Asn
			180					185					190		
Tyr	Val	Thr	Asn	Ile	Leu	Ser	Lys	Leu	Asp	Ala	Gly	Asn	Arg	Thr	Glu
		195					200					205			
Ala	Ala	Asn	Ile	Ala	Lys	Glu	Ser	Gly	Trp	Leu					
		210					215								

(2) INFORMATION FOR SEQ ID NO:3641:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 431 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...431

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3641:

Gly	Ser	Arg	Asn	Asn	Asn	Phe	Lys	Lys	Glu	Lys	Arg	His	Met	His	Ile
1				5					10					15	
Phe	Asp	Glu	Leu	Lys	Asp	Arg	Gly	Leu	Ile	Phe	Gln	Thr	Thr	Asp	Glu
			20					25					30		
Glu	Ala	Leu	Arg	Lys	Ala	Leu	Glu	Glu	Gly	Gln	Val	Ser	Tyr	Tyr	Thr
		35					40					45			
Gly	Tyr	Asp	Pro	Thr	Ala	Asp	Ser	Leu	His	Leu	Gly	His	Leu	Val	Ala
		50				55					60				
Ile	Leu	Thr	Ser	Arg	Arg	Leu	Gln	Leu	Ala	Gly	His	Lys	Pro	Tyr	Ala
65				70						75					80
Leu	Val	Gly	Gly	Ala	Thr	Gly	Leu	Ile	Gly	Asp	Pro	Ser	Phe	Lys	Asp
			85						90					95	
Ala	Glu	Arg	Ser	Leu	Gln	Thr	Lys	Asp	Thr	Val	Asp	Gly	Trp	Val	Lys
			100					105					110		
Ser	Ile	Gln	Gly	Gln	Leu	Ser	Arg	Phe	Leu	Asp	Phe	Glu	Asn	Gly	Glu
		115					120					125			

Asn	Lys	Ala	Val	Met	Val	Asn	Asn	Tyr	Asp	Trp	Phe	Gly	Ser	Ile	Ser	130	135	140
Phe	Ile	Asp	Phe	Leu	Arg	Asp	Ile	Gly	Lys	Tyr	Phe	Thr	Val	Asn	Tyr	145	150	155
Met	Met	Ser	Lys	Glu	Ser	Val	Lys	Lys	Arg	Ile	Glu	Thr	Gly	Ile	Ser	165	170	175
Tyr	Thr	Glu	Phe	Ala	Tyr	Gln	Ile	Met	Gln	Gly	Tyr	Asp	Phe	Phe	Val	180	185	190
Leu	Asn	Gln	Asp	His	Asn	Val	Thr	Leu	Gln	Ile	Gly	Gly	Ser	Asp	Gln	195	200	205
Trp	Gly	Asn	Met	Thr	Ala	Gly	Thr	Glu	Leu	Leu	Arg	Arg	Lys	Ala	Asp	210	215	220
Lys	Thr	Gly	His	Val	Ile	Thr	Val	Pro	Leu	Ile	Thr	Asp	Ala	Thr	Gly	225	230	235
Lys	Lys	Phe	Gly	Lys	Ser	Glu	Gly	Asn	Ala	Val	Trp	Leu	Asn	Pro	Glu	245	250	255
Lys	Thr	Ser	Pro	Tyr	Glu	Met	Tyr	Gln	Phe	Trp	Met	Asn	Val	Met	Asp	260	265	270
Ala	Asp	Ala	Val	Arg	Phe	Leu	Lys	Ile	Phe	Thr	Phe	Leu	Ser	Leu	Asp	275	280	285
Glu	Ile	Glu	Asp	Ile	Arg	Lys	Gln	Phe	Glu	Ala	Ala	Pro	His	Glu	Arg	290	295	300
Leu	Ala	Gln	Lys	Val	Leu	Ala	Arg	Glu	Val	Val	Thr	Leu	Val	His	Gly	305	310	315
Glu	Glu	Ala	Tyr	Lys	Glu	Ala	Leu	Asn	Ile	Thr	Glu	Gln	Leu	Phe	Ala	325	330	335
Gly	Asn	Ile	Lys	Asn	Leu	Ser	Val	Lys	Glu	Leu	Lys	Gln	Gly	Leu	Arg	340	345	350
Gly	Val	Pro	Asn	Tyr	Gln	Val	Gln	Ala	Asp	Glu	Asn	Asn	Asn	Ile	Val	355	360	365
Glu	Leu	Leu	Val	Ser	Ser	Gly	Ile	Val	Asn	Ser	Lys	Arg	Gln	Ala	Arg	370	375	380
Glu	Asp	Val	Gln	Asn	Gly	Ala	Ile	Tyr	Val	Asn	Gly	Asp	Arg	Ile	Gln	385	390	395
Glu	Leu	Asp	Tyr	Val	Leu	Ser	Asp	Ala	Asp	Lys	Leu	Glu	Asn	Glu	Leu	405	410	415
Thr	Val	Ile	Arg	Arg	Gly	Lys	Lys	Lys	Tyr	Phe	Val	Leu	Thr	Tyr		420	425	430

(2) INFORMATION FOR SEQ ID NO:3642:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...87

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3642:

Pro	Tyr	Arg	Lys	Arg	Gln	Gln	Ile	Met	Lys	Met	Ser	Thr	Phe	Phe	Lys
1			5					10					15		
Lys	Ser	Phe	Trp	Pro	Thr	Phe	Met	Ile	Val	Asn	Gln	Thr	Val	Ile	Leu
		20					25					30			
Phe	His	Leu	Lys	Asp	Gly	Leu	Asp	Arg	Gln	Tyr	Leu	Thr	Thr	Glu	Ser
	35					40					45				
Ile	Tyr	Trp	Val	Ile	Gly	Thr	Phe	Ile	Phe	Gly	Asn	Ile	Leu	Val	Ala
	50				55					60					
Val	Phe	Ser	Asn	Met	Lys	Ile	Trp	Asp	Lys	Lys	Lys	Asn	Gly	Ser	Lys
65				70				75							80
Lys	Lys	Tyr	Ile	Leu	Lys	Lys									
				85											

(2) INFORMATION FOR SEQ ID NO:3643:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3643:

Thr	Leu	Arg	Asn	Leu	Leu	Thr	Asp	Lys	Ile	Leu	Ala	Leu	Asp	Phe	Leu
1			5					10					15		
Arg	Asn	Lys	Ile	Trp	Tyr	Ser	Ser	Ser	Met	Asn	Tyr	Glu	Ala	Ser	Lys
		20					25					30			
Gln	Leu	Thr	Asp	Ala	Arg	Phe	Lys	Cys	Leu	Val	Gly	Val	Gln	Arg	Thr
	35					40					45				
Thr	Phe	Glu	Glu	Ile	Leu	Ala	Val	Leu	Lys	Thr	Ala	Tyr	Gln	Leu	Lys
	50				55					60					
His	Thr	Lys	Gly	Gly	Arg	Glu	Pro	Lys	Leu	Ser	Leu	Glu	Asp	Leu	Leu
65				70				75							80
Met	Ala	Thr	Leu	Gln	Tyr	Val	Arg	Glu	Tyr	Arg	Thr	Tyr	Glu	Gln	Ile
			85					90					95		
Ala	Ala	Val	Phe	Gly	Ile	His	Glu	Ser	Asn	Leu	Leu	Arg	Arg	Ser	Gln
		100					105					110			
Trp	Val	Glu	Val	Thr	Leu	Val	Gln	Ser	Ile	Leu	Gln	Phe	Gln	Glu	Leu
	115					120					125				
Leu	Ser	Val	Leu	Arg	Thr	Arg									
	130					135									

(2) INFORMATION FOR SEQ ID NO:3644:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 304 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...304

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3644:

Phe	Leu	Arg	Asn	Gln	Ser	Leu	Pro	Ser	Arg	Leu	Asp	Ser	Arg	Lys	Ser	1	5	10	15
Gln	Ile	Thr	Leu	Gly	Glu	Ile	Phe	Lys	Arg	Val	Gly	Ala	Glu	Val	Glu	20	25	30	
Ile	Asp	Glu	Ser	Tyr	Thr	Ala	Pro	Phe	Val	Met	Ala	His	Phe	Lys	Ser	35	40	45	
Ser	Arg	Pro	Asp	Ala	Lys	Thr	Leu	Ile	Phe	Tyr	Asn	His	Tyr	Asp	Thr	50	55	60	
Val	Pro	Ala	Asp	Gly	Asp	Gln	Val	Trp	Thr	Glu	Asp	Pro	Phe	Thr	Leu	65	70	75	80
Ser	Val	Arg	Asn	Gly	Phe	Met	Tyr	Gly	Arg	Gly	Val	Asp	Asp	Asp	Lys	85	90	95	
Gly	His	Ile	Thr	Ala	Arg	Leu	Ser	Ala	Leu	Arg	Lys	Tyr	Met	Gln	His	100	105	110	
His	Asp	Asp	Leu	Pro	Val	Asn	Ile	Ser	Phe	Ile	Met	Glu	Gly	Ala	Glu	115	120	125	
Glu	Ser	Ala	Ser	Thr	Asp	Leu	Asp	Lys	Tyr	Leu	Glu	Lys	His	Ala	Asp	130	135	140	
Lys	Leu	His	Gly	Ala	Asp	Leu	Leu	Val	Trp	Glu	Gln	Gly	Thr	Lys	Asn	145	150	155	160
Ala	Leu	Glu	Gln	Leu	Glu	Ile	Ser	Gly	Gly	Asn	Lys	Gly	Ile	Val	Thr	165	170	175	
Phe	Asp	Ala	Lys	Val	Lys	Ser	Ala	Asp	Val	Asp	Ile	His	Ser	Ser	Tyr	180	185	190	
Gly	Gly	Val	Val	Glu	Ser	Ala	Pro	Trp	Tyr	Leu	Leu	Gln	Ala	Leu	Gln	195	200	205	
Ser	Leu	Arg	Ala	Ala	Asp	Gly	Arg	Ile	Leu	Val	Glu	Gly	Leu	Tyr	Glu	210	215	220	
Glu	Val	His	Glu	Pro	Asn	Glu	Arg	Glu	Met	Ala	Leu	Leu	Glu	Thr	Tyr	225	230	235	240
Gly	Gln	Arg	Asn	Pro	Glu	Glu	Val	Ser	Arg	Ile	Tyr	Gly	Leu	Glu	Leu	245	250	255	
Pro	Leu	Leu	Gln	Glu	Glu	Arg	Met	Ala	Phe	Leu	Lys	Arg	Phe	Phe	Phe	260	265	270	
Glu	Pro	Ala	Leu	Asn	Ile	Glu	Gly	Ile	Gln	Ser	Gly	Tyr	Gln	Gly	Gln	275	280	285	
Gly	Val	Lys	Thr	Ile	Val	Pro	Ala	Glu	Ala	Ser	Ala	Lys	Leu	Glu	Val	290	295	300	

(2) INFORMATION FOR SEQ ID NO:3645:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 148 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...148
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3645:

```

Asn Lys Arg Lys Lys Leu Thr Lys Glu Thr Gly Met Glu His Thr Phe
 1              5              10              15
Phe Ile Ile Lys Pro Asp Gly Val Lys Arg Gly Leu Val Gly Glu Val
      20              25              30
Leu Lys Arg Ile Glu Gln Arg Gly Phe Thr Ile Glu Lys Leu Glu Phe
      35              40              45
Arg Ser Gln Val Ser Glu Glu Leu Ile Asp Gln His Tyr Gln Asp Leu
      50              55              60
Val Gly Gln Ser Phe Tyr Pro Pro Ile Arg Glu Phe Met Thr Ser Gly
65              70              75              80
Pro Val Leu Val Gly Val Ile Ser Gly Pro Lys Val Ile Glu Thr Trp
      85              90              95
Arg Thr Met Met Gly Ala Thr Arg Pro Glu Glu Ala Leu Pro Gly Thr
      100             105             110
Ile Arg Gly Asp Phe Ala Lys Ala Ala Gly Glu Asn Glu Ile Ile Gln
      115             120             125
Asn Val Val His Gly Ser Asp Ser Glu Glu Ser Ala Lys Arg Glu Ile
      130             135             140
Ala Leu Trp Phe
145

```

(2) INFORMATION FOR SEQ ID NO:3646:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 182 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...182

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3646:

Gln	Lys	Arg	Lys	Gln	Phe	Thr	Lys	Lys	Asn	Asp	Gly	Gly	Ala	Asn	Met
1				5					10					15	
Ala	Gln	Lys	Gly	Val	Ser	Leu	Ile	Lys	Ala	Ala	Phe	Asp	Thr	Asp	Asn
			20					25					30		
Phe	Leu	Met	Arg	Phe	Ser	Glu	Lys	Val	Leu	Asp	Ile	Val	Thr	Ala	Asn
		35					40					45			
Leu	Leu	Phe	Val	Val	Ser	Cys	Leu	Pro	Ile	Val	Thr	Ile	Gly	Val	Ala
	50					55					60				
Lys	Ile	Ser	Leu	Tyr	Glu	Thr	Met	Phe	Glu	Val	Lys	Lys	Ser	Arg	Arg
65					70				75					80	
Val	Pro	Val	Phe	Lys	Ile	Tyr	Leu	Arg	Ser	Phe	Lys	Gln	Asn	Leu	Lys
				85				90					95		
Leu	Gly	Leu	Gln	Leu	Gly	Leu	Met	Glu	Leu	Gly	Ile	Val	Phe	Leu	Thr
			100					105					110		
Leu	Ser	Asp	Leu	Tyr	Leu	Phe	Trp	Gly	Gln	Thr	Ala	Leu	Pro	Phe	Gln
		115					120					125			
Leu	Leu	Lys	Ala	Ile	Cys	Leu	Gly	Ile	Leu	Ile	Phe	Leu	Thr	Ile	Val
	130					135					140				
Met	Leu	Ala	Ser	Tyr	Pro	Ile	Ala	Ala	Arg	Tyr	Asp	Leu	Ser	Trp	Lys
145					150				155					160	
Glu	Ile	Leu	Gln	Lys	Gly	Leu	Met	Leu	Ala	Ser	Phe	Asn	Tyr	Pro	Ala
				165				170						175	
Leu	His	His	Glu	Trp	Asn										
			180												

(2) INFORMATION FOR SEQ ID NO:3647:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...151

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3647:

Lys	Lys	Arg	Lys	Ile	Trp	Pro	Ala	Arg	Phe	Leu	Ile	Ile	Met	Ala	Ile
1				5					10				15		
Arg	Thr	Ser	Phe	Leu	Ile	Lys	Cys	Ile	Ser	Phe	Leu	Arg	Glu	Val	Gly
			20				25					30			
Lys	Met	Thr	Glu	Ile	Asn	Trp	Lys	Asp	Asn	Leu	Arg	Ile	Ala	Trp	Phe
		35				40					45				
Gly	Asn	Phe	Leu	Thr	Gly	Ala	Ser	Ile	Ser	Leu	Val	Val	Pro	Phe	Met
	50					55					60				

Pro	Ile	Phe	Val	Glu	Asn	Leu	Cys	Val	Gly	Ser	Gln	Gln	Val	Ala	Phe
65					70				75						80
Tyr	Ala	Gly	Leu	Ala	Ile	Ser	Val	Ser	Ala	Ile	Ser	Ala	Ala	Leu	Phe
				85					90						95
Ser	Pro	Ile	Trp	Gly	Ile	Leu	Ala	Asp	Lys	Tyr	Gly	Arg	Lys	Pro	Met
			100					105					110		
Met	Ile	Leu	Gly	Arg	Ser	Cys	Tyr	Asp	Tyr	His	Tyr	Gly	Arg	Leu	Gly
		115					120					125			
Leu	Cys	Pro	Lys	Tyr	Leu	Leu	Val	Asn	Leu	Ser	Ser	Phe	Thr	Lys	Arg
	130						135				140				
Cys	Ile	Cys	Arg	Phe	Cys	Ser									
145					150										

(2) INFORMATION FOR SEQ ID NO:3648:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...194

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3648:

Tyr	Arg	Arg	Lys	Gly	Ile	Arg	Lys	Asn	Met	Ala	Asn	Val	Ile	Ile	Glu
1				5				10					15		
Lys	Ala	Lys	Glu	Arg	Met	Thr	Gln	Ser	His	Gln	Ser	Leu	Ala	Arg	Glu
			20					25					30		
Phe	Gly	Gly	Ile	Arg	Ala	Gly	Arg	Ala	Asn	Ala	Ser	Leu	Leu	Asp	Arg
		35				40						45			
Val	His	Val	Glu	Tyr	Tyr	Gly	Val	Glu	Thr	Pro	Leu	Asn	Gln	Ile	Ala
	50				55					60					
Ser	Ile	Thr	Ile	Pro	Glu	Ala	Arg	Val	Leu	Leu	Val	Thr	Pro	Phe	Asp
65					70				75						80
Lys	Ser	Ser	Leu	Lys	Asp	Ile	Glu	Arg	Ala	Leu	Asn	Ala	Ser	Asp	Leu
			85					90						95	
Gly	Ile	Thr	Pro	Ala	Asn	Asp	Gly	Ser	Val	Ile	Arg	Leu	Val	Ile	Pro
			100					105					110		
Ala	Leu	Thr	Glu	Glu	Thr	Arg	Arg	Asp	Leu	Ala	Lys	Glu	Val	Lys	Lys
		115				120						125			
Val	Gly	Glu	Asn	Ala	Lys	Val	Ala	Val	Arg	Asn	Ile	Arg	Arg	Asp	Ala
	130				135					140					
Met	Asp	Glu	Ala	Lys	Lys	Gln	Glu	Lys	Ala	Gln	Glu	Ile	Thr	Glu	Asp
145					150				155						160
Glu	Leu	Lys	Thr	Leu	Glu	Lys	Asp	Ile	Gln	Lys	Val	Thr	Asp	Asp	Ala
			165					170					175		
Val	Lys	His	Ile	Asp	Asp	Met	Thr	Ala	Asn	Lys	Glu	Lys	Glu	Leu	Leu
			180					185					190		

Glu Val

(2) INFORMATION FOR SEQ ID NO:3649:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...118

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3649:

Gly	Gly	Arg	Lys	Met	Lys	Ser	Lys	Glu	Glu	Ile	Asn	Met	Leu	Gly	Phe	
1				5				10						15		
Thr	Ile	Val	Ala	Tyr	Ala	Gly	Asp	Ala	Arg	Ser	Asp	Leu	Met	Asp	Ala	
			20					25					30			
Leu	Ala	Phe	Ala	Arg	Asp	Gly	Tyr	Phe	Glu	Gln	Ala	Arg	Glu	Leu	Val	
		35					40					45				
Glu	Ser	Ala	Asn	Asp	Ser	Ile	Val	Ser	Ala	His	Arg	Glu	Gln	Thr	Asn	
	50					55				60						
Leu	Leu	Ala	Glu	Glu	Ala	Ser	Gly	Asp	Asn	Phe	Glu	Val	Ser	Phe	Ile	
65					70					75					80	
Met	Ile	His	Gly	Gln	Asp	Thr	Leu	Met	Thr	Thr	Met	Leu	Leu	Tyr	Asp	
			85						90					95		
Gln	Val	Lys	Phe	Phe	Ile	Asp	Glu	Tyr	Glu	Arg	Ile	Arg	Lys	Ile	Glu	
			100					105					110			
Glu	His	Ile	Gly	Leu	Gln											
					115											

(2) INFORMATION FOR SEQ ID NO:3650:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...282

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3650:

Asn	Lys	Arg	Lys	Asn	Ser	Ile	Lys	Glu	Glu	Ile	Met	Glu	Lys	Gln	Thr
1				5					10					15	
Val	Ala	Val	Leu	Gly	Pro	Gly	Ser	Trp	Gly	Thr	Ala	Leu	Ser	Gln	Val
			20					25					30		
Leu	Asn	Asp	Asn	Gly	His	Glu	Val	Arg	Ile	Trp	Gly	Asn	Leu	Pro	Glu
		35					40					45			
Gln	Ile	Asn	Glu	Ile	Asn	Thr	His	His	Thr	Asn	Lys	His	Tyr	Phe	Lys
	50					55					60				
Asp	Val	Val	Leu	Asp	Glu	Asn	Ile	Ile	Ala	Tyr	Thr	Asp	Leu	Ala	Glu
65					70					75					80
Thr	Leu	Lys	Asp	Val	Asp	Ala	Ile	Leu	Phe	Val	Val	Pro	Thr	Lys	Val
			85						90					95	
Thr	Arg	Leu	Val	Ala	Gln	Gln	Val	Ala	Gln	Thr	Leu	Asp	His	Lys	Val
			100					105					110		
Ile	Ile	Met	His	Ala	Ser	Lys	Gly	Leu	Glu	Pro	Asp	Ser	His	Lys	Arg
		115					120					125			
Leu	Ser	Thr	Ile	Leu	Glu	Glu	Glu	Ile	Pro	Glu	His	Leu	Arg	Ser	Asp
	130					135					140				
Ile	Val	Val	Val	Ser	Gly	Pro	Ser	His	Ala	Glu	Glu	Thr	Ile	Val	Arg
145					150					155					160
Asp	Leu	Thr	Leu	Ile	Thr	Ala	Ala	Ser	Lys	Asp	Leu	Gln	Thr	Ala	Gln
			165						170					175	
Tyr	Val	Gln	Glu	Leu	Phe	Ser	Asn	His	Tyr	Phe	Arg	Leu	Tyr	Thr	Asn
		180						185					190		
Thr	Asp	Val	Ile	Gly	Val	Glu	Thr	Ala	Gly	Ala	Leu	Lys	Asn	Ile	Ile
	195						200					205			
Ala	Val	Gly	Ala	Gly	Ala	Leu	His	Gly	Leu	Gly	Phe	Gly	Asp	Asn	Ala
	210					215					220				
Lys	Ala	Ala	Ile	Ile	Ala	Arg	Gly	Leu	Ala	Glu	Ile	Thr	Arg	Leu	Gly
225					230					235					240
Val	Ala	Leu	Gly	Ala	Ser	Pro	Leu	Thr	Tyr	Ser	Gly	Leu	Ser	Gly	Val
			245						250					255	
Gly	Asp	Leu	Ile	Val	Thr	Gly	Thr	Ser	Ile	His	Ser	Arg	Asn	Trp	Arg
		260					265						270		
Ala	Gly	Asp	Ala	Leu	Gly	Arg	Gly	Glu	Ser						
		275					280								

(2) INFORMATION FOR SEQ ID NO:3651:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...91

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3651:

Glu	Lys	Arg	Lys	Glu	Met	Tyr	Tyr	Thr	Leu	Glu	Glu	Lys	Glu	Val	Phe
1				5					10					15	
Met	Arg	Glu	Ala	Leu	Arg	Glu	Ala	Glu	Ile	Ala	Leu	Glu	His	Asp	Glu
			20					25					30		
Ile	Pro	Ile	Gly	Cys	Val	Ile	Val	Lys	Asp	Gly	Glu	Ile	Ile	Gly	Arg
			35				40					45			
Gly	His	Asn	Ala	Arg	Glu	Glu	Leu	Gln	Arg	Ala	Val	Met	His	Ala	Glu
	50					55					60				
Ile	Met	Ala	Ile	Glu	Asp	Ala	Asn	Leu	Ser	Glu	Glu	Ser	Trp	Arg	Leu
65					70					75					80
Leu	Asp	Cys	Thr	Leu	Phe	Val	Thr	Val	Gln	His					
				85					90						

(2) INFORMATION FOR SEQ ID NO:3652:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 88 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...88

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3652:

Lys	Glu	Arg	Lys	Met	Val	Tyr	Leu	Val	Leu	Gly	Ile	Leu	Leu	Leu	Leu
1				5					10					15	
Leu	Tyr	Val	Phe	Ala	Thr	Pro	Glu	Ser	Ile	Lys	Gly	Thr	Val	Asn	Ile
			20					25					30		
Val	Ala	Met	Val	Cys	Ile	Leu	Val	Ala	Leu	Leu	Ile	Leu	Leu	Val	Leu
			35				40					45			
Ser	Phe	Leu	Lys	Ile	Phe	Gln	Leu	Pro	Thr	Glu	Ile	Phe	Leu	Ala	Ile
	50					55					60				
Ala	Met	Leu	Ile	Leu	Ala	Tyr	Phe	Ser	Val	Arg	Asp	Ile	Thr	Leu	Met
65					70					75					80
Pro	Val	Lys	Lys	Ser	Lys	Arg	Arg								
					85										

(2) INFORMATION FOR SEQ ID NO:3653:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 201 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...201
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3653:

```

Ala Arg Arg Lys Leu Thr Thr Asn Lys Asn Ser Arg Ile Gln Ala Glu
1      5      10      15
Lys Glu Arg Lys Lys Arg Asp Lys Ile Ala Lys Gln Tyr Ala Asp Asn
20      25      30
Leu Val Leu Ala Met Gly Pro Ala Glu Arg Ala Tyr Gln Asp Tyr Phe
35      40      45
Gly Phe Thr Glu Thr Leu Thr Gln Glu Glu Arg Lys Trp Glu Lys Ile
50      55      60
Leu Phe Gly Lys Asn Arg Ala Glu Arg Ala Ile Lys Ala Lys Gln Tyr
65      70      75      80
Gln Lys Glu Leu Glu Lys Asp Gln Arg Ile Ala Ser Gln Asp Pro Ile
85      90      95
Glu Arg Lys Gln Lys Gln Thr Trp Leu Leu Asn Ser Tyr Phe Arg Glu
100     105     110
Leu Pro Glu Glu Lys Ala Arg Phe Ser Arg Leu Leu Leu Glu Tyr Arg
115     120     125
Lys Asn Gly Glu Val Pro Phe Ser Thr Glu Tyr Leu Ser Asp His Leu
130     135     140
Ile Asp Phe Phe Tyr Lys Met Lys Ala Phe Glu Phe Glu Ile Ala Pro
145     150     155     160
Glu Gln Val Arg Asp Phe Leu Lys Lys Ser Leu Gln Glu Asp Tyr Arg
165     170     175
Ser Ser Ala Gln Gly Ser Trp Ile Glu Gly Ile Leu Leu Asn Cys Leu
180     185     190
Lys Pro Phe Leu Glu Arg Leu Val Ile
195     200

```

(2) INFORMATION FOR SEQ ID NO:3654:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 98 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...98

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3654:

Lys	Arg	Arg	Asn	Lys	Met	Val	Lys	Val	Leu	Ala	Ala	Cys	Gly	Asn	Gly
1			5						10					15	
Met	Gly	Ser	Ser	Met	Val	Ile	Lys	Met	Lys	Val	Glu	Asn	Ala	Leu	Arg
			20					25					30		
Lys	Leu	Asn	Gln	Thr	Asp	Phe	Thr	Val	Asn	Ser	Cys	Ser	Val	Gly	Glu
		35					40					45			
Ala	Lys	Gly	Leu	Ala	Val	Gly	Tyr	Asp	Ile	Val	Ile	Ala	Ser	Leu	His
	50					55					60				
Leu	Ile	Gln	Glu	Leu	Glu	Gly	Arg	Thr	Asn	Gly	Lys	Leu	Ile	Gly	Leu
65					70					75				80	
Asp	Asn	Leu	Met	Asp	Asp	Lys	Glu	Ile	Thr	Glu	Lys	Leu	Ser	Gln	Ala
				85					90					95	
Leu	Gln														

(2) INFORMATION FOR SEQ ID NO:3655:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...227

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3655:

Lys	Arg	Arg	Lys	Lys	Met	Lys	Lys	Phe	Val	Ala	Glu	Leu	Ile	Gly	Thr
1			5						10					15	
Phe	Met	Leu	Val	Phe	Val	Gly	Thr	Gly	Ala	Val	Val	Phe	Gly	Asn	Gly
			20					25					30		
Leu	Asp	Gly	Leu	Gly	His	Leu	Gly	Ile	Ala	Phe	Ala	Phe	Gly	Leu	Ala
		35					40					45			
Ile	Val	Val	Ala	Ala	Tyr	Ser	Ile	Gly	Thr	Val	Ser	Gly	Ala	His	Leu
	50					55					60				
Asn	Pro	Ala	Val	Ser	Ile	Ala	Met	Phe	Val	Asn	Lys	Arg	Leu	Ser	Ser
65					70					75				80	
Ser	Glu	Leu	Val	Asn	Tyr	Ile	Leu	Gly	Gln	Val	Val	Gly	Ala	Phe	Ile
				85					90					95	
Ala	Ser	Gly	Ala	Val	Phe	Phe	Leu	Leu	Ala	Asn	Ser	Gly	Met	Ser	Thr
		100						105					110		
Ala	Ser	Leu	Gly	Glu	Asn	Ala	Leu	Ala	Asn	Gly	Val	Thr	Val	Phe	Gly
		115					120					125			
Gly	Phe	Leu	Phe	Glu	Val	Ile	Ala	Thr	Phe	Leu	Phe	Val	Leu	Val	Ile
	130					135					140				
Met	Thr	Val	Thr	Ser	Glu	Ser	Lys	Gly	Asn	Gly	Ala	Ile	Ala	Gly	Leu


```

145          150          155          160
Val Ile Gly Leu Ser Leu Met Ala Met Ile Leu Val Gly Leu Lys Ile
          165          170          175
Thr Gly Leu Ser Val Asn Pro Ala Arg Ser Leu Ala Pro Ala Val Leu
          180          185          190
Val Gly Gly Ala Ala Leu Gln Gln Val Trp Ile Phe Ile Leu Ala Pro
          195          200          205
Ile Ala Gly Gly Val Leu Ala Ala Leu Val Ala Lys Asn Phe Leu Gly
          210          215          220
Thr Glu Glu
225

```

(2) INFORMATION FOR SEQ ID NO:3656:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 419 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...419

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3656:

```

Tyr Asn Gly Lys Asn Lys Phe Lys Arg Ser Phe Phe Met Thr Tyr Pro
1          5          10          15
Asn Leu Leu Asp Arg Phe Leu Thr Tyr Val Lys Val Asn Thr Arg Ser
          20          25          30
Asp Glu His Ser Thr Thr Thr Pro Ser Thr Gln Ser Gln Val Asp Phe
          35          40          45
Ala Thr Asn Val Leu Ile Pro Glu Met Lys Arg Val Gly Leu Gln Asn
          50          55          60
Val Tyr Tyr Leu Pro Asn Gly Phe Ala Ile Gly Thr Leu Pro Ala Asn
          65          70          75          80
Asp Pro Ser Leu Thr Arg Lys Ile Gly Phe Ile Ser His Met Asp Thr
          85          90          95
Ala Asp Phe Asn Ala Glu Gly Val Asn Pro Gln Val Ile Glu Asn Tyr
          100          105          110
Asp Gly Gly Val Ile Glu Leu Gly Asn Ser Gly Phe Lys Leu Asp Pro
          115          120          125
Ala Asp Phe Lys Ser Leu Glu Lys Tyr Pro Gly Gln Thr Leu Ile Thr
          130          135          140
Thr Asp Gly Thr Thr Leu Leu Gly Ala Asp Asp Lys Ser Gly Ile Ala
          145          150          155          160
Glu Ile Met Thr Ala Ile Glu Tyr Leu Thr Ala His Pro Glu Ile Lys
          165          170          175
His Cys Glu Ile Arg Val Gly Phe Gly Pro Asp Glu Glu Ile Gly Val
          180          185          190
Gly Ala Asn Lys Phe Asp Ala Glu Asp Phe Asp Val Asp Phe Ala Tyr

```

		195					200				205				
Thr	Val	Asp	Gly	Gly	Pro	Leu	Gly	Glu	Leu	Gln	Tyr	Glu	Thr	Phe	Ser
	210						215				220				
Ala	Ala	Gly	Ala	Glu	Leu	His	Phe	Gln	Gly	Arg	Asn	Val	His	Pro	Gly
225						230				235					240
Thr	Ala	Lys	Gly	Gln	Met	Val	Asn	Ala	Leu	Gln	Leu	Ala	Ile	Asp	Phe
			245						250					255	
His	Asn	Gln	Leu	Pro	Glu	Asn	Asp	Arg	Pro	Glu	Leu	Thr	Glu	Gly	Tyr
		260						265					270		
Gln	Gly	Phe	Tyr	His	Leu	Met	Asp	Val	Thr	Gly	Ser	Val	Glu	Glu	Ala
	275						280					285			
Arg	Ala	Ser	Tyr	Ile	Ile	Arg	Asp	Phe	Glu	Lys	Asp	Ala	Phe	Glu	Ala
	290					295					300				
Arg	Lys	Ala	Ser	Met	Gln	Ser	Ile	Ala	Asp	Lys	Met	Asn	Glu	Glu	Leu
305					310					315					320
Gly	Ser	Asn	Arg	Val	Thr	Leu	Asn	Leu	Thr	Asp	Gln	Tyr	Tyr	Asn	Met
			325						330					335	
Lys	Glu	Val	Ile	Glu	Lys	Asp	Met	Thr	Pro	Ile	Thr	Val	Ala	Lys	Ala
		340						345				350			
Val	Met	Glu	Asp	Leu	Gly	Ile	Thr	Pro	Ile	Ile	Glu	Pro	Ile	Arg	Gly
	355						360					365			
Gly	Thr	Asp	Gly	Ser	Lys	Ile	Ser	Phe	Met	Gly	Ile	Pro	Thr	Pro	Asn
	370					375					380				
Ile	Phe	Ala	Gly	Gly	Glu	Asn	Met	His	Gly	Arg	Phe	Glu	Tyr	Val	Ser
385					390					395					400
Leu	Gln	Thr	Met	Glu	Arg	Ala	Val	Asp	Thr	Ile	Ile	Gly	Ile	Val	Ala
			405						410					415	
Tyr	Lys	Gly													

(2) INFORMATION FOR SEQ ID NO:3657:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 263 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3657:

Glu	Asp	Gly	Asn	Met	Lys	Lys	Asn	Ser	Leu	Tyr	Ile	Ile	Ser	Ser	Leu
1				5					10					15	
Phe	Phe	Ala	Cys	Val	Leu	Phe	Val	Tyr	Ala	Thr	Ala	Thr	Asn	Phe	Gln
			20					25					30		
Asn	Ser	Thr	Ser	Ala	Arg	Gln	Val	Lys	Thr	Glu	Thr	Tyr	Thr	Asn	Thr
		35				40					45				
Val	Thr	Asn	Val	Pro	Ile	Asp	Ile	Arg	Tyr	Asn	Ser	Asp	Lys	Tyr	Phe

50		55		60	
Ile Ser Gly Phe Ala Ser Glu Val Ser Val Val Leu Thr Gly Ala Asn					
65		70		75	80
Arg Leu Ser Leu Ala Ser Glu Met Gln Glu Ser Thr Arg Lys Phe Lys					
	85		90		95
Val Thr Ala Asp Leu Thr Asp Ala Gly Val Gly Thr Ile Glu Val Pro					
	100		105		110
Leu Ser Ile Glu Asp Leu Pro Asn Gly Leu Thr Ala Val Ala Thr Pro					
	115		120		125
Gln Lys Ile Thr Val Lys Ile Gly Lys Lys Ala Gln Lys Asp Lys Val					
	130		135		140
Lys Ile Val Pro Glu Ile Asp Pro Ser Gln Ile Asp Ser Arg Val Gln					
145		150		155	160
Ile Glu Asn Val Met Val Ser Asp Lys Glu Val Ser Ile Thr Ser Asp					
	165		170		175
Gln Glu Thr Leu Asp Arg Ile Asp Lys Ile Ile Ala Val Leu Pro Thr					
	180		185		190
Ser Glu Arg Ile Thr Gly Asn Tyr Ser Gly Ser Val Pro Leu Gln Ala					
	195		200		205
Ile Asp Arg Asn Gly Val Val Leu Pro Ala Val Ile Thr Pro Phe Asp					
210		215		220	
Thr Ile Met Lys Val Thr Thr Lys Pro Val Ala Pro Ser Ser Ser Thr					
225		230		235	240
Ser Asn Ser Ser Thr Ser Ser Ser Ser Glu Thr Ser Ser Ser Thr Lys					
	245		250		255
Ala Thr Ser Ser Lys Thr Asn					
	260				

(2) INFORMATION FOR SEQ ID NO:3658:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...158

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3658:

Asn Lys Gly Lys Gly Glu Arg Arg Met Lys Val Ile Phe Leu Ala Asp	
1	5 10 15
Val Lys Gly Lys Gly Lys Lys Gly Glu Ile Lys Glu Val Pro Thr Gly	
	20 25 30
Tyr Ala Gln Asn Phe Leu Ile Lys Lys Asn Leu Ala Lys Glu Ala Thr	
	35 40 45
Ala Gln Ala Val Gly Glu Leu Arg Gly Lys Gln Lys Ser Glu Glu Lys	
	50 55 60
Ala His Ala Glu Met Ile Ala Glu Gly Lys Ala Ile Lys Ala Gln Leu	

65					70					75				80
Glu	Ala	Glu	Glu	Thr	Val	Val	Glu	Phe	Val	Glu	Lys	Val	Gly	Pro Asp
				85					90				95	
Gly	Arg	Thr	Phe	Gly	Ser	Ile	Thr	Asn	Lys	Lys	Ile	Ala	Glu	Leu
			100					105				110		
Gln	Lys	Gln	Phe	Gly	Ile	Lys	Ile	Asp	Lys	Arg	His	Ile	Gln	Val Gln
		115					120				125			
Ala	Pro	Ile	Arg	Ala	Val	Gly	Leu	Ile	Asp	Val	Pro	Val	Lys	Ile Tyr
	130						135				140			
Gln	Asp	Ile	Thr	Ser	Val	Ile	Asn	Leu	Arg	Val	Lys	Glu	Gly	
145					150					155				

(2) INFORMATION FOR SEQ ID NO:3659:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 521 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...521

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3659:

Leu	Lys	Gly	Asn	Thr	Met	Glu	Glu	Gln	Ser	Glu	Ile	Val	Arg	Ser	Lys
1				5					10					15	
Lys	Glu	Phe	Ala	Phe	Ala	Ser	Ser	Thr	Ile	Leu	Ser	Gln	Val	Gly	Arg
			20					25					30		
Gly	Ile	Ile	Val	Gly	Leu	Ile	Val	Gly	Ile	Ile	Val	Gly	Ser	Phe	Arg
		35					40					45			
Phe	Leu	Ile	Glu	Lys	Gly	Phe	His	Leu	Ile	Gln	Gly	Val	Tyr	Gln	Asp
	50				55					60					
Gln	Gly	Tyr	Leu	Val	Arg	Asn	Leu	Phe	Val	Leu	Val	Leu	Phe	Tyr	Ile
65				70					75					80	
Leu	Ile	Cys	Trp	Leu	Ser	Ala	Lys	Leu	Thr	Arg	Ser	Glu	Lys	Asp	Ile
			85						90				95		
Lys	Gly	Ser	Gly	Ile	Pro	Gln	Val	Glu	Ala	Glu	Leu	Lys	Gly	Leu	Met
			100					105					110		
Ser	Leu	Asn	Trp	Trp	Gly	Ile	Leu	Trp	Lys	Lys	Tyr	Val	Leu	Gly	Ile
		115					120					125			
Leu	Ala	Ile	Ala	Ser	Gly	Leu	Met	Leu	Gly	Arg	Glu	Gly	Pro	Ser	Ile
	130					135					140				
Gln	Leu	Gly	Ala	Val	Gly	Gly	Lys	Gly	Ile	Ala	Lys	Trp	Leu	Lys	Ser
145				150					155					160	
Ser	Pro	Val	Glu	Glu	Arg	Ser	Leu	Ile	Ala	Ser	Gly	Ala	Ala	Ala	Gly
			165					170					175		
Leu	Ala	Ala	Ala	Phe	Asn	Ala	Pro	Ile	Ala	Ala	Leu	Leu	Phe	Val	Val
		180					185						190		
Glu	Glu	Val	Tyr	His	His	Phe	Ser	Arg	Phe	Phe	Trp	Val	Ser	Thr	Leu

(A) NAME/KEY: misc_feature

(B) LOCATION 1...422

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3660:

Val	Gly	Gly	Asn	Met	Lys	Ala	Glu	Ile	Ile	Ala	Val	Gly	Thr	Glu	Ile
1				5					10					15	
Leu	Thr	Gly	Gln	Ile	Val	Asn	Thr	Asn	Ala	Gln	Phe	Leu	Ser	Glu	Lys
			20					25					30		
Leu	Ala	Glu	Ile	Gly	Val	Asp	Val	Tyr	Phe	Gln	Thr	Ala	Val	Gly	Asp
		35					40					45			
Asn	Glu	Val	Arg	Leu	Leu	Ser	Leu	Leu	Glu	Ile	Ala	Ser	Gln	Arg	Ser
	50					55					60				
Ser	Leu	Val	Ile	Leu	Thr	Gly	Gly	Leu	Gly	Pro	Thr	Glu	Asp	Asp	Leu
65					70					75					80
Thr	Lys	Gln	Thr	Leu	Ala	Lys	Phe	Leu	Gly	Lys	Ala	Leu	Val	Phe	Asp
			85						90					95	
Pro	Gln	Ala	Gln	Glu	Lys	Leu	Asp	Ile	Phe	Phe	Ala	Leu	Arg	Pro	Asp
		100						105					110		
Tyr	Ala	Arg	Thr	Pro	Asn	Asn	Glu	Arg	Gln	Ala	Gln	Ile	Val	Glu	Gly
	115						120					125			
Ala	Ile	Pro	Leu	Pro	Asn	Glu	Thr	Gly	Leu	Ala	Val	Gly	Gly	Lys	Leu
	130					135					140				
Glu	Val	Asp	Gly	Val	Thr	Tyr	Val	Val	Leu	Pro	Gly	Pro	Pro	Ser	Glu
145					150					155					160
Leu	Lys	Pro	Met	Val	Leu	Asn	Gln	Leu	Leu	Pro	Lys	Leu	Met	Thr	Gly
			165					170						175	
Ser	Lys	Leu	Tyr	Ser	Arg	Val	Leu	Arg	Phe	Phe	Gly	Ile	Gly	Glu	Ser
		180					185					190			
Gln	Leu	Val	Thr	Ile	Leu	Ala	Asp	Leu	Ile	Asp	Asn	Gln	Ile	Asp	Pro
	195						200					205			
Thr	Leu	Ala	Pro	Tyr	Ala	Lys	Thr	Gly	Glu	Val	Thr	Leu	Arg	Leu	Ser
	210					215					220				
Thr	Lys	Ala	Ser	Ser	Gln	Glu	Glu	Ala	Asn	Gln	Ala	Leu	Asp	Ile	Leu
225					230					235					240
Glu	Asn	Gln	Ile	Leu	Asp	Cys	Gln	Thr	Phe	Glu	Gly	Ile	Ser	Leu	Arg
			245					250						255	
Asp	Phe	Cys	Tyr	Gly	Tyr	Gly	Glu	Glu	Thr	Ser	Leu	Ala	Ser	Ile	Val
		260					265						270		
Val	Glu	Glu	Leu	Lys	Arg	Gln	Gly	Lys	Thr	Ile	Ala	Ala	Ala	Glu	Ser
	275						280					285			
Leu	Thr	Ala	Gly	Leu	Phe	Gln	Ala	Thr	Val	Ala	Asn	Phe	Ser	Gly	Ala
	290					295					300				
Ser	Ser	Ile	Phe	Lys	Gly	Gly	Phe	Val	Thr	Tyr	Ser	Leu	Glu	Glu	Lys
305					310					315					320
Ser	Arg	Met	Leu	Asp	Ile	Pro	Ala	Lys	Asn	Leu	Glu	Glu	His	Gly	Val
			325					330						335	
Val	Ser	Glu	Phe	Thr	Ala	Gln	Lys	Met	Ala	Glu	Gln	Ala	Arg	Ser	Lys
		340						345					350		
Thr	Gln	Ser	Asp	Phe	Gly	Ile	Ser	Leu	Thr	Gly	Val	Ala	Gly	Pro	Asp
	355					360						365			
Ser	Leu	Glu	Gly	His	Pro	Val	Gly	Thr	Val	Phe	Ile	Gly	Leu	Ala	Gln
	370					375					380				
Glu	Gln	Gly	Thr	Glu	Val	Ile	Lys	Val	Asn	Ile	Gly	Gly	Arg	Ser	Arg
385					390					395					400
Ala	Asp	Val	Arg	His	Ile	Ala	Val	Met	His	Ala	Phe	Asn	Leu	Val	Arg
			405					410						415	

Lys Ala Leu Leu Ser Asp
420

(2) INFORMATION FOR SEQ ID NO:3661:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...67

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3661:

Lys	Met	Gly	Lys	Lys	Lys	Glu	Asn	Gln	Ile	Glu	Lys	Leu	Pro	Leu	Tyr
1			5						10					15	
Leu	Glu	Lys	Leu	Leu	Lys	Leu	Ser	Ile	Leu	Lys	Ser	Ser	Met	Gly	Gln
			20					25					30		
Ser	Glu	Asn	Val	Leu	Glu	Lys	Gly	Ala	Ser	Lys	Arg	Phe	Ile	Leu	Pro
		35					40					45			
Thr	Met	Leu	Asn	Ser	Leu	Met	Lys	Ile	Ile	Ala	Ser	Thr	Arg	Ser	Arg
	50					55					60				
Asp	Gln	Ala													
65															

(2) INFORMATION FOR SEQ ID NO:3662:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...81

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3662:

Val	Gly	Gly	Lys	Ser	Arg	Ala	Phe	Ile	Leu	Ala	Glu	Gly	Thr	Arg	Met
1			5						10					15	
Gly	His	Ile	His	Leu	Ser	Val	Lys	Asp	Ser	Arg	Lys	Ser	Ser	Gln	Phe

		20					25				30				
Tyr	Gln	Lys	Val	Leu	Gly	Leu	Glu	Asn	Lys	Phe	Ser	Val	Pro	Gly	Ala
		35					40					45			
Ser	Trp	Ile	Ala	Ala	Gly	Asp	Tyr	His	His	His	Leu	Ala	Val	Asn	Glu
	50					55					60				
Trp	Gly	Gly	Lys	Gly	Leu	Ala	Ser	Arg	Lys	Gln	Gly	Leu	Pro	Gly	Leu
65					70					75					80
Ala															

(2) INFORMATION FOR SEQ ID NO:3663:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 89 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...89
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3663:

Lys	Gln	Cys	Phe	Glu	Gln	Pro	Ala	Ala	Ser	Cys	Leu	Val	Cys	Ser	Leu
1				5					10					15	
Ile	Phe	Ile	Glu	Phe	His	Ser	Thr	Val	Thr	Tyr	Gly	Gln	Met	Leu	Ile
			20					25					30		
Leu	Leu	Phe	Phe	Tyr	Ala	Ile	Ser	Asn	Phe	Asn	Trp	Pro	Ala	Leu	Thr
		35					40					45			
Pro	Ile	Leu	Ser	Val	Leu	Pro	Ala	Thr	Lys	Ser	Pro	Leu	Arg	Arg	Ser
	50					55					60				
Ser	Ala	Asn	Leu	Ser	Ser	Thr	Ser	Val	Cys	Arg	Val	Leu	Arg	Ser	Gly
65					70					75					80
Arg	Ala	Pro	Ile	Ser	Gly	Ser	Tyr	Pro							
				85											

(2) INFORMATION FOR SEQ ID NO:3664:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 219 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...219

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3664:

Gly	Glu	Cys	Leu	Gly	Ile	Leu	Gly	Ile	Asn	Gly	Ala	Gly	Lys	Thr	Ser
1				5					10					15	
Thr	Leu	Lys	Met	Ile	Tyr	Ser	Leu	Thr	Ser	Ile	Ser	Ser	Gly	Glu	Ile
			20					25					30		
Asp	Ile	Leu	Gly	Gln	Asn	Ile	Glu	Thr	Asn	Arg	Arg	Lys	Ser	Lys	Ser
			35				40					45			
Cys	Leu	Gly	Ile	Val	Gly	Gln	Glu	Asp	Met	Leu	Asp	Met	Thr	Leu	Asn
			50			55					60				
Val	Tyr	Asp	Asn	Leu	Phe	Ala	His	Gly	Leu	Cys	Tyr	Gly	Ile	Ser	Ser
65					70					75				80	
Val	Glu	Leu	Arg	Lys	Arg	Ile	Asp	Ser	Leu	Leu	Asp	Phe	Val	Gln	Leu
				85					90					95	
Ser	Lys	His	Ala	Gln	Lys	Met	Val	Asn	Gln	Leu	Ser	Ser	Gly	Met	Arg
			100					105					110		
Arg	Arg	Leu	Val	Leu	Ala	Arg	Ala	Leu	Ile	Asn	Arg	Pro	Asp	Ile	Ile
			115				120						125		
Ile	Leu	Asp	Glu	Pro	Thr	Val	Gly	Leu	Asp	Ile	Gln	Ser	Arg	Asn	Ile
			130			135					140				
Ile	Trp	Asp	Lys	Leu	Leu	Glu	Leu	Lys	Glu	Leu	Gly	Val	Ser	Ile	Ile
145				150						155				160	
Ile	Thr	Ser	His	Tyr	Met	Asn	Glu	Ile	Glu	Tyr	Leu	Thr	Asp	Arg	Val
				165					170					175	
Leu	Met	Leu	His	Gln	Gly	Thr	Ile	Lys	Glu	Glu	Gly	Thr	Val	Glu	Asp
			180					185					190		
Leu	Leu	Ile	Lys	Tyr	Asp	Ala	Asp	Asn	Leu	Glu	Thr	Leu	Phe	Leu	Gly
			195				200						205		
Leu	Thr	Gly	Thr	Glu	Lys	Glu	Asp	Leu	His	Val					
			210			215									

(2) INFORMATION FOR SEQ ID NO:3665:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 130 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3665:

Ser Ser Leu Lys Ile Phe Pro Ser Phe Asn Ile Asn Ala Arg Ser Val

1		5		10		15
Phe	Glu	Ala	Asn	Ser	Ile	Pro
		20			25	30
Ala	Pro	Thr	Asn	Ser	Leu	Thr
	35			40		45
Leu	Ser	Lys	Ala	Pro	Val	Ser
	50			55		60
Ala	Ile	Asn	Ala	Leu	Ala	Thr
65			70			75
Arg	Val	Pro	Thr	Lys	Ser	Phe
			85			90
Ser	Lys	Phe	Ser	Thr	Phe	Leu
		100			105	
Lys	Gly	Ser	Ala	Ile	Phe	Ser
	115			120		125
Tyr	Ala					
	130					

(2) INFORMATION FOR SEQ ID NO:3666:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 178 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...178

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3666:

Lys	Thr	Leu	Lys	Glu	Arg	Lys	Lys	Met	Asn	Leu	Lys	Asp	Tyr	Ile	Ala
1			5					10						15	
Thr	Ile	Glu	Asn	Tyr	Pro	Lys	Glu	Gly	Ile	Thr	Phe	Arg	Asp	Ile	Ser
		20					25					30			
Pro	Leu	Met	Ala	Asp	Gly	Asn	Ala	Tyr	Ser	Tyr	Ala	Val	Arg	Glu	Ile
		35				40					45				
Val	Gln	Tyr	Ala	Thr	Asp	Lys	Lys	Val	Asp	Met	Ile	Val	Gly	Pro	Glu
	50					55				60					
Ala	Arg	Gly	Phe	Ile	Val	Gly	Cys	Pro	Val	Ala	Phe	Glu	Leu	Gly	Ile
65					70					75					80
Gly	Phe	Ala	Pro	Val	Arg	Lys	Pro	Gly	Lys	Leu	Pro	Arg	Glu	Val	Ile
				85				90					95		
Ser	Ala	Asp	Tyr	Glu	Lys	Glu	Tyr	Gly	Val	Asp	Thr	Leu	Thr	Met	His
		100						105				110			
Ala	Asp	Ala	Ile	Lys	Pro	Gly	Gln	Arg	Val	Leu	Ile	Val	Asp	Asp	Leu
	115					120				125					
Leu	Ala	Thr	Gly	Gly	Thr	Val	Lys	Ala	Thr	Ile	Glu	Met	Ile	Glu	Lys

[illegible]

(2) INFORMATION FOR SEQ ID NO:3667:

- ```
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 63 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...63

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3667:
```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Ser | Leu | Asn | Trp | Ile | Phe | Ala | Glu | Cys | Lys | Leu | Leu | Lys | Leu | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Cys | His | Thr | Met | Tyr | Thr | Thr | Trp | Ala | Leu | Val | Val | Ala | Asn | Cys | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Tyr | Asn | Ile | Arg | Arg | Val | Leu | Trp | Gly | Lys | Ala | Ile | Gly | Ile | Gly |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Glu | Phe | Ile | Ala | Phe | Val | Ser | Leu | Leu | Trp | Glu | Leu | Ala | Gln |     |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:3668:

- ```
(i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 64 amino acids
      (B) TYPE: amino acid
      (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
      (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:
      (A) NAME/KEY: misc_feature
      (B) LOCATION 1...64

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3668:
```

Arg	Gly	Leu	Lys	Arg	Phe	Ser	Lys	Ser	Ile	Arg	Arg	Lys	Arg	Met	Lys
1				5					10					15	
Glu	Ile	Ala	Phe	Asp	Ala	Phe	Tyr	Gln	Leu	Tyr	Gln	Asn	Asp	Gln	Leu
			20					25					30		
Ser	Leu	Val	Asp	Val	Arg	Glu	Val	Asp	Glu	Phe	Ala	Ala	Leu	His	Leu
		35					40					45			
Glu	Gly	Ala	His	Asn	Leu	Pro	Leu	Ser	Gln	Leu	Ala	Asp	Ser	Tyr	Asp
	50					55					60				

(2) INFORMATION FOR SEQ ID NO:3669:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 175 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3669:

Arg	Gly	Leu	Lys	Arg	Phe	Leu	Lys	Ser	Ile	Asn	Lys	Gly	Val	Gln	Glu
1				5					10					15	
Val	Arg	Leu	Ile	Leu	Tyr	Glu	Lys	Gln	Gly	Glu	Lys	Phe	Met	Lys	Val
			20					25					30		
Glu	Leu	Gln	Ile	Ser	Glu	Thr	Tyr	Glu	Glu	Glu	Lys	Leu	Ile	Val	Gln
		35					40					45			
Ala	Pro	Gln	Pro	Thr	Asp	Lys	Val	Gln	Lys	Val	Ile	Glu	Phe	Ala	Glu
	50					55					60				
Asn	Leu	Asp	Gln	Arg	Glu	Lys	Ile	Lys	Gly	Lys	Ser	Asp	Asp	Gln	Val
65					70				75					80	
Tyr	Leu	Val	Glu	Ile	Gly	Lys	Ile	Gln	Arg	Phe	Tyr	Ile	Glu	Asn	Arg
			85					90					95		
Lys	Val	Leu	Ala	Glu	Thr	Ala	Ser	Gln	Thr	Tyr	Ser	Ile	Asp	Leu	Arg
		100						105					110		
Leu	Tyr	Gln	Val	Pro	Lys	Leu	Leu	Pro	Ser	Asn	Phe	Ile	Gln	Ile	Ser
		115					120					125			
Gln	Ser	Glu	Ile	Ile	Asn	Ile	Asp	Ser	Ile	Ser	His	Leu	Lys	Leu	Thr
	130					135					140				
Pro	Asn	Gly	Leu	Val	Glu	Ile	Phe	Leu	Lys	Asn	Glu	Ser	Phe	Thr	Tyr
145					150				155					160	
Ser	Ser	Arg	Arg	Tyr	Leu	Lys	Thr	Ile	Lys	Glu	Lys	Leu	Glu	Leu	
				165				170					175		

(2) INFORMATION FOR SEQ ID NO:3670:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 amino acids

(B) TYPE: amino acid

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...139
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3670:

```

Arg Gly Leu Lys Arg Phe Ser Lys Ser Ile Ile Leu Asp Ser Asn Gln
1      5      10      15
Lys Ala Leu Tyr Asn Ser Asn Met Lys Ser Thr Lys Glu Glu Ile Gln
20     25     30
Thr Ile Lys Thr Leu Leu Lys Asp Ser Arg Thr Ala Lys Tyr His Lys
35     40     45
Arg Leu Gln Ile Val Leu Phe Arg Leu Met Gly Lys Ser Tyr Lys Glu
50     55     60
Ile Ile Glu Leu Leu Asp Cys Asn Gln Thr Thr Ile Trp Arg Asn Val
65     70     75     80
Lys Lys Tyr Glu Glu Phe Gly Leu Asp Ser Leu Leu Gln Glu Thr Arg
85     90     95
Gly Gly Arg Asn His Ala Tyr Met Thr Val Glu Glu Glu Lys Ala Phe
100    105    110
Leu Ala Arg His Leu Lys Ala Thr Glu Ala Gly Glu Phe Val Thr Ile
115    120    125
Pro Tyr Phe Arg Leu Ile Ser Phe Leu His Thr
130    135

```

(2) INFORMATION FOR SEQ ID NO:3671:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 228 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...228
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3671:

```

Arg Gly Leu Lys Arg Phe Ser Lys Ser Ile Ser Thr Phe Phe Glu Ile
1      5      10      15
Gly Ala Ser Met Lys Ile His Lys Thr Val Asn Pro Val Ala Tyr Glu

```

		20					25				30						
Asn	Thr	Tyr	Tyr	Leu	Glu	Gly	Glu	Lys	His	Leu	Ile	Val	Val	Asp	Pro		
		35					40					45					
Gly	Ser	His	Trp	Glu	Ala	Ile	Arg	Gln	Thr	Ile	Glu	Lys	Ile	Asn	Lys		
		50				55					60						
Pro	Ile	Cys	Ala	Ile	Leu	Leu	Thr	His	Ala	His	Tyr	Asp	His	Ile	Met		
65					70					75					80		
Ser	Leu	Asp	Leu	Val	Arg	Glu	Thr	Phe	Gly	Asn	Pro	Pro	Val	Tyr	Ile		
				85					90					95			
Ala	Glu	Ser	Glu	Ala	Ser	Trp	Leu	Tyr	Thr	Pro	Val	Asp	Asn	Leu	Ser		
			100					105					110				
Gly	Leu	Pro	Arg	His	Asp	Asp	Met	Ala	Asp	Val	Val	Thr	Lys	Pro	Ala		
		115					120					125					
Glu	His	Thr	Phe	Val	Phe	His	Glu	Glu	Tyr	Gln	Leu	Glu	Glu	Phe	Arg		
		130				135					140						
Phe	Lys	Val	Leu	Pro	Thr	Pro	Gly	His	Ser	Ile	Gly	Gly	Val	Ser	Leu		
145					150				155						160		
Val	Phe	Pro	Asp	Ala	His	Leu	Val	Leu	Thr	Gly	Asp	Ala	Leu	Phe	Arg		
				165					170					175			
Glu	Thr	Ile	Gly	Arg	Thr	Asp	Leu	Pro	Thr	Gly	Ser	Met	Glu	Gln	Leu		
			180				185						190				
Leu	His	Ser	Ile	Gln	Thr	Gln	Leu	Phe	Thr	Leu	Pro	Asn	Tyr	Asp	Val		
		195				200						205					
Tyr	Pro	Gly	His	Gly	Pro	Ala	Thr	Thr	Ile	Ala	His	Glu	Lys	Ala	Phe		
	210					215					220						
Asn	Pro	Phe	Phe														
225																	

(2) INFORMATION FOR SEQ ID NO:3672:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...78

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3672:

Val	Leu	Leu	Lys	Phe	Phe	Val	Ser	Gln	Ile	Asn	Cys	Trp	Gln	Arg	Cys		
1				5					10					15			
Met	Arg	Arg	Gly	Ala	His	Gln	Leu	Phe	Phe	Leu	Asp	Ile	Glu	Ile	Arg		
			20					25					30				
His	Glu	Glu	Met	Lys	Gly	Leu	Asp	Val	Ala	Arg	Lys	Ile	Arg	Asp	Arg		
		35					40					45					
Asp	Ser	Tyr	Ala	Leu	Ile	Val	Leu	Val	Thr	Ser	Ser	Leu	Glu	Val	Tyr		
	50					55					60						
Ala	Pro	Val	Leu	Ser	Leu	Pro	Ser	Val	Cys	Ser	Gly	Leu	Tyr				

(2) INFORMATION FOR SEQ ID NO:3673:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...63

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3673:

```

Leu Leu Leu Lys Trp Asn Gly Ala Arg Glu Lys Leu Ser Thr Lys Thr
1      5      10      15
Val Pro Arg Leu Thr Lys Lys Ser Lys Ser Arg Arg Arg Tyr Leu Asn
      20      25      30
Pro Val Val Lys Lys Ile Lys Glu Asp Val Arg Gly Ile Thr Asp Leu
      35      40      45
Pro His Pro Ile Phe Thr Gly Phe Asp Cys Leu Lys Tyr Asn Gln
      50      55      60

```

(2) INFORMATION FOR SEQ ID NO:3674:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...63

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3674:

```

Phe Ser Leu Asn Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys
1      5      10      15
Lys Trp Gly Lys Lys Asn Lys Lys Lys Lys Lys Lys Lys Lys Lys
      20      25      30
Lys Lys Lys Lys Lys Arg Glu Lys Lys Lys Lys Arg Glu Lys Arg Arg
      35      40      45

```

Gly Gly Arg Lys Arg Gly Gly Arg Glu Arg Arg Lys Lys Glu Gly
 50 55 60

(2) INFORMATION FOR SEQ ID NO:3675:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...83

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3675:

Asn	Ala	Leu	Lys	Lys	Leu	Leu	Pro	Phe	Val	Val	Phe	Gln	Phe	Leu	Ile
1				5					10					15	
Trp	His	Lys	Lys	Gly	Asp	Lys	Met	Ala	Gln	Ile	Lys	Ile	Thr	Leu	Thr
			20					25					30		
Lys	Ser	Pro	Ile	Gly	Arg	Ile	Pro	Ser	Gln	Arg	Lys	Thr	Val	Val	Ala
		35				40					45				
Leu	Gly	Leu	Gly	Lys	Leu	Asn	Ser	Ser	Val	Ile	Lys	Glu	Asp	Asn	Ala
	50				55				60						
Ala	Ile	Arg	Gly	Met	Ile	Thr	Ala	Val	Ser	His	Leu	Val	Thr	Val	Glu
65					70				75						80
Glu	Val	Asn													

(2) INFORMATION FOR SEQ ID NO:3676:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1769 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1769

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3676:

Lys	Phe	Met	Asn	Lys	Gly	Leu	Phe	Glu	Lys	Arg	Cys	Lys	Tyr	Ser	Ile
1			5					10						15	
Arg	Lys	Phe	Ser	Leu	Gly	Val	Ala	Ser	Val	Met	Ile	Gly	Ala	Ala	Phe
		20						25					30		
Phe	Gly	Thr	Ser	Pro	Val	Leu	Ala	Asp	Ser	Val	Gln	Ser	Gly	Ser	Thr
		35					40					45			
Ala	Asn	Leu	Pro	Ala	Asp	Leu	Ala	Thr	Ala	Leu	Ala	Thr	Ala	Lys	Glu
	50					55					60				
Asn	Asp	Gly	Arg	Asp	Phe	Glu	Ala	Pro	Lys	Val	Gly	Glu	Asp	Gln	Gly
65					70					75					80
Ser	Pro	Glu	Val	Thr	Asp	Gly	Pro	Lys	Thr	Glu	Glu	Glu	Leu	Leu	Ala
				85					90					95	
Leu	Glu	Lys	Glu	Lys	Pro	Ala	Glu	Glu	Lys	Pro	Lys	Glu	Asp	Lys	Pro
			100					105					110		
Ala	Ala	Ala	Lys	Pro	Glu	Thr	Pro	Lys	Thr	Val	Thr	Pro	Glu	Trp	Gln
		115					120						125		
Thr	Val	Glu	Lys	Lys	Glu	Gln	Gln	Gly	Thr	Val	Thr	Ile	Arg	Glu	Glu
		130				135						140			
Lys	Gly	Val	Arg	Tyr	Asn	Gln	Leu	Ser	Ser	Thr	Ala	Gln	Asn	Asp	Asn
145					150					155					160
Ala	Gly	Lys	Pro	Ala	Leu	Phe	Glu	Lys	Lys	Gly	Leu	Thr	Val	Asp	Ala
				165					170					175	
Asn	Gly	Asn	Ala	Thr	Val	Asp	Leu	Thr	Phe	Lys	Glu	Asp	Ser	Glu	Lys
			180					185						190	
Gly	Lys	Ser	Arg	Phe	Gly	Val	Phe	Leu	Lys	Phe	Lys	Asp	Thr	Asn	Asn
		195				200						205			
Asn	Val	Phe	Val	Gly	Tyr	Asp	Lys	Asp	Gly	Trp	Phe	Trp	Glu	Tyr	Lys
	210					215					220				
Ser	Pro	Thr	Thr	Ser	Thr	Trp	Tyr	Arg	Gly	Ser	Arg	Val	Ala	Ala	Pro
225					230					235					240
Glu	Thr	Gly	Ser	Thr	Asn	Arg	Leu	Ser	Ile	Thr	Leu	Lys	Ser	Asp	Gly
				245					250					255	
Gln	Leu	Asn	Ala	Ser	Asn	Asn	Asp	Val	Asn	Leu	Phe	Asp	Thr	Val	Thr
			260					265					270		
Leu	Pro	Ala	Ala	Val	Asn	Asp	His	Leu	Lys	Asn	Glu	Lys	Lys	Ile	Leu
		275					280					285			
Leu	Lys	Ala	Gly	Ser	Tyr	Asp	Asp	Glu	Arg	Thr	Val	Val	Ser	Val	Lys
	290					295					300				
Thr	Asp	Asn	Gln	Glu	Arg	Val	Lys	Thr	Glu	Asp	Thr	Pro	Ala	Gln	Lys
305					310					315					320
Glu	Thr	Gly	Pro	Val	Val	Asp	Asp	Arg	Lys	Val	Thr	Tyr	Asp	Thr	Ile
				325					330					335	
Gln	Ser	Lys	Val	Leu	Lys	Ala	Val	Ile	Asp	Gln	Ala	Phe	Pro	Arg	Val
			340					345					350		
Lys	Glu	Tyr	Thr	Leu	Asn	Gly	His	Thr	Leu	Pro	Gly	Gln	Val	Gln	Gln
		355					360					365			
Phe	Asn	Gln	Val	Phe	Ile	Asn	Asn	His	Arg	Ile	Thr	Pro	Glu	Val	Thr
	370					375				380					
Tyr	Lys	Lys	Ile	Asn	Glu	Thr	Thr	Ala	Glu	Tyr	Leu	Met	Lys	Leu	Arg
385					390					395					400
Asp	Asp	Ala	His	Leu	Ile	Asn	Ala	Glu	Met	Thr	Val	Arg	Leu	Gln	Val
				405					410					415	
Val	Asp	Asn	Gln	Leu	His	Phe	Asp	Val	Thr	Lys	Ile	Val	Asn	His	Asn
			420					425					430		
Gln	Val	Thr	Pro	Gly	Gln	Lys	Ile	Asp	Asp	Glu	Arg	Lys	Leu	Leu	Ser
		435					440					445			
Ser	Ile	Ser	Phe	Leu	Gly	Asn	Ala	Leu	Val	Ser	Val	Ser	Ser	Asp	Gln

450	455	460
Thr Gly Ala Lys Phe Asp	Gly Ala Thr Met Ser Asn Asn Thr His Val	
465	470	475
Ser Gly Asp Asp His Ile Asp	Val Thr Asn Pro Met Lys Asp Leu Ala	480
	485	490
Lys Gly Tyr Met Tyr Gly Phe Val	Ser Thr Asp Lys Leu Ala Ala Gly	495
	500	505
Val Trp Ser Asn Ser Gln Asn Ser	Tyr Gly Gly Gly Ser Asn Asp Trp	510
	515	520
Thr Arg Leu Thr Ala Tyr Lys Glu Thr	Val Gly Asn Ala Asn Tyr Val	525
	530	535
Gly Ile His Ser Ser Glu Trp Gln Trp	Glu Lys Ala Tyr Lys Gly Ile	540
545	550	555
Val Phe Pro Glu Tyr Thr Lys Glu Leu	Pro Ser Ala Lys Val Val Ile	560
	565	570
Thr Glu Asp Ala Asn Ala Asp Lys Lys	Val Asp Trp Gln Asp Gly Ala	575
	580	585
Ile Ala Tyr Arg Ser Ile Met Asn Asn	Pro Gln Gly Trp Glu Lys Val	590
	595	600
Lys Asp Ile Thr Ala Tyr Arg Ile Ala	Met Asn Phe Gly Ser Gln Ala	605
610	615	620
Gln Asn Pro Phe Leu Met Thr Leu Asp	Gly Ile Lys Lys Ile Asn Leu	625
625	630	635
His Thr Asp Gly Leu Gly Gln Gly Val	Leu Leu Lys Gly Tyr Gly Ser	640
	645	650
Glu Gly His Asp Ser Gly His Leu Asn	Tyr Ala Asp Ile Gly Lys Arg	655
	660	665
Ile Gly Gly Val Glu Asp Phe Lys Thr	Leu Ile Glu Lys Ala Lys Lys	670
	675	680
Tyr Gly Ala His Leu Gly Ile His Val	Asn Ala Ser Glu Thr Tyr Pro	685
690	695	700
Glu Ser Lys Tyr Phe Asn Glu Lys Ile	Leu Arg Lys Asn Pro Asp Gly	705
705	710	715
Ser Tyr Ser Tyr Gly Trp Asn Trp Leu	Asp Gln Gly Ile Asn Ile Asp	720
	725	730
Ala Ala Tyr Asp Leu Ala His Gly Arg	Leu Ala Arg Trp Glu Asp Leu	735
	740	745
Lys Lys Lys Leu Gly Asp Gly Leu Asp	Phe Ile Tyr Val Asp Val Trp	750
	755	760
Gly Asn Gly Gln Ser Gly Asp Asn Gly	Ala Trp Ala Thr His Val Leu	765
770	775	780
Ala Lys Glu Ile Asn Lys Gln Gly Trp	Arg Phe Ala Ile Glu Trp Gly	785
785	790	795
His Gly Gly Glu Tyr Asp Ser Thr Phe	His His Trp Ala Ala Asp Leu	800
	805	810
Thr Tyr Gly Gly Tyr Thr Asn Lys Gly	Ile Asn Ser Ala Ile Thr Arg	815
	820	825
Phe Ile Arg Asn His Gln Lys Asp Ala	Trp Val Gly Asp Tyr Arg Ser	830
	835	840
Tyr Gly Gly Ala Ala Asn Tyr Pro Leu	Leu Gly Gly Tyr Ser Met Lys	845
850	855	860
Asp Phe Glu Gly Trp Gln Gly Arg Ser	Asp Tyr Asn Gly Tyr Val Thr	865
865	870	875
Asn Leu Phe Ala His Asp Val Met Thr	Lys Tyr Phe Gln His Phe Thr	880
	885	890
Val Ser Lys Trp Glu Asn Gly Thr Pro	Val Thr Met Thr Asp Asn Gly	895
	900	905
		910

Ser	Thr	Tyr	Lys	Trp	Thr	Pro	Glu	Met	Arg	Val	Glu	Leu	Val	Asp	Ala	915	920	925
Asp	Asn	Asn	Lys	Val	Val	Val	Thr	Arg	Lys	Ser	Asn	Asp	Val	Asn	Ser	930	935	940
Pro	Leu	Tyr	Arg	Glu	Arg	Thr	Val	Thr	Leu	Asn	Gly	Arg	Val	Ile	Gln	945	950	955
Asp	Gly	Ser	Ala	Tyr	Leu	Thr	Pro	Trp	Asn	Trp	Asp	Ala	Asn	Gly	Lys	965	970	975
Lys	Leu	Ser	Thr	Asp	Lys	Glu	Lys	Met	Tyr	Tyr	Phe	Asn	Thr	Gln	Ala	980	985	990
Gly	Ala	Thr	Thr	Trp	Thr	Leu	Pro	Ser	Asp	Trp	Ala	Lys	Ser	Lys	Val	995	1000	1005
Tyr	Leu	Tyr	Lys	Leu	Thr	Asp	Gln	Gly	Lys	Thr	Glu	Glu	Gln	Glu	Leu	1010	1015	1020
Thr	Val	Lys	Asp	Gly	Lys	Ile	Thr	Leu	Asp	Leu	Leu	Ala	Asn	Gln	Pro	1025	1030	1035
Tyr	Val	Leu	Tyr	Arg	Ser	Lys	Gln	Thr	Asn	Pro	Glu	Met	Ser	Trp	Ser	1045	1050	1055
Glu	Gly	Met	His	Ile	Tyr	Asp	Gln	Gly	Phe	Asn	Ser	Gly	Thr	Leu	Lys	1060	1065	1070
His	Trp	Thr	Ile	Ser	Gly	Asp	Ala	Ser	Lys	Ala	Glu	Ile	Val	Lys	Ser	1075	1080	1085
Gln	Gly	Ala	Asn	Asp	Met	Leu	Arg	Ile	Gln	Gly	Asn	Lys	Glu	Lys	Val	1090	1095	1100
Ser	Leu	Thr	Gln	Lys	Leu	Thr	Gly	Leu	Lys	Pro	Asn	Thr	Lys	Tyr	Ala	1105	1110	1115
Val	Tyr	Val	Gly	Val	Asp	Asn	Arg	Ser	Asn	Ala	Lys	Ala	Ser	Ile	Thr	1125	1130	1135
Val	Asn	Thr	Gly	Glu	Lys	Glu	Val	Thr	Thr	Tyr	Thr	Asn	Lys	Ser	Leu	1140	1145	1150
Ala	Leu	Asn	Tyr	Val	Lys	Ala	Tyr	Ala	His	Asn	Thr	Arg	Arg	Asn	Asn	1155	1160	1165
Ala	Thr	Val	Asp	Asp	Thr	Ser	Tyr	Phe	Gln	Asn	Met	Tyr	Ala	Phe	Phe	1170	1175	1180
Thr	Thr	Gly	Ser	Asp	Val	Ser	Asn	Val	Thr	Leu	Thr	Leu	Ser	Arg	Glu	1185	1190	1195
Ala	Gly	Asp	Gln	Ala	Thr	Tyr	Phe	Asp	Glu	Ile	Arg	Thr	Phe	Glu	Asn	1205	1210	1215
Asn	Ser	Ser	Met	Tyr	Gly	Asp	Lys	His	Asp	Thr	Gly	Lys	Gly	Thr	Phe	1220	1225	1230
Lys	Gln	Asp	Phe	Glu	Asn	Val	Ala	Gln	Gly	Ile	Phe	Pro	Phe	Val	Val	1235	1240	1245
Gly	Gly	Val	Glu	Gly	Val	Glu	Asp	Asn	Arg	Thr	His	Leu	Ser	Glu	Lys	1250	1255	1260
His	Asp	Pro	Tyr	Thr	Gln	Arg	Gly	Trp	Asn	Gly	Lys	Lys	Val	Asp	Asp	1265	1270	1275
Val	Ile	Glu	Gly	Asn	Trp	Ser	Leu	Lys	Thr	Asn	Gly	Leu	Val	Ser	Arg	1285	1290	1295
Arg	Asn	Leu	Val	Tyr	Gln	Thr	Ile	Pro	Gln	Asn	Phe	Arg	Phe	Glu	Ala	1300	1305	1310
Gly	Lys	Thr	Tyr	Arg	Val	Thr	Phe	Glu	Tyr	Glu	Ala	Gly	Ser	Asp	Asn	1315	1320	1325
Thr	Tyr	Ala	Phe	Val	Val	Gly	Lys	Gly	Glu	Phe	Gln	Ser	Gly	Arg	Arg	1330	1335	1340
Gly	Thr	Gln	Ala	Ser	Asn	Leu	Glu	Met	His	Glu	Leu	Pro	Asn	Thr	Trp	1345	1350	1355
Thr	Asp	Ser	Lys	Lys	Ala	Lys	Lys	Ala	Thr	Phe	Leu	Val	Thr	Gly	Ala			

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...618

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3677:

```

Ile Ser Met Asn Lys Lys Leu Thr Asp Tyr Val Ile Asp Leu Val Glu
1      5      10      15
Ile Leu Asn Lys Gln Gln Lys Gln Val Phe Trp Gly Ile Phe Asp Ile
20      25      30
Phe Ser Met Val Val Ser Ile Ile Val Ser Tyr Ile Leu Phe Tyr Gly
35      40      45
Leu Ile Asn Pro Ala Pro Val Asp Tyr Ile Ile Tyr Thr Ser Leu Ala
50      55      60
Phe Leu Phe Tyr Gln Leu Met Ile Gly Phe Trp Gly Leu Asn Ala Ser
65      70      75      80
Ile Ser Arg Tyr Ser Lys Ile Thr Asp Phe Met Lys Ile Phe Phe Gly
85      90      95
Val Thr Ala Ser Ser Val Leu Ser Tyr Ser Ile Cys Tyr Ala Phe Leu
100     105     110
Pro Leu Phe Ser Ile Arg Phe Ile Ile Leu Phe Ile Leu Leu Ser Thr
115     120     125
Phe Leu Ile Leu Leu Pro Arg Ile Thr Trp Gln Leu Ile Tyr Ser Arg
130     135     140
Arg Lys Lys Gly Ser Gly Asp Gly Glu His Arg Arg Thr Phe Leu Ile
145     150     155     160
Gly Ala Gly Asp Gly Gly Ala Leu Phe Met Asp Ser Tyr Gln His Pro
165     170     175
Thr Ser Glu Leu Glu Leu Val Gly Ile Leu Asp Lys Asp Ser Lys Lys
180     185     190
Lys Gly Gln Lys Leu Gly Gly Ile Pro Val Leu Gly Ser Tyr Asp Asn
195     200     205
Leu Pro Glu Leu Ala Lys Arg His Gln Ile Glu Arg Val Ile Val Ala
210     215     220
Ile Pro Ser Leu Asp Pro Ser Glu Tyr Glu Arg Ile Leu Gln Met Cys
225     230     235     240
Asn Lys Leu Gly Val Lys Cys Tyr Lys Met Pro Lys Val Glu Thr Val
245     250     255
Val Gln Gly Leu His Gln Ala Gly Thr Gly Phe Gln Lys Ile Asp Ile
260     265     270
Thr Asp Leu Leu Gly Arg Gln Glu Ile Arg Leu Asp Glu Ser Arg Leu
275     280     285
Gly Ala Glu Leu Thr Gly Lys Thr Ile Leu Val Thr Gly Ala Gly Gly
290     295     300
Ser Ile Gly Ser Glu Ile Cys Arg Gln Val Ser Arg Phe Asn Pro Glu
305     310     315     320
Arg Ile Val Leu Leu Gly His Gly Glu Asn Ser Ile Tyr Leu Val Tyr
325     330     335

```

His	Glu	Leu	Ile	Arg	Lys	Phe	Gln	Gly	Ile	Asp	Tyr	Val	Pro	Val	Ile
			340					345					350		
Ala	Asp	Ile	Gln	Asp	Tyr	Asp	Arg	Leu	Leu	Gln	Val	Phe	Glu	Gln	Tyr
		355					360					365			
Lys	Pro	Ala	Ile	Val	Tyr	His	Ala	Ala	Ala	His	Lys	His	Val	Pro	Met
	370					375					380				
Met	Glu	Arg	Asn	Pro	Lys	Glu	Ala	Phe	Lys	Asn	Asn	Ile	Arg	Gly	Thr
385					390					395					400
Tyr	Asn	Val	Ala	Arg	Ala	Val	Asp	Glu	Ala	Lys	Val	Ser	Lys	Met	Val
			405						410					415	
Met	Ile	Ser	Thr	Asp	Lys	Ala	Val	Asn	Pro	Pro	Asn	Val	Met	Gly	Ala
			420					425					430		
Thr	Lys	Arg	Val	Ala	Glu	Leu	Ile	Val	Thr	Gly	Phe	Asn	Gln	Arg	Ser
		435					440					445			
Gln	Ser	Thr	Tyr	Cys	Ala	Val	Arg	Phe	Gly	Asn	Val	Leu	Gly	Ser	Arg
	450					455					460				
Gly	Ser	Val	Ile	Pro	Val	Phe	Glu	Arg	Gln	Ile	Ala	Glu	Gly	Gly	Pro
465					470					475					480
Val	Thr	Val	Thr	Asp	Phe	Arg	Met	Thr	Arg	Tyr	Phe	Met	Thr	Ile	Pro
			485						490					495	
Glu	Ala	Ser	Arg	Leu	Val	Ile	His	Ala	Gly	Ala	Tyr	Ala	Lys	Asp	Gly
			500					505					510		
Glu	Val	Phe	Ile	Leu	Asp	Met	Gly	Lys	Pro	Val	Lys	Ile	Tyr	Asp	Leu
		515					520					525			
Ala	Lys	Lys	Met	Val	Leu	Leu	Ser	Gly	His	Thr	Glu	Ser	Glu	Ile	Pro
	530					535						540			
Ile	Val	Glu	Val	Gly	Ile	Arg	Pro	Gly	Glu	Lys	Leu	Tyr	Glu	Glu	Leu
545					550					555					560
Leu	Val	Ser	Thr	Glu	Leu	Val	Asp	Asn	Gln	Val	Met	Asp	Lys	Ile	Phe
			565						570					575	
Val	Gly	Lys	Val	Asn	Val	Met	Pro	Leu	Glu	Ser	Ile	Asn	Gln	Lys	Ile
			580					585					590		
Gly	Glu	Phe	Arg	Thr	Leu	Ser	Gly	Asp	Glu	Leu	Lys	Gln	Ala	Ile	Ile
		595					600					605			
Ala	Phe	Ala	Asn	Gln	Thr	Thr	His	Ile	Glu						
	610					615									

(2) INFORMATION FOR SEQ ID NO:3678:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...437

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3678:

Tyr	Pro	Met	Lys	Gly	Val	Asn	Met	Glu	Lys	Gln	Gln	Pro	Ser	Lys	Ala
1			5					10						15	
Ala	Leu	Leu	Ser	Ile	Ile	Pro	Gly	Leu	Gly	Gln	Ile	Tyr	Asn	Lys	Gln
			20					25					30		
Lys	Ala	Lys	Gly	Phe	Ile	Phe	Leu	Gly	Val	Thr	Ile	Val	Phe	Val	Leu
		35					40					45			
Tyr	Phe	Leu	Ala	Leu	Ala	Thr	Pro	Glu	Leu	Ser	Asn	Leu	Ile	Thr	Leu
	50					55					60				
Gly	Asp	Lys	Pro	Gly	Arg	Asp	Asn	Ser	Leu	Phe	Met	Leu	Ile	Arg	Gly
65				70						75				80	
Ala	Phe	His	Leu	Ile	Phe	Val	Ile	Val	Tyr	Val	Leu	Phe	Tyr	Phe	Ser
			85						90					95	
Asn	Ile	Lys	Asp	Ala	His	Thr	Ile	Ala	Lys	Arg	Ile	Asn	Asn	Gly	Ile
		100						105					110		
Pro	Val	Pro	Arg	Thr	Leu	Lys	Asp	Met	Ile	Lys	Gly	Ile	Tyr	Glu	Asn
		115					120					125			
Gly	Phe	Pro	Tyr	Leu	Leu	Ile	Ile	Pro	Ser	Tyr	Val	Ala	Met	Thr	Phe
	130					135					140				
Ala	Ile	Ile	Phe	Pro	Val	Ile	Val	Thr	Leu	Met	Ile	Ala	Phe	Thr	Asn
145				150						155					160
Tyr	Asp	Phe	Gln	His	Leu	Pro	Pro	Asn	Lys	Leu	Leu	Asp	Trp	Val	Gly
			165					170						175	
Leu	Thr	Asn	Phe	Thr	Asn	Ile	Trp	Ser	Leu	Ser	Thr	Phe	Arg	Ser	Ala
		180					185					190			
Phe	Gly	Ser	Val	Leu	Ser	Trp	Thr	Ile	Ile	Trp	Ala	Leu	Ala	Ala	Ser
	195					200					205				
Thr	Leu	Gln	Ile	Val	Ile	Gly	Ile	Phe	Thr	Ala	Ile	Ile	Ala	Asn	Gln
	210					215					220				
Pro	Phe	Ile	Lys	Gly	Lys	Arg	Ile	Phe	Gly	Val	Ile	Phe	Leu	Leu	Pro
225				230						235					240
Trp	Ala	Val	Pro	Ala	Phe	Ile	Thr	Ile	Leu	Thr	Phe	Ser	Asn	Met	Phe
			245						250					255	
Asn	Asp	Ser	Val	Gly	Ala	Ile	Asn	Thr	Gln	Val	Leu	Pro	Ile	Leu	Ala
		260					265						270		
Lys	Phe	Leu	Pro	Phe	Leu	Asp	Gly	Ala	Leu	Ile	Pro	Trp	Lys	Thr	Asp
	275					280						285			
Pro	Thr	Trp	Thr	Lys	Ile	Ala	Leu	Ile	Met	Met	Gln	Gly	Trp	Leu	Gly
	290				295						300				
Phe	Pro	Tyr	Ile	Tyr	Val	Leu	Thr	Leu	Gly	Ile	Leu	Gln	Ser	Ile	Pro
305				310						315					320
Asn	Asp	Leu	Tyr	Glu	Ala	Ala	Tyr	Ile	Asp	Gly	Ala	Asn	Ala	Trp	Gln
			325						330					335	
Lys	Phe	Arg	Asn	Ile	Thr	Phe	Pro	Met	Ile	Leu	Ala	Val	Ala	Ala	Pro
		340					345						350		
Thr	Leu	Ile	Ser	Gln	Tyr	Thr	Phe	Asn	Phe	Asn	Asn	Phe	Ser	Ile	Met
	355					360						365			
Tyr	Leu	Phe	Asn	Gly	Gly	Gly	Pro	Gly	Ser	Val	Gly	Gly	Gly	Ala	Gly
	370				375						380				
Ser	Thr	Asp	Ile	Leu	Ile	Ser	Trp	Ile	Tyr	Arg	Leu	Thr	Thr	Gly	Thr
385				390						395					400
Ser	Pro	Gln	Tyr	Ser	Met	Ala	Ala	Ala	Val	Thr	Leu	Ile	Ile	Ser	Ile
			405						410					415	
Ile	Val	Ile	Ser	Ile	Ser	Met	Val	Ala	Phe	Lys	Lys	Leu	His	Ala	Phe
		420					425						430		
Asp	Met	Glu	Asp	Val											
		435													

(2) INFORMATION FOR SEQ ID NO:3679:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...218

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3679:

Asn	Thr	Met	Lys	Asp	Lys	Gln	Thr	Phe	Leu	Met	Lys	Gly	Ser	Phe	Ala	
1			5					10						15		
Leu	Leu	Leu	Phe	Val	Ile	Leu	Gly	Tyr	Met	Val	Lys	Phe	Tyr	Pro	Glu	
			20					25					30			
Met	Leu	Val	Asn	Phe	Asp	Gln	Ser	Ile	Gln	Thr	Ala	Ile	Arg	Gly	Asn	
			35				40					45				
Leu	Pro	Asn	Tyr	Leu	Thr	Ile	Leu	Phe	Arg	Ser	Leu	Thr	Arg	Leu	Ile	
			50			55					60					
Asp	Ile	Pro	Val	Ile	Ile	Thr	Trp	Val	Val	Ile	Thr	Ala	Phe	Val	Phe	
65					70					75					80	
Tyr	Arg	Lys	Arg	Trp	Lys	Ile	Lys	Ser	Phe	Phe	Met	Leu	Gly	Asn	Leu	
			85						90					95		
Ala	Leu	Ala	Gly	Leu	Leu	Ile	Val	Thr	Phe	Lys	Asn	Ile	Tyr	Gln	Arg	
			100					105					110			
Pro	Gln	Pro	Ala	Ile	Leu	His	Leu	Val	Glu	Glu	Lys	Gly	Phe	Ser	Phe	
			115				120					125				
Pro	Ser	Gly	His	Ser	Leu	Ala	Val	Thr	Leu	Met	Val	Gly	Thr	Leu	Ile	
			130			135					140					
Val	Ile	Leu	Ser	Gln	Arg	Ile	Lys	Asp	Pro	Val	Trp	Arg	Lys	Ile	Val	
145					150					155					160	
Gln	Ile	Val	Leu	Gly	Leu	Tyr	Leu	Val	Ser	Val	Leu	Val	Ser	Arg	Val	
				165					170					175		
Tyr	Leu	Gly	Val	His	Tyr	Pro	Ser	Asp	Val	Leu	Ala	Ser	Leu	Cys	Val	
			180					185					190			
Gly	Leu	Gly	Val	Leu	Phe	Ile	Glu	Phe	Pro	Phe	Tyr	Asp	Lys	Leu	Arg	
			195				200					205				
Phe	Gln	Trp	Arg	Phe	Lys	Gly	Lys	Gln	Lys							
			210				215									

(2) INFORMATION FOR SEQ ID NO:3680:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3680:

```
Asn His Met Asn Ile Thr Asn Leu Phe Ser Ile Lys Thr Gly Cys Asp
1          5          10          15
Glu Thr Asp Arg Gln Leu Gln Lys Leu Phe Phe Gln Leu Asp Leu Gln
          20          25          30
Leu Gly Glu Leu Thr Asp Gln Leu Arg Lys Leu Asp Ser Asn Phe Val
          35          40          45
Pro Arg Ser Gln Phe Val Asp Thr Leu Asp Leu Asn Asp Val Glu Tyr
          50          55          60
Lys Glu Ile Leu Asn Tyr Phe Ile Phe His Arg Asn Asp Ser Glu Glu
65          70          75          80
Ser Leu Val Glu Trp Leu Tyr Asp Trp Ile Ser Thr Asn Arg Tyr Glu
          85          90          95
Leu Pro Lys Glu Phe Ser Ile Arg Met Ala His Lys Tyr His Glu Ser
          100          105          110
Val Thr Glu Val Phe Gly Asp Glu
          115          120
```

(2) INFORMATION FOR SEQ ID NO:3681:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 81 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...81

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3681:

```
Thr Asn Met Lys Arg Ile Ala Val Leu Thr Ser Gly Gly Asp Ala Pro
1          5          10          15
Gly Met Asn Ala Ala Ile Arg Ala Val Val Arg Gln Ala Ile Ser Glu
          20          25          30
Gly Met Glu Val Phe Gly Ile Tyr Asp Gly Tyr Ala Gly Met Val Ala
          35          40          45
Gly Glu Asn Ser Ser Pro Lys Cys Ser Phe Ser Arg Gly His His Phe
          50          55          60
```

Ser Trp Trp Tyr Phe Ser Ser Leu Ser Ser Leu Ser Lys Phe Arg Ser
65 70 75 80
Thr

(2) INFORMATION FOR SEQ ID NO:3682:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 155 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3682:

Asp Asn Met Lys Gln Thr Lys Thr Thr Lys Ile Ala Leu Val Ser Leu
1 5 10 15
Leu Thr Ala Leu Ser Val Val Leu Gly Tyr Phe Leu Lys Phe Pro Thr
20 25 30
Pro Thr Gly Ile Leu Thr Leu Leu Asp Ala Gly Val Phe Phe Ala Ala
35 40 45
Phe Tyr Phe Gly Ser Arg Glu Gly Ala Val Val Gly Gly Leu Ala Ser
50 55 60
Phe Leu Ile Asp Leu Leu Ser Gly Tyr Pro Gln Trp Met Phe Phe Ser
65 70 75 80
Leu Val Asn His Gly Leu Gln Gly Phe Phe Ala Gly Phe Lys Gly Lys
85 90 95
Ser Gln Trp Leu Gly Leu Ile Leu Ala Thr Ile Ala Met Val Gly Gly
100 105 110
Tyr Ala Leu Gly Ser Thr Leu Met Asn Gly Trp Ala Ala Leu Pro
115 120 125
Glu Ile Leu Pro Asn Phe Met Gln Asn Met Val Gly Met Ile Val Gly
130 135 140
Phe Ile Leu Ser Gln Ser Ile Lys Lys Ile Lys
145 150 155

(2) INFORMATION FOR SEQ ID NO:3683:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 163 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...163

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3683:

```

Ile Ser Met Asn Leu Asn Asp Ile Lys Asp Leu Met Thr Gln Phe Asp
1          5          10          15
Gln Ser Ser Leu Arg Glu Phe Ser Tyr Lys Asn Gly Thr Asp Glu Leu
          20          25          30
Gln Phe Ser Lys Asn Glu Ala Arg Pro Val Pro Glu Val Ala Thr Gln
          35          40          45
Val Ala Pro Ala Pro Val Leu Ala Thr Pro Ser Pro Val Ala Pro Thr
          50          55          60
Ser Ala Pro Ala Glu Thr Val Ala Glu Glu Val Pro Ala Pro Ala Glu
65          70          75          80
Ala Ser Val Ala Ser Glu Gly Asn Leu Val Glu Ser Pro Leu Val Gly
          85          90          95
Val Val Tyr Leu Ala Ala Gly Pro Asp Lys Pro Ala Phe Val Thr Val
          100          105          110
Gly Asp Ser Val Lys Lys Gly Gln Thr Leu Val Ile Ile Glu Ala Met
          115          120          125
Lys Val Met Asn Glu Ile Pro Ala Pro Lys Asp Gly Val Val Thr Glu
          130          135          140
Ile Leu Val Ser Asn Glu Glu Met Val Glu Phe Gly Lys Gly Leu Val
145          150          155          160
Arg Ile Lys
  
```

(2) INFORMATION FOR SEQ ID NO:3684:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 434 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...434

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3684:

```

Arg Ser Met Lys Val Asn Leu Asp Tyr Leu Gly Arg Leu Phe Thr Glu
1          5          10          15
Asn Glu Leu Thr Glu Glu Glu Arg Gln Leu Ala Glu Lys Leu Pro Ala
          20          25          30
Met Arg Lys Glu Lys Gly Lys Leu Phe Cys Gln Arg Cys Asn Ser Thr
  
```


(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3685:

```

Arg Ser Met Lys Trp Thr Lys Ile Ile Lys Lys Ile Glu Glu Gln Ile
1      5      10      15
Glu Ala Gly Ile Tyr Pro Gly Ala Ser Phe Ala Tyr Phe Lys Asp Asn
      20      25      30
Gln Trp Thr Glu Phe Tyr Leu Gly Gln Ser Asp Pro Glu His Gly Leu
      35      40      45
Gln Thr Glu Ala Gly Leu Val Tyr Asp Leu Ala Ser Val Ser Lys Val
      50      55      60
Val Gly Val Gly Thr Val Cys Thr Phe Leu Trp Glu Ile Gly Gln Leu
65      70      75      80
Asp Ile Asp Arg Leu Val Ile Asp Phe Leu Pro Glu Ser Asp Tyr Pro
      85      90      95
Asp Ile Thr Ile Arg Gln Leu Leu Thr His Ala Thr Asp Leu Asp Pro
      100     105     110
Phe Ile Pro Asn Arg Asp Leu Leu Thr Ala Pro Glu Leu Lys Glu Ala
      115     120     125
Met Phe His Leu Asn Arg Arg Ser Gln Pro Ala Phe Leu Tyr Ser Asp
      130     135     140
Val His Phe Leu Leu Leu Gly Phe Ile Leu Glu Arg Ile Phe Asn Gln
145     150     155     160
Asp Leu Asp Val Ile Leu Lys Asp Gln Val Trp Lys Pro Trp Gly Met
      165     170     175
Thr Glu Thr Lys Phe Gly Pro Val Glu Leu Ala Val Pro Thr Val Arg
      180     185     190
Gly Val Glu Ala Gly Ile Val His Asp Pro Lys Ala Arg Leu Leu Gly
      195     200     205
Arg His Ala Gly Ser Ala Gly Leu Phe Ser Thr Ile Lys Asp Leu Gln
210     215     220
Ile Phe Leu Glu His Tyr Leu Ala Asp Asp Phe Ala Arg Asp Leu Asn
225     230     235     240
Gln Asn Phe Ser Pro Leu Asp Asp Lys Glu Arg Ser Leu Ala Trp Asn
      245     250     255
Leu Glu Gly Asp Trp Leu Asp His Thr Gly Tyr Thr Gly Thr Phe Ile
      260     265     270
Met Trp Asn Arg Gln Lys Gln Glu Ala Thr Ile Phe Leu Ser Asn Arg
      275     280     285
Thr Tyr Glu Lys Asp Glu Arg Ala Gln Trp Ile Leu Asp Arg Asn Gln
      290     295     300
Val Met Asn Leu Ile Arg Lys Glu Glu
305     310

```

(2) INFORMATION FOR SEQ ID NO:3686:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...160

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3686:

Leu	Leu	Met	Lys	Trp	Thr	Ala	Leu	Pro	Val	Arg	Ser	Ser	Lys	Lys	Leu
1			5						10				15		
Val	Met	Val	Ser	Thr	Ser	Thr	Thr	Val	Ser	Gly	Met	Val	Ser	Val	Trp
		20						25				30			
Met	Ser	Met	Asn	Ser	His	Leu	Ser	Trp	Lys	Glu	Thr	Thr	Trp	Ser	Ser
		35				40					45				
Lys	Lys	Ala	Cys	Ala	Ser	Leu	Leu	Asn	Gln	Val	Ser	Ile	Ser	Leu	Val
	50					55				60					
Lys	Ser	Val	Phe	Val	Leu	Lys	Thr	Ala	Val	Leu	Leu	Pro	Arg	Met	Ala
65				70					75					80	
Ser	Thr	Ser	Leu	Gln	Ala	Pro	Ala	Lys	Ile	Cys	Phe	Ile	Leu	Ile	Lys
			85					90					95		
Leu	Tyr	Ser	Pro	Tyr	Ala	Phe	Leu	Ser	Lys	Tyr	Leu	Gly	Ala	Ile	Leu
		100						105					110		
Leu	Ser	Phe	Phe	Cys	Tyr	Tyr	Ala	Lys	Glu	Ile	Gly	Cys	Asn	Asn	Leu
	115						120					125			
Thr	Leu	Ser	Val	Trp	Asn	Asp	Asn	Glu	Gly	Ala	Leu	Arg	Phe	Tyr	Gln
	130					135					140				
Arg	Gln	Gly	Met	Lys	Pro	Gln	Glu	Thr	Thr	Met	Glu	Met	Ile	Ile	Asp
145				150					155					160	

(2) INFORMATION FOR SEQ ID NO:3687:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 654 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...654

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3687:

Ser	Leu	Met	Lys	Lys	Gln	Asn	Asn	Gly	Leu	Ile	Lys	Asn	Pro	Phe	Leu
1				5					10					15	
Trp	Leu	Leu	Phe	Ile	Phe	Phe	Leu	Val	Thr	Gly	Phe	Gln	Tyr	Phe	Tyr
			20					25				30			
Ser	Gly	Asn	Asn	Ser	Gly	Gly	Ser	Gln	Gln	Ile	Asn	Tyr	Thr	Glu	Leu
		35					40				45				
Val	Gln	Glu	Ile	Thr	Asp	Gly	Asn	Val	Lys	Glu	Leu	Thr	Tyr	Gln	Pro
	50					55					60				
Asn	Gly	Ser	Val	Ile	Glu	Val	Ser	Gly	Val	Tyr	Lys	Asn	Pro	Lys	Thr
65					70					75				80	
Ser	Lys	Glu	Gly	Thr	Gly	Ile	Gln	Phe	Phe	Thr	Pro	Ser	Val	Thr	Lys
				85					90					95	
Val	Glu	Lys	Phe	Thr	Ser	Thr	Ile	Leu	Pro	Ala	Asp	Thr	Thr	Val	Ser
			100					105					110		
Glu	Leu	Gln	Lys	Leu	Ala	Thr	Asp	His	Lys	Ala	Glu	Val	Thr	Val	Lys
	115						120					125			
His	Glu	Ser	Ser	Ser	Gly	Ile	Trp	Ile	Asn	Leu	Leu	Val	Ser	Ile	Val
	130					135					140				
Pro	Phe	Gly	Ile	Leu	Phe	Phe	Phe	Leu	Phe	Ser	Met	Met	Gly	Asn	Met
145					150					155				160	
Gly	Gly	Gly	Asn	Gly	Arg	Asn	Pro	Met	Ser	Phe	Gly	Arg	Ser	Lys	Ala
			165						170					175	
Lys	Ala	Ala	Asn	Lys	Glu	Asp	Ile	Lys	Val	Arg	Phe	Ser	Asp	Val	Ala
			180					185					190		
Gly	Ala	Glu	Glu	Glu	Lys	Gln	Glu	Leu	Val	Glu	Val	Val	Glu	Phe	Leu
	195						200					205			
Lys	Asp	Pro	Lys	Arg	Phe	Thr	Lys	Leu	Gly	Ala	Arg	Ile	Pro	Ala	Gly
	210					215					220				
Val	Leu	Leu	Glu	Gly	Pro	Pro	Gly	Thr	Gly	Lys	Thr	Leu	Leu	Ala	Lys
225					230					235				240	
Ala	Val	Ala	Gly	Glu	Ala	Gly	Val	Pro	Phe	Phe	Ser	Ile	Ser	Gly	Ser
			245						250					255	
Asp	Phe	Val	Glu	Met	Phe	Val	Gly	Val	Gly	Ala	Ser	Arg	Val	Arg	Ser
		260					265						270		
Leu	Phe	Glu	Asp	Ala	Lys	Lys	Ala	Ala	Pro	Ala	Ile	Ile	Phe	Ile	Asp
	275						280					285			
Glu	Ile	Asp	Ala	Val	Gly	Arg	Gln	Arg	Gly	Val	Gly	Leu	Gly	Gly	Gly
	290				295					300					
Asn	Asp	Glu	Arg	Glu	Gln	Thr	Leu	Asn	Gln	Leu	Leu	Ile	Glu	Met	Asp
305					310				315					320	
Gly	Phe	Glu	Gly	Asn	Glu	Gly	Ile	Ile	Val	Ile	Ala	Ala	Thr	Asn	Arg
			325						330					335	
Ser	Asp	Val	Leu	Asp	Pro	Ala	Leu	Leu	Arg	Pro	Gly	Arg	Phe	Asp	Arg
		340					345						350		
Lys	Val	Leu	Val	Gly	Arg	Pro	Asp	Val	Lys	Gly	Arg	Glu	Ala	Ile	Leu
	355						360					365			
Lys	Val	His	Ala	Lys	Asn	Lys	Pro	Leu	Ala	Glu	Asp	Val	Asp	Leu	Lys
	370					375					380				
Leu	Val	Ala	Gln	Gln	Thr	Pro	Gly	Phe	Val	Gly	Ala	Asp	Leu	Glu	Asn
385					390					395				400	
Val	Leu	Asn	Glu	Ala	Ala	Leu	Val	Ala	Ala	Arg	Arg	Asn	Lys	Ser	Ile
			405					410						415	

Val	Leu	Pro	Val	Leu	Asn	Lys	Gly	Val	Val	Asp	Ala	Gly	Ile	Lys	Ala
50						55					60				
Ala	Leu	Ala	Leu	Asn	Met	Asp	Ile	His	Lys	Lys	Met	His	Phe	Asp	Arg
65					70					75					80
Lys	Asn	Tyr	Phe	Tyr	Pro	Asp	Asn	Pro	Lys	Ala	Tyr	Gln	Ile	Ser	Gln
				85					90					95	
Phe	Asp	Glu	Pro	Ile	Gly	Tyr	Asn	Gly	Trp	Ile	Glu	Val	Glu	Leu	Glu
			100					105					110		
Asp	Gly	Thr	Thr	Lys	Lys	Ile	Gly	Ile	Glu	Arg	Ala	His	Leu	Glu	Glu
		115					120					125			
Asp	Ala	Gly	Lys	Asn	Thr	His	Gly	Thr	Asp	Gly	Tyr	Ser	Tyr	Val	Asp
	130					135					140				
Leu	Asn	Arg	Gln	Gly	Val	Pro	Leu	Ile	Glu	Ile	Val	Ser	Glu	Ala	Asp
145					150				155						160
Met	Arg	Ser	Pro	Glu	Glu	Ala	Tyr	Ala	Tyr	Leu	Thr	Ala	Leu	Lys	Glu
				165					170					175	
Val	Ile	Gln	Tyr	Ala	Gly	Ile	Ser	Asp	Val	Lys	Met	Glu	Glu	Gly	Ser
			180					185					190		
Met	Arg	Val	Asp	Ala	Asn	Ile	Ser	Leu	Val	Leu	Met	Val	Lys	Arg	Asn
	195					200						205			
Ser	Val	Pro	Arg	Leu	Asn										
	210														

(2) INFORMATION FOR SEQ ID NO:3689:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 432 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3689:

Pro	Ile	Met	Lys	Ser	Asp	Lys	Thr	Ile	Ile	Arg	Lys	Ile	His	Met	Glu
1			5					10					15		
Gln	Leu	His	Phe	Ile	Thr	Lys	Leu	Leu	Asp	Ile	Lys	Asp	Pro	Asn	Ile
		20					25					30			
Lys	Ile	Leu	Asp	Ile	Ile	Asn	Met	Asp	Thr	His	Lys	Glu	Ile	Ile	Ala
	35					40					45				
Lys	Leu	Asp	Tyr	Glu	Ala	Pro	Ser	Cys	Pro	Asp	Cys	Gly	Ser	Leu	Met
	50				55					60					
Lys	Lys	Tyr	Asp	Phe	Gln	Lys	Pro	Ser	Lys	Ile	Pro	Tyr	Leu	Glu	Thr
65				70					75					80	
Thr	Gly	Met	Pro	Ser	Arg	Ile	Leu	Leu	Arg	Lys	Arg	Arg	Phe	Lys	Cys
			85					90					95		
Tyr	His	Cys	Ser	Lys	Met	Met	Val	Ala	Glu	Thr	Pro	Leu	Val	Lys	Lys
			100					105					110		

Asn	His	Gln	Ile	Pro	Arg	Ile	Ile	Asn	Gln	Lys	Ile	Ala	Gln	Lys	Leu	115	120	125
Ile	Glu	Lys	Ile	Ser	Met	Thr	Asp	Ile	Ala	His	Gln	Leu	Ala	Ile	Ser	130	135	140
Thr	Ser	Thr	Val	Ile	Arg	Lys	Leu	Asn	Asp	Phe	His	Phe	Glu	His	Asp	145	150	155
Phe	Ser	Arg	Leu	Pro	Lys	Ile	Met	Ser	Trp	Asp	Glu	Tyr	Ala	Phe	Thr	165	170	175
Lys	Gly	Lys	Met	Ser	Phe	Ile	Ala	Gln	Asp	Phe	Asp	Asn	Leu	Asn	Ile	180	185	190
Ile	Thr	Val	Leu	Glu	Gly	Arg	Thr	Gln	Ala	Val	Ile	Arg	Asn	His	Phe	195	200	205
Leu	Arg	Tyr	Asp	Arg	Ala	Val	Arg	Cys	Gln	Val	Lys	Ile	Ile	Thr	Met	210	215	220
Asp	Met	Phe	Ser	Pro	Tyr	Tyr	Asp	Leu	Ala	Lys	Gln	Leu	Phe	Pro	Cys	225	230	235
Ala	Lys	Ile	Val	Leu	Asp	Arg	Phe	His	Ile	Ile	Gln	His	Leu	Ser	Arg	245	250	255
Ala	Met	Ser	Arg	Phe	Arg	Val	Gln	Ile	Met	Asn	Gln	Phe	Glu	Arg	Lys	260	265	270
Ser	His	Glu	Tyr	Lys	Ala	Ile	Lys	Arg	Tyr	Trp	Lys	Leu	Ile	Gln	Gln	275	280	285
Asp	Ser	Arg	Lys	Leu	Ser	Asp	Lys	Arg	Phe	Tyr	Arg	Pro	Thr	Phe	Arg	290	295	300
Met	His	Leu	Thr	Asn	Lys	Glu	Ile	Leu	Asp	Lys	Ile	Leu	Ser	Tyr	Ser	305	310	315
Glu	Asp	Leu	Lys	His	His	Tyr	Gln	Ile	Tyr	Gln	Leu	Leu	Leu	Phe	His	325	330	335
Phe	Gln	Asn	Lys	Asp	Pro	Glu	Lys	Phe	Phe	Gly	Leu	Ile	Glu	Asp	Thr	340	345	350
Leu	Lys	Gln	Val	His	Pro	Ile	Phe	Gln	Thr	Val	Phe	Lys	Thr	Phe	Leu	355	360	365
Lys	Asn	Lys	Glu	Lys	Ile	Val	Asn	Ala	Leu	Gln	Leu	Pro	Tyr	Ser	Asn	370	375	380
Ala	Lys	Leu	Glu	Ala	Thr	Asn	Asn	Leu	Ile	Lys	Leu	Ile	Lys	Arg	Asn	385	390	395
Ala	Phe	Gly	Phe	Arg	Asn	Phe	Glu	Asn	Phe	Lys	Lys	Arg	Ile	Phe	Ile	405	410	415
Ala	Leu	Asn	Ile	Lys	Lys	Glu	Arg	Thr	Asn	Phe	Val	Leu	Ser	Arg	Ala	420	425	430

(2) INFORMATION FOR SEQ ID NO:3690:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

(B) LOCATION 1...426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3690:

Lys	Ile	Met	Lys	Ile	Ser	Trp	Asn	Gly	Phe	Ser	Lys	Lys	Ser	Tyr	Gln	1	5	10	15
Glu	Arg	Leu	Glu	Leu	Leu	Lys	Ala	Gln	Ala	Leu	Leu	Ser	Pro	Glu	Arg	20	25	30	
Gln	Ala	Ser	Leu	Glu	Lys	Asp	Glu	Gln	Met	Ser	Val	Thr	Val	Ala	Asp	35	40	45	
Gln	Leu	Ser	Glu	Asn	Val	Val	Gly	Thr	Phe	Ser	Leu	Pro	Tyr	Ser	Leu	50	55	60	
Val	Pro	Glu	Val	Leu	Val	Asn	Gly	Gln	Glu	Tyr	Thr	Val	Pro	Tyr	Val	65	70	75	80
Thr	Glu	Glu	Pro	Ser	Val	Val	Ala	Ala	Ala	Ser	Tyr	Ala	Ser	Lys	Ile	85	90	95	
Ile	Lys	Arg	Ala	Gly	Gly	Phe	Thr	Ala	Gln	Val	His	Gln	Arg	Gln	Met	100	105	110	
Ile	Gly	Gln	Val	Ala	Leu	Tyr	Gln	Ile	Ala	Asn	Pro	Lys	Leu	Ala	Gln	115	120	125	
Glu	Lys	Ile	Ala	Ser	Lys	Lys	Ala	Glu	Leu	Leu	Glu	Leu	Ala	Asn	Gln	130	135	140	
Ala	Tyr	Pro	Ser	Ile	Val	Lys	Arg	Gly	Gly	Gly	Ala	Arg	Asp	Leu	His	145	150	155	160
Val	Glu	Gln	Ile	Lys	Gly	Glu	Pro	Asp	Phe	Leu	Val	Val	Tyr	Ile	His	165	170	175	
Val	Asp	Thr	Gln	Glu	Ala	Met	Gly	Ala	Asn	Met	Leu	Asn	Thr	Met	Leu	180	185	190	
Glu	Ala	Leu	Lys	Pro	Val	Leu	Glu	Glu	Leu	Ser	Gln	Gly	Gln	Ser	Leu	195	200	205	
Met	Gly	Ile	Leu	Ser	Asn	Tyr	Ala	Thr	Asp	Ser	Leu	Val	Thr	Ala	Ser	210	215	220	
Cys	Arg	Ile	Ala	Phe	Arg	Tyr	Leu	Ser	Arg	Gln	Lys	Asp	Gln	Gly	Arg	225	230	235	240
Glu	Ile	Ala	Glu	Lys	Ile	Ala	Leu	Ala	Ser	Gln	Phe	Ala	Gln	Ala	Asp	245	250	255	
Pro	Tyr	Arg	Ala	Ala	Thr	His	Asn	Lys	Gly	Ile	Phe	Asn	Gly	Ile	Asp	260	265	270	
Ala	Ile	Leu	Ile	Ala	Thr	Gly	Asn	Asp	Trp	Arg	Ala	Ile	Glu	Ala	Gly	275	280	285	
Ala	His	Ala	Phe	Ala	Ser	Arg	Asp	Gly	Arg	Tyr	Gln	Gly	Leu	Ser	Cys	290	295	300	
Trp	Thr	Leu	Asp	Leu	Glu	Arg	Glu	Glu	Leu	Val	Gly	Glu	Met	Thr	Leu	305	310	315	320
Pro	Met	Pro	Val	Ala	Thr	Lys	Gly	Gly	Ser	Ile	Gly	Leu	Asn	Pro	Arg	325	330	335	
Val	Ala	Leu	Ser	His	Asp	Leu	Leu	Gly	Asn	Pro	Ser	Ala	Arg	Glu	Leu	340	345	350	
Ala	Gln	Ile	Ile	Val	Ser	Ile	Gly	Leu	Ala	Gln	Asn	Phe	Ala	Ala	Leu	355	360	365	
Lys	Ala	Leu	Val	Ser	Thr	Gly	Ile	Gln	Gln	Gly	His	Met	Lys	Leu	Gln	370	375	380	
Ala	Lys	Ser	Leu	Ala	Leu	Leu	Ala	Gly	Ala	Ser	Glu	Ser	Glu	Val	Ala	385	390	395	400
Pro	Leu	Val	Glu	Arg	Leu	Ile	Ser	Asp	Lys	Thr	Phe	Asn	Leu	Glu	Thr	405	410	415	

Leu Ser Glu Gly Ser Val Lys
275

(2) INFORMATION FOR SEQ ID NO:3692:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...82

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3692:

Glu	Ile	Met	Lys	Arg	Ile	Leu	Ile	Ala	Pro	Val	Arg	Phe	Tyr	Gln	Arg
1			5					10					15		
Phe	Ile	Ser	Pro	Val	Phe	Pro	Pro	Ser	Cys	Arg	Phe	Glu	Leu	Thr	Cys
			20					25				30			
Ser	Asn	Tyr	Met	Ile	Gln	Ala	Ile	Glu	Lys	His	Gly	Phe	Lys	Gly	Val
			35				40				45				
Leu	Met	Gly	Leu	Ala	Arg	Ile	Leu	Arg	Cys	His	Pro	Trp	Ser	Lys	Thr
			50			55				60					
Gly	Lys	Asp	Pro	Val	Pro	Asp	His	Phe	Ser	Leu	Lys	Arg	Asn	Gln	Glu
65					70				75					80	
Gly	Glu														

(2) INFORMATION FOR SEQ ID NO:3693:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...87

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3693:

Tyr Ser Met Lys Ile Lys Glu Gln Thr Arg Lys Leu Ala Ala Gly Cys

1				5					10					15		
Ser	Lys	Gln	Cys	Phe	Glu	Val	Val	Asp	Glu	Thr	Asp	Glu	Val	Ser	Ser	
			20					25					30			
Lys	Gln	Cys	Phe	Glu	Val	Val	Asp	Glu	Thr	Asp	Glu	Val	Ser	Asn	His	
		35					40					45				
Thr	Tyr	Gly	Lys	Ala	Lys	Leu	Thr	Trp	Phe	Glu	Glu	Ile	Phe	Glu	Glu	
	50					55					60					
Tyr	Lys	Met	Met	Gly	Lys	Ala	Gly	Gln	Leu	Val	Phe	Phe	Asp	Val	Tyr	
65					70					75					80	
Arg	Leu	Val	Arg	Gln	Val	Ser										
					85											

(2) INFORMATION FOR SEQ ID NO:3694:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 81 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...81

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3694:

Tyr	Ser	Met	Lys	Ile	Lys	Glu	Gln	Thr	Arg	Lys	Leu	Ala	Ala	Gly	Cys	
1				5				10						15		
Ser	Lys	His	Arg	Phe	Glu	Val	Ala	Asp	Arg	Thr	Asp	Glu	Val	Ser	Ser	
			20					25					30			
Lys	His	Cys	Phe	Glu	Val	Val	Asp	Arg	Thr	Asp	Glu	Val	Ser	Ser	Lys	
		35					40					45				
His	Arg	Phe	Glu	Val	Val	Asp	Arg	Thr	Asp	Glu	Val	Ser	Asn	His	Thr	
	50					55					60					
Tyr	Gly	Lys	Val	Lys	Leu	Thr	Trp	Phe	Glu	Glu	Ser	Phe	Glu	Glu	Tyr	
65					70					75					80	
Lys																

(2) INFORMATION FOR SEQ ID NO:3695:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3695:

Tyr	Ser	Met	Lys	Ile	Gln	Glu	Gln	Thr	Arg	Lys	Leu	Ala	Ala	Ser	Cys
1				5				10						15	
Ser	Lys	His	Cys	Phe	Glu	Val	Val	Asp	Lys	Thr	Asp	Lys	Val	Ser	His
			20					25					30		
Ile	Tyr	Thr	Val	Arg	Arg	Arg	Trp	Arg	Gly	Leu	Lys	Arg	Phe	Leu	Lys
		35					40					45			
Ser	Ile	Lys	Ile	Leu	Lys	Ile	Leu	Ser	Ser	Ile	Leu				
	50					55					60				

(2) INFORMATION FOR SEQ ID NO:3696:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 112 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3696:

Tyr	Ser	Met	Lys	Ile	Lys	Glu	Gln	Thr	Arg	Lys	Leu	Ala	Ala	Gly	Cys
1				5				10						15	
Ser	Lys	His	Ser	Phe	Glu	Val	Val	Asp	Glu	Thr	Asp	Glu	Val	Ser	Ser
			20					25					30		
Lys	His	Gly	Phe	Glu	Val	Val	Asp	Glu	Thr	Asp	Glu	Val	Ser	Ser	Lys
		35					40					45			
His	Gly	Ser	Glu	Val	Val	Asp	Glu	Thr	Asp	Glu	Val	Ser	Ser	Lys	His
	50					55					60				
Gly	Phe	Glu	Val	Val	Asp	Glu	Thr	Asp	Glu	Val	Ser	Ser	Lys	His	Gly
65					70				75					80	
Phe	Glu	Ile	Val	Asp	Glu	Thr	Asp	Glu	Val	Ser	Asn	His	Thr	Tyr	Gly
			85					90					95		
Lys	Ala	Thr	Leu	Thr	Trp	Phe	Glu	Glu	Ile	Phe	Glu	Glu	Tyr	Lys	Asn
			100					105					110		

(2) INFORMATION FOR SEQ ID NO:3697:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3697:

Tyr	Ser	Met	Lys	Ile	Lys	Val	Gln	Thr	Arg	Lys	Leu	Ala	Ala	Gly	Cys
1				5				10						15	
Ser	Lys	His	Cys	Phe	Lys	Val	Val	Asp	Gly	Thr	Asp	Glu	Val	Ser	Ser
		20						25					30		
Lys	His	Cys	Phe	Glu	Val	Val	Asp	Arg	Thr	Asp	Glu	Val	Ser	Asn	His
		35					40					45			
Ile	Tyr	Gly	Lys	Val	Lys	Leu	Thr	Trp	Phe	Glu	Glu	Ile	Phe	Glu	Glu
	50					55					60				
Tyr	Lys	Ser	Leu	His	Asn	Lys	Thr	His	Ile	Thr	Lys	Val	Leu	Met	Asn
65					70					75					80
Cys	Thr	Pro	Lys	Val	Arg	Gln	Lys	Lys	Ser	Asn	Phe	Trp	Gly	Ser	Val
				85					90					95	
His	Ser	Thr	Pro	Asp	Thr	Met	Arg	Phe	Phe	Asn	Phe	Lys	Asp	Phe	Leu
			100					105					110		
Gln	Leu	Leu	Leu	Thr	His	Ile	Lys	Leu	Phe						
			115				120								

(2) INFORMATION FOR SEQ ID NO:3698:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...70

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3698:

Tyr	Ser	Met	Lys	Ile	Lys	Glu	Gln	Thr	Arg	Lys	Leu	Ala	Ala	Gly	Cys
1				5				10						15	
Ser	Lys	His	Cys	Phe	Glu	Val	Ala	Asp	Arg	Thr	Asp	Glu	Val	Ser	Ser
		20						25					30		


```

Lys His Cys Phe Glu Val Ala Asp Arg Thr Asp Glu Val Ser Asn His
   35           40           45
Thr Tyr Asp Lys Ala Thr Leu Thr Arg Phe Glu Glu Ile Phe Glu Glu
   50           55           60
Tyr Lys Gly Val Pro Arg
65           70

```

(2) INFORMATION FOR SEQ ID NO:3699:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 151 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...151
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3699:

```

Leu Gln Met Lys Leu Thr Asp Tyr Val Lys Gln Val Ser Leu Glu Asp
1           5           10           15
Phe Gly Arg Pro Phe Ile His His Val Gln Trp Asn Arg Arg Leu Arg
   20           25           30
Ser Thr Gly Gly Arg Phe Phe Pro Lys Asp Gly His Leu Asp Phe Asn
   35           40           45
Pro Lys Val Tyr Gln Glu Leu Gly Leu Asp Val Phe Arg Lys Ile Val
   50           55           60
Arg His Glu Leu Cys His Tyr His Leu Tyr Phe Gln Gly Lys Gly Tyr
65           70           75           80
Gln His Lys Asp Arg Asp Phe Lys Glu Leu Leu Lys Ala Val Asp Gly
   85           90           95
Leu Arg Phe Val Pro Ser Leu Pro Asn Ser Asn Ser Lys Pro Leu Lys
   100          105          110
Leu Tyr Arg Cys Gln Ser Cys Gln Gln Thr Tyr Gln Arg Lys Arg Arg
   115          120          125
Ile Asp Thr Lys Arg Tyr Arg Cys Gly Leu Cys Arg Gly Lys Leu Leu
   130          135          140
Leu Ile Asn Gln Pro Glu Asp
145          150

```

(2) INFORMATION FOR SEQ ID NO:3700:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 661 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...661

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3700:

Glu	Gly	Met	Asn	Val	Leu	Asn	Ile	Lys	Glu	Lys	Asp	Ile	Leu	Gln	Phe
1				5					10					15	
Leu	Ile	Lys	Asn	Lys	Glu	Arg	Phe	Val	Thr	Ser	Lys	Glu	Leu	Ala	Glu
			20					25					30		
Tyr	Leu	Ser	Cys	Ser	Asp	Arg	Thr	Val	Arg	Asn	Val	Leu	Lys	Leu	Ile
		35					40					45			
Glu	Lys	Thr	Met	Ile	Ile	Gln	Gly	Val	Arg	Leu	Ile	Ser	Lys	Gln	Gly
	50					55					60				
Gln	Gly	Tyr	Gln	Ile	Phe	Phe	Glu	Asn	Gln	Gly	Ala	Tyr	Gln	Glu	Phe
65					70				75					80	
Arg	Gln	Thr	Tyr	Glu	Leu	Glu	Glu	Asp	Tyr	Thr	Lys	Thr	Ala	Val	Ser
			85					90						95	
Lys	Gly	Asp	Asp	Arg	Leu	Val	Phe	Ile	Leu	Asn	Lys	Leu	Leu	Phe	Glu
		100						105					110		
Gln	Val	Pro	Val	Leu	Phe	Asp	Asp	Leu	Ala	Asp	Glu	Leu	Tyr	Val	Ser
	115					120						125			
Arg	Ser	Thr	Leu	Ser	His	Asp	Phe	Arg	Lys	Ile	Arg	Val	Met	Leu	Ser
	130					135					140				
Glu	Tyr	Asn	Leu	Ser	Ile	Glu	Ser	Arg	Ala	Asn	Lys	Gly	Val	Tyr	Val
145					150				155					160	
Ser	Gly	Glu	Glu	Arg	Asp	Lys	Arg	Arg	Phe	Ile	Ile	Asn	Tyr	Phe	Leu
			165					170					175		
Glu	Asn	Gln	Phe	Phe	Lys	Thr	Ile	His	Cys	Tyr	Val	Lys	Phe	Asn	Phe
		180					185					190			
Phe	Asp	Gln	Thr	Val	Pro	Leu	Glu	Glu	Phe	Ala	Arg	Ile	Val	Leu	Asp
	195					200					205				
Glu	Cys	Gln	Glu	Ala	Asn	Leu	Lys	Leu	Ser	Asp	Phe	Val	Leu	Gln	Asn
	210				215					220					
Leu	Val	Val	His	Ile	Ala	Leu	Ser	Val	Ile	Arg	Leu	Lys	Ser	Gly	Phe
225				230					235					240	
Glu	Ile	Lys	Asn	Ile	Asp	Cys	Gln	Met	Thr	Asp	Asp	Ala	Thr	Glu	Arg
			245					250					255		
Lys	Val	Ala	Gln	Arg	Ile	Leu	Ser	Lys	Val	Arg	Glu	Val	Thr	Asn	Gln
		260					265					270			
Glu	Phe	Pro	Val	Gln	Glu	Ile	Asp	Tyr	Ile	Thr	Leu	His	Leu	Leu	Ala
	275					280					285				
Lys	Ser	Gln	Gln	Cys	Gln	Lys	Asn	Gln	Lys	Asn	Ile	Ser	Glu	Glu	Val
	290				295					300					
Leu	Lys	Lys	Ser	Leu	Phe	Lys	Thr	Phe	Gln	Asn	Leu	Gly	Leu	Asp	Asp
305				310				315						320	
Met	Tyr	Asn	Phe	Ser	Ser	Asp	Phe	Gln	Leu	Ile	Glu	Gly	Leu	Ile	Thr
			325					330					335		
His	Leu	Met	Thr	Leu	Gln	Val	Arg	Leu	Glu	Ser	Arg	Ile	Thr	Leu	Asn
		340					345					350			
Asn	Pro	Leu	Val	Asp	Glu	Ile	Lys	Gln	Asn	Tyr	Ser	Asp	Ile	Phe	Phe

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3701:

```
Arg Leu Met Lys Gln Leu Ile Ser Leu Lys Asn Ile Phe Arg Ser Tyr
1          5          10          15
Arg Asn Gly Asp Gln Glu Leu Gln Val Leu Lys Asn Ile Asn Leu Glu
20        25        30
Val Asn Glu Gly Glu Phe Val Ala Ile Met Gly Pro Ser Gly Ser Gly
35        40        45
Lys Ser Thr Leu Met Asn Thr Ile Gly Met Leu Asp Thr Pro Thr Ser
50        55        60
Gly Glu Tyr Tyr Leu Glu Gly Gln Glu Val Ala Gly Leu Gly Glu Lys
65        70        75        80
Gln Leu Ala Lys Val Arg Asn Gln Gln Ile Gly Phe Val Phe Gln Gln
85        90        95
Phe Phe Leu Leu Ser Lys Leu Asn Ala Leu Gln Asn Val Glu Leu Pro
100       105       110
Leu Ile Tyr Ala Gly Val Ser Ser Ser Lys Arg Arg Lys Leu Ala Glu
115       120       125
Glu Tyr Leu Asp Lys Val Glu Leu Thr Glu Arg Ser His His Leu Pro
130       135       140
Ser Glu Leu Ser Gly Gly Gln Lys Gln Arg Val Ala Ile Ala Arg Ala
145       150       155       160
Leu Val Asn Asn Pro Ser Ile Ile Leu Ala Asp Glu Pro Thr Gly Ala
165       170       175
Leu Asp Thr Lys Thr Gly Asn Gln Ile Met Gln Leu Leu Val Asp Leu
180       185       190
Asn Lys Glu Gly Lys Thr Ile Ile Met Val Thr His Glu Pro Glu Ile
195       200       205
Ala Ala Tyr Ala Lys Arg Gln Ile Val Ile Arg Asp Gly Val Ile Ser
210       215       220
Ser Asp Ser Ala Gln Leu Gly Lys Glu Glu Asn
225       230       235
```

(2) INFORMATION FOR SEQ ID NO:3702:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...370

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3702:

```
Val Pro Met Asn Ile Ile Leu Ile Ala Lys Leu Leu Arg Glu Asn Thr
1          5          10          15
Asn Thr Lys Ala Asn Ala Leu Asn Asn Gly Trp Ala Arg Ser Gly Ser
```


(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...382

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3703:

Gln	Gln	Met	Lys	Ile	Asp	Lys	Tyr	Ser	Ala	Ile	Leu	Gly	Asn	Tyr	His
1				5					10					15	
Val	Gly	Phe	His	Asn	Met	Ser	Thr	Leu	Thr	Asp	His	Arg	Pro	Val	Ala
			20					25					30		
Ser	Leu	Pro	Phe	Gly	Gly	Lys	Tyr	Arg	Leu	Ile	Asp	Phe	Pro	Leu	Ser
		35					40					45			
Ser	Leu	Ala	Asn	Ala	Gly	Val	Arg	Ser	Val	Phe	Gly	Ile	Phe	Gln	Gln
		50				55					60				
Asp	Asn	Ile	Ser	Ser	Val	Phe	Asp	His	Ile	Arg	Ser	Gly	Arg	Glu	Trp
65					70				75					80	
Gly	Leu	Ser	Thr	Leu	Leu	Ser	His	Tyr	Tyr	Leu	Gly	Ile	Tyr	Asn	Thr
			85					90						95	
Arg	Val	Glu	Ser	Ser	Thr	Val	Gly	Lys	Glu	Tyr	Tyr	Gln	Gln	Leu	Leu
			100					105					110		
Thr	Tyr	Leu	Lys	Arg	Ser	Gly	Ser	Asn	Gln	Thr	Val	Ala	Leu	Asn	Cys
		115				120						125			
Asp	Val	Leu	Ile	Asn	Ile	Asp	Leu	Asn	Gln	Val	Phe	His	Leu	His	Ser
		130				135					140				
Thr	Thr	Lys	Glu	Pro	Ile	Thr	Val	Val	Tyr	Lys	Lys	Leu	Ala	Lys	Lys
145					150				155					160	
Asp	Ile	Ser	Glu	Val	Asn	Ala	Ile	Leu	Asp	Val	Asp	Glu	Thr	Asp	His
			165					170					175		
Val	Leu	Ser	His	Lys	Leu	Phe	Asp	Ser	Lys	Ser	Thr	Ala	Glu	Thr	Phe
			180					185					190		
Asn	Met	Ser	Thr	Asp	Ile	Phe	Val	Val	Asp	Thr	Pro	Trp	Leu	Ile	Glu
		195				200						205			
His	Leu	Glu	Glu	Glu	Ala	Lys	Lys	Glu	His	Pro	Glu	Lys	Leu	Arg	Tyr
		210				215					220				
Val	Leu	Arg	Asp	Leu	Ala	Val	Lys	Glu	Gly	Ala	Phe	Ala	Tyr	Glu	Tyr
225					230				235					240	
Thr	Gly	Tyr	Leu	Ala	Asn	Ile	His	Ser	Val	Lys	Ser	Tyr	Tyr	Gln	Ala
			245						250					255	
Asn	Ile	Asp	Met	Leu	Glu	Ser	Gln	Lys	Phe	Tyr	Ser	Leu	Phe	Ser	Pro
		260						265					270		
Asn	Gln	Lys	Ile	Tyr	Thr	Lys	Val	Lys	Asn	Glu	Glu	Pro	Thr	Tyr	Tyr
		275				280						285			
Ala	Asn	Thr	Ser	Lys	Val	Ser	Thr	Ser	Gln	Phe	Ala	Ser	Gly	Ser	Ile
		290				295					300				
Ile	Glu	Gly	Gln	Val	Ala	Asn	Ser	Val	Leu	Ser	Arg	Asn	Ile	His	Val
305					310				315					320	
His	Lys	Asp	Ser	Leu	Val	Lys	Asp	Ser	Leu	Leu	Phe	Pro	Arg	Val	Val
			325						330				335		
Ile	Gly	Glu	Gly	Ala	Gln	Val	Glu	Tyr	Ala	Ile	Leu	Asp	Lys	Gly	Val
			340					345					350		
Glu	Val	Glu	Pro	Gly	Val	Val	Ile	Arg	Gly	Thr	Ala	Glu	His	Pro	Val
		355					360					365			
Val	Val	Lys	Lys	Gly	Ala	Lys	Val	Thr	Glu	Asp	Ile	His	Ser		
		370				375						380			

(2) INFORMATION FOR SEQ ID NO:3704:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...236

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3704:

Cys	Lys	Met	Asn	Gln	Val	Ile	Asn	Ala	Met	Arg	Lys	Arg	Val	Cys	Asp
1			5					10						15	
Ala	Asn	Gln	Ser	Leu	Pro	Lys	His	Gly	Leu	Val	Lys	Phe	Thr	Trp	Gly
		20						25					30		
Asn	Val	Ser	Glu	Val	Asn	Arg	Glu	Leu	Gly	Val	Ile	Val	Ile	Lys	Pro
		35					40					45			
Ser	Gly	Val	Asp	Tyr	Asp	Glu	Leu	Thr	Pro	Glu	Asn	Met	Val	Val	Thr
	50					55					60				
Asp	Leu	Asp	Gly	Lys	Ile	Leu	Glu	Gly	Asp	Leu	Arg	Pro	Ser	Ser	Asp
65					70					75					80
Leu	Pro	Thr	His	Val	Gln	Leu	Tyr	Lys	Ala	Trp	Ser	Glu	Ile	Gly	Ser
			85						90					95	
Val	Val	His	Thr	His	Ser	Thr	Glu	Ala	Val	Gly	Trp	Ala	Gln	Ala	Gly
			100					105					110		
Arg	Asp	Ile	Pro	Phe	Tyr	Gly	Thr	Thr	His	Ala	Asp	Tyr	Phe	Tyr	Gly
	115					120						125			
Ser	Ile	Pro	Cys	Ala	Arg	Ser	Leu	Thr	Lys	Asp	Glu	Val	Glu	Val	Ala
	130					135					140				
Tyr	Glu	Lys	Asp	Thr	Gly	Leu	Val	Ile	Val	Glu	Glu	Phe	Glu	His	Arg
145					150					155					160
Gly	Leu	Asn	Pro	Val	Glu	Val	Pro	Gly	Ile	Val	Val	Arg	Asn	His	Gly
			165						170					175	
Pro	Phe	Thr	Trp	Gly	Lys	Asn	Pro	Glu	Asp	Ala	Val	Tyr	His	Ser	Val
			180					185					190		
Val	Leu	Glu	Glu	Val	Ser	Lys	Met	Asn	Arg	Phe	Thr	Glu	Gln	Ile	Asn
		195					200					205			
Ser	Arg	Val	Glu	Pro	Ala	Pro	Gln	Tyr	Ile	Leu	Glu	Lys	His	Tyr	Gln
	210					215					220				
Arg	Lys	His	Gly	Pro	Asn	Ala	Tyr	Tyr	Gly	Gln	Lys				
225					230					235					

(2) INFORMATION FOR SEQ ID NO:3705:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 721 amino acids
- (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...721

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3705:

```

Asn Lys Met Asn Lys Pro Thr Ile Leu Arg Leu Ile Lys Tyr Leu Ser
1      5      10      15
Ile Ser Phe Leu Ser Leu Val Ile Ala Ala Ile Val Leu Gly Gly Gly
20      25      30
Val Phe Phe Tyr Tyr Val Ser Lys Ala Pro Ser Leu Ser Glu Ser Lys
35      40      45
Leu Val Ala Thr Thr Ser Ser Lys Ile Tyr Asp Asn Lys Asn Gln Leu
50      55      60
Ile Ala Asp Leu Gly Ser Glu Arg Arg Val Asn Ala Gln Ala Asn Asp
65      70      75      80
Ile Pro Thr Asp Leu Val Lys Ala Ile Val Ser Ile Glu Asp His Arg
85      90      95
Phe Phe Asp His Arg Gly Ile Asp Thr Ile Arg Ile Leu Gly Ala Phe
100     105     110
Leu Arg Asn Leu Gln Ser Asn Ser Leu Gln Gly Gly Ser Thr Leu Thr
115     120     125
Gln Gln Leu Ile Lys Leu Thr Tyr Phe Ser Thr Ser Thr Ser Asp Gln
130     135     140
Thr Ile Ser Arg Lys Ala Gln Glu Ala Trp Leu Ala Ile Gln Leu Glu
145     150     155     160
Gln Lys Ala Thr Lys Gln Glu Ile Leu Thr Tyr Tyr Ile Asn Lys Val
165     170     175
Tyr Met Ser Asn Gly Asn Tyr Gly Met Gln Thr Ala Ala Gln Asn Tyr
180     185     190
Tyr Gly Lys Asp Leu Asn Asn Leu Ser Leu Pro Gln Leu Ala Leu Leu
195     200     205
Ala Gly Met Pro Gln Ala Pro Asn Gln Tyr Asp Pro Tyr Ser His Pro
210     215     220
Glu Ala Ala Gln Asp Arg Arg Asn Leu Val Leu Ser Glu Met Lys Asn
225     230     235     240
Gln Gly Tyr Ile Ser Ala Glu Gln Tyr Glu Lys Ala Val Asn Thr Pro
245     250     255
Ile Thr Asp Gly Leu Gln Ser Leu Lys Ser Ala Ser Asn Tyr Pro Ala
260     265     270
Tyr Met Asp Asn Tyr Leu Lys Glu Val Ile Asn Gln Val Glu Glu Glu
275     280     285
Thr Gly Tyr Asn Leu Leu Thr Thr Gly Met Asp Val Tyr Thr Asn Val
290     295     300
Asp Gln Glu Ala Gln Lys His Leu Trp Asp Ile Tyr Asn Thr Asp Glu
305     310     315     320
Tyr Val Ala Tyr Pro Asp Asp Glu Leu Gln Val Ala Ser Thr Ile Val
325     330     335

```


(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3706:

Lys	Lys	Met	Lys	Gln	Thr	Lys	Arg	Ile	Lys	Arg	Trp	Arg	Tyr	Tyr	Leu
1				5					10					15	
Arg	Arg	Phe	Ala	Tyr	Gln	Ile	Lys	Ile	Leu	Arg	Val	Leu	Gln	Ser	Ile
		20						25					30		
Ser	Arg	Glu	Lys	Tyr	Asp	Glu	Lys	Ile	Ser	Ala	Ser	Leu	Val	Tyr	Gly
		35					40					45			
Phe	Leu	Ser	Ala	Val	Ala	Val	Asn	Phe	Phe	Phe	Gln	Pro	Gly	His	Val
	50					55					60				
Tyr	Ser	Ser	Gly	Ala	Thr	Gly	Leu	Ala	Gln	Ile	Ile	Ser	Ala	Leu	Ser
65					70				75					80	
Asn	His	Trp	Phe	Gly	Phe	His	Ile	Pro	Ile	Ser	Leu	Thr	Phe	Tyr	Ala
				85					90					95	
Ile	Asn	Phe	Pro	Leu	Met	Val	Leu	Ala	Trp	Tyr	Gln	Ile	Gly	His	Lys
			100					105					110		
Phe	Thr	Val	Phe	Thr	Phe	Ile	Thr	Val	Ser	Met	Ser	Ser	Phe	Phe	Ile
		115					120					125			
Gln	Phe	Val	Pro	Val	Ala	Thr	Leu	Thr	Glu	Asp	Pro	Ile	Ile	Asn	Ala
	130					135					140				
Leu	Phe	Gly	Gly	Val	Val	Met	Gly	Leu	Gly	Ile	Gly	Phe	Ala	Leu	Arg
145					150				155					160	
Asn	Asn	Ile	Ser	Ser	Gly	Gly	Thr	Asp	Ile	Val	Ser	Leu	Thr	Ile	Arg
			165					170						175	
Lys	Lys	Thr	Gly	Lys	Asn	Val	Gly	Ser	Ile	Ser	Phe	Leu	Val	Asn	Gly
		180					185					190			
Thr	Ile	Met	Leu	Ile	Ala	Gly	Leu	Thr	Phe	Gly	Trp	Lys	Tyr	Ala	Leu
		195					200					205			
Tyr	Ser	Met	Ile	Thr	Ile	Phe	Val	Ser	Ser	Arg	Val	Thr	Asp	Ala	Val
	210					215					220				
Phe	Thr	Lys	Gln	Lys	Arg	Met	Gln	Ala	Met	Ile	Val	Thr	Asn	His	Pro
225					230				235					240	
Glu	Lys	Val	Ile	Glu	Lys	Ile	His	Lys	Lys	Leu	His	Arg	Gly	Ala	Thr
			245					250					255		
Met	Ile	His	Asp	Ala	Glu	Gly	Thr	Tyr	Asn	His	Glu	Arg	Lys	Ala	Val
		260				265						270			
Leu	Ile	Thr	Val	Ile	Thr	Arg	Ala	Glu	Phe	Asn	Glu	Phe	Lys	Gln	Ile
		275				280					285				
Met	Thr	Gln	Val	Asp	Pro	Ser	Ser	Phe	Val	Ser	Val	Ser	Glu	Asn	Val
	290				295						300				
His	Ile	Leu	Gly	Arg	Phe	Val	Glu	Ile	Asp	Asn					
305					310					315					

(2) INFORMATION FOR SEQ ID NO:3707:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 310 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...310
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3707:

Lys	Thr	Val	Lys	Ser	Ile	Lys	Arg	Phe	Ala	Leu	Ser	Ala	Met	Gly	Val
1			5					10					15		
Ala	Met	Leu	Leu	Val	Leu	Thr	Gly	Cys	Val	Asn	Val	Asp	Lys	Thr	Thr
		20					25					30			
Gly	Gln	Pro	Thr	Gly	Phe	Ile	Trp	Asn	Thr	Ile	Gly	Ala	Pro	Met	Ala
	35					40					45				
Glu	Ala	Ile	Lys	Tyr	Phe	Ala	Thr	Asp	Lys	Gly	Leu	Gly	Phe	Gly	Val
	50				55					60					
Ala	Ile	Ile	Ile	Val	Thr	Ile	Ile	Val	Arg	Leu	Ile	Ile	Leu	Pro	Leu
65				70				75						80	
Gly	Ile	Tyr	Gln	Ser	Trp	Lys	Ala	Thr	Leu	His	Ser	Glu	Lys	Met	Asn
		85					90					95			
Ala	Leu	Lys	His	Val	Leu	Glu	Pro	His	Gln	Thr	Arg	Leu	Lys	Glu	Ala
		100					105					110			
Thr	Thr	Gln	Glu	Glu	Lys	Leu	Glu	Ala	Gln	Gln	Ala	Leu	Phe	Ala	Ala
	115					120						125			
Gln	Lys	Glu	His	Gly	Ile	Ser	Met	Phe	Gly	Gly	Val	Gly	Cys	Phe	Pro
130					135						140				
Ile	Leu	Leu	Gln	Met	Pro	Phe	Phe	Ser	Ala	Ile	Tyr	Phe	Ala	Ala	Gln
145				150					155					160	
His	Thr	Glu	Gly	Val	Ala	Gln	Ala	Ser	Tyr	Leu	Gly	Ile	Pro	Leu	Gly
		165						170					175		
Ser	Pro	Ser	Met	Ile	Leu	Val	Ala	Cys	Ala	Gly	Val	Leu	Tyr	Tyr	Leu
		180					185					190			
Gln	Ser	Leu	Leu	Ser	Leu	His	Gly	Val	Lys	Asp	Glu	Met	Gln	Arg	Glu
	195					200						205			
Gln	Ile	Lys	Lys	Met	Ile	Tyr	Met	Ser	Pro	Leu	Met	Ile	Val	Val	Phe
210					215					220					
Ser	Leu	Phe	Ser	Pro	Ala	Ser	Val	Thr	Leu	Tyr	Trp	Val	Val	Gly	Gly
225				230					235					240	
Phe	Met	Met	Ile	Leu	Gln	Gln	Phe	Ile	Val	Asn	Tyr	Ile	Val	Arg	Pro
		245						250					255		
Lys	Leu	Arg	Lys	Lys	Val	Arg	Glu	Glu	Leu	Ala	Lys	Asn	Pro	Pro	Lys
	260					265						270			
Ala	Ser	Ala	Phe	Ser	Lys	Pro	Ser	Gly	Arg	Lys	Asp	Val	Thr	Pro	Glu
	275					280						285			
Gln	Pro	Thr	Ala	Ile	Thr	Ser	Lys	Lys	Lys	His	Lys	Asn	Arg	Asn	Ala

290	295	300
Gly Lys Gln Arg Ser Arg		
305	310	

(2) INFORMATION FOR SEQ ID NO:3708:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...306

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3708:

Ile	Met	Val	Lys	Glu	Phe	Lys	Glu	Gly	Ser	Met	Lys	Asn	Ser	Ile	Met
1				5				10						15	
Asp	Thr	Lys	Phe	Asp	Arg	Arg	Ile	Leu	Leu	Leu	Asn	Lys	Ile	Ile	Ile
			20					25					30		
Val	Phe	Ile	Val	Leu	Met	Thr	Leu	Leu	Pro	Leu	Leu	Tyr	Ile	Val	Val
		35				40						45			
Ala	Ser	Phe	Met	Asp	Pro	Lys	Val	Leu	Val	Ser	Arg	Gly	Ile	Ser	Phe
	50					55					60				
Asn	Pro	Ala	Asp	Trp	Thr	Val	Glu	Gly	Tyr	Gln	Arg	Val	Phe	Ser	Asp
65				70					75					80	
Gln	Ser	Ile	Leu	Arg	Gly	Phe	Ile	Asn	Ser	Leu	Leu	Tyr	Ser	Phe	Gly
			85					90						95	
Phe	Ala	Ala	Leu	Thr	Val	Leu	Leu	Ser	Val	Phe	Thr	Ala	Tyr	Pro	Leu
		100						105					110		
Ser	Lys	Lys	Asp	Leu	Val	Gly	Arg	Arg	Trp	Ile	Asn	Tyr	Phe	Leu	Ile
	115					120						125			
Val	Thr	Met	Phe	Phe	Gly	Gly	Gly	Leu	Val	Pro	Thr	Tyr	Leu	Leu	Val
	130				135						140				
Lys	Glu	Leu	Gly	Met	Leu	Asn	Thr	Pro	Trp	Ala	Ile	Ile	Val	Pro	Gly
145				150					155					160	
Ala	Val	Asn	Val	Trp	Asn	Ile	Ile	Leu	Ala	Arg	Ala	Tyr	Phe	Gln	Gly
			165					170						175	
Leu	Pro	Glu	Glu	Leu	Val	Glu	Ala	Ala	Val	Ile	Asp	Gly	Ala	Asn	Asp
		180					185						190		
Leu	Gln	Ile	Phe	Phe	Lys	Ile	Met	Leu	Pro	Leu	Ala	Lys	Pro	Ile	Met
	195				200							205			
Phe	Val	Leu	Phe	Leu	Tyr	Ala	Phe	Val	Gly	Gln	Trp	Asn	Ser	Tyr	Phe
	210				215					220					
Asp	Ala	Met	Ile	Tyr	Ile	Lys	Asp	Pro	Asn	Leu	Glu	Pro	Leu	Gln	Leu
225				230					235					240	
Val	Leu	Arg	Lys	Ile	Leu	Ile	Gln	Ser	Gln	Pro	Gly	Gln	Asp	Met	Ile
			245				250						255		
Gly	Ala	Gln	Ala	Ala	Met	Asn	Glu	Met	Lys	Arg	Leu	Ala	Glu	Leu	Ile

	260		265		270
Lys	Tyr	Ala	Thr	Ile	Val
	275		280		285
Pro	Phe	Phe	Gln	Lys	Tyr
	290		295		300
Lys	Gly				
305					

(2) INFORMATION FOR SEQ ID NO:3709:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3709:

Leu	Val	Val	Lys	Ile	Ile	Gln	Lys	Gly	Ile	Phe	Ile	Met	Ser	Gln	Ala
1			5					10						15	
Ile	Ser	Leu	Asn	Gln	Ser	Thr	Trp	Ala	Ser	Lys	Leu	Lys	Ala	Met	Gly
		20						25					30		
Pro	Gly	Ile	Leu	Met	Ala	Thr	Ala	Ala	Val	Gly	Gly	Ser	His	Ile	Val
		35					40					45			
Ser	Ser	Thr	Gln	Ala	Gly	Gly	Ser	Tyr	Gly	Trp	Ser	Leu	Leu	Leu	Leu
	50				55				60						
Val	Ile	Leu	Ala	Asn	Val	Phe	Lys	Tyr	Pro	Phe	Phe	Arg	Phe	Gly	Ala
65				70					75					80	
Glu	Tyr	Thr	Ala	Asp	Thr	Gly	Lys	Thr	Leu	Val	Glu	Gly	Tyr	Ala	Glu
			85					90					95		
Lys	Gly	Lys	Leu	Tyr	Leu	Trp	Ile	Phe	Phe	Ile	Leu	Asn	Val	Phe	Ser
		100						105					110		
Ala	Met	Val	Asn	Thr	Ala	Gly	Val	Ala	Ile	Leu	Cys	Ser	Ala	Ile	Ile
		115				120					125				
Ala	Ser	Ala	Phe	Pro	Met	Ile	Gly	Leu	Ser	Ile	Thr	Gln	Trp	Ser	Leu
	130					135					140				
Ile	Leu	Val	Ala	Ile	Ile	Trp	Ala	Met	Leu	Leu	Phe	Gly	Gly	Tyr	Lys
145				150					155					160	
Leu	Leu	Asp	Gly	Met	Val	Lys	Trp	Ile	Met	Ser	Ala	Leu	Thr	Ile	Ala
			165					170					175		
Thr	Val	Leu	Ala	Val	Ile	Ile	Ala	Ala	Val	Lys	His	Pro	Glu	Tyr	Ser
		180					185					190			
Ser	Asp	Phe	Val	Glu	Lys	Thr	Pro	Trp	Gln	Met	Ala	Ala	Leu	Pro	Ser
	195						200					205			
Ser	Ser	Pro	Ser												
210															

(2) INFORMATION FOR SEQ ID NO:3710:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...81

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3710:

Tyr	Ser	Ser	Lys	Ile	Ser	Ser	Asn	His	Val	Ser	Val	Ala	Leu	Pro	Tyr
1				5					10					15	
Val	Trp	Leu	Leu	Thr	Ser	Ser	Val	Ser	Ser	Thr	Thr	Ser	Lys	Gln	Cys
			20				25						30		
Phe	Glu	Leu	Thr	Ser	Ser	Val	Ser	Ser	Thr	Thr	Ser	Lys	Thr	Cys	Phe
		35					40					45			
Glu	Leu	Thr	Ser	Ser	Val	Leu	Ser	Thr	Thr	Ser	Lys	Gln	Cys	Phe	Glu
	50					55					60				
Gln	Pro	Ala	Ala	Ser	Phe	Leu	Val	Cys	Ser	Leu	Ile	Phe	Ile	Glu	Tyr
65					70					75					80
Lys															

(2) INFORMATION FOR SEQ ID NO:3711:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...66

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3711:

Tyr	Ser	Ser	Lys	Ile	Ser	Ser	Asn	His	Val	Ser	Val	Thr	Leu	Pro	Tyr
1				5					10					15	

Ile	Trp	Leu	Leu	Thr	Ser	Ser	Val	Leu	Ser	Thr	Thr	Ser	Lys	Gln	Cys
		20						25					30		
Phe	Glu	Gln	Pro	Ala	Ala	Ser	Phe	Leu	Val	Cys	Ser	Leu	Ile	Ser	Ile
		35					40					45			
Glu	Tyr	Glu	Lys	Lys	Tyr	Ser	Gly	Tyr	Ser	Leu	Thr	Leu	Thr	Thr	Pro
	50					55					60				
Pro	Asp														
65															

(2) INFORMATION FOR SEQ ID NO:3712:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...486

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3712:

Leu	Leu	Ser	Lys	Ile	Gly	Leu	Thr	Thr	Thr	Leu	Lys	Asn	Ala	Trp	Thr
1				5					10					15	
Thr	Ser	Arg	Gln	Val	Asn	Phe	Phe	Trp	Val	Ala	Asn	Phe	Asn	Leu	Lys
			20					25					30		
Phe	Gly	Ile	Pro	Thr	Leu	Tyr	Thr	Leu	Ser	Ser	Gly	Arg	Val	Leu	Ser
		35					40					45			
Ser	Ile	Asp	Ala	Arg	Tyr	Gly	Gly	Thr	His	Asp	Ser	Lys	Ser	Lys	Ile
		50				55					60				
Asn	Ile	Ala	Thr	Ser	Tyr	Ser	Asp	Asp	Asn	Gly	Lys	Thr	Trp	Ser	Glu
65					70					75				80	
Pro	Ile	Phe	Ala	Met	Lys	Phe	Asn	Asp	Tyr	Glu	Glu	Gln	Leu	Val	Tyr
				85					90					95	
Trp	Pro	Arg	Asp	Asn	Lys	Leu	Lys	Asn	Ser	Gln	Ile	Ser	Gly	Ser	Ala
			100					105					110		
Ser	Phe	Ile	Asp	Ser	Ser	Ile	Val	Glu	Asp	Lys	Lys	Ser	Gly	Lys	Thr
		115				120						125			
Ile	Leu	Leu	Ala	Asp	Val	Met	Pro	Ala	Gly	Ile	Gly	Asn	Asn	Asn	Ala
		130				135					140				
Asn	Lys	Ala	Asp	Ser	Gly	Phe	Lys	Glu	Ile	Asn	Gly	His	Tyr	Tyr	Leu
145					150					155				160	
Lys	Leu	Lys	Lys	Asn	Gly	Asp	Asn	Asp	Phe	Arg	Tyr	Thr	Val	Arg	Glu
				165					170					175	
Lys	Gly	Val	Val	Tyr	Asp	Glu	Thr	Thr	Asn	Lys	Pro	Thr	Asn	Tyr	Thr
			180					185					190		
Ile	Asn	Asp	Lys	Tyr	Glu	Val	Leu	Glu	Gly	Gly	Lys	Ser	Leu	Thr	Val
		195				200						205			
Glu	Gln	Tyr	Ser	Val	Asp	Phe	Asp	Ser	Gly	Ser	Leu	Arg	Glu	Arg	His
		210				215					220				

Asn	Gly	Lys	Gln	Val	Pro	Met	Asn	Val	Phe	Tyr	Lys	Asp	Ser	Leu	Phe	225	230	235	240
Lys	Val	Thr	Pro	Thr	Asn	Tyr	Ile	Ala	Met	Thr	Thr	Ser	Gln	Asn	Arg		245	250	255
Gly	Glu	Ser	Trp	Glu	Gln	Phe	Lys	Leu	Leu	Pro	Pro	Phe	Leu	Gly	Glu	260	265		270
Lys	His	Asn	Gly	Thr	Tyr	Leu	Cys	Pro	Gly	Gln	Gly	Leu	Ala	Leu	Lys	275	280		285
Ser	Ser	Asn	Arg	Leu	Ile	Phe	Ala	Thr	Tyr	Thr	Ser	Gly	Glu	Leu	Thr	290	295	300	
Tyr	Leu	Ile	Ser	Asp	Asp	Ser	Gly	Gln	Thr	Trp	Lys	Lys	Ser	Ser	Ala	305	310	315	320
Ser	Ile	Pro	Phe	Glu	Asn	Ala	Thr	Ala	Glu	Ala	Gln	Met	Val	Glu	Leu		325	330	335
Arg	Asp	Gly	Val	Ile	Arg	Thr	Phe	Phe	Arg	Thr	Thr	Thr	Gly	Lys	Ile	340	345		350
Ala	Tyr	Met	Thr	Ser	Arg	Asp	Ser	Gly	Glu	Thr	Trp	Ser	Lys	Val	Ser	355	360	365	
Tyr	Ile	Asp	Gly	Ile	Gln	Gln	Thr	Ser	Tyr	Gly	Thr	Gln	Val	Ser	Ala	370	375	380	
Ile	Lys	Tyr	Ser	Gln	Leu	Ile	Asp	Gly	Lys	Glu	Ala	Val	Ile	Leu	Ser	385	390	395	400
Thr	Pro	Asn	Ser	Arg	Ser	Gly	Arg	Lys	Gly	Gly	Gln	Leu	Val	Val	Gly		405	410	415
Leu	Val	Asn	Lys	Glu	Asp	Asp	Ser	Ile	Asp	Trp	Arg	Tyr	His	Tyr	Asp	420	425		430
Ile	Asp	Leu	Pro	Ser	Tyr	Gly	Tyr	Ala	Tyr	Ser	Ala	Ile	Thr	Glu	Leu	435	440		445
Pro	Asn	His	His	Ile	Gly	Val	Leu	Phe	Glu	Lys	Tyr	Asp	Ser	Trp	Ser	450	455	460	
Arg	Asn	Glu	Leu	His	Leu	Ser	Asn	Val	Val	Gln	Tyr	Ile	Asp	Leu	Glu	465	470	475	480
Ile	Asn	Asp	Leu	Thr	Lys												485		

(2) INFORMATION FOR SEQ ID NO:3713:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...356

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3713:

Ile	Lys	Ser	Lys	Asn	Leu	Lys	Lys	Gly	Glu	Thr	Met	Leu	Ala	Ile	Glu	1	5	10	15
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	---	---	----	----

Glu	Ser	Gln	Lys	Leu	Thr	Leu	Ser	Asn	Leu	Pro	Ser	Leu	Ser	Leu	Phe
			20					25					30		
Thr	Gly	Thr	Asp	Gln	Gly	Gln	Phe	Glu	Val	Met	Lys	Ser	Gln	Val	Leu
		35					40					45			
Lys	Gln	Ile	Gly	Tyr	Asp	Ser	Ala	Asp	Leu	Asn	Phe	Ala	Tyr	Phe	Asp
			50					55							
Met	Lys	Glu	Val	Val	Tyr	Lys	Asp	Val	Glu	Leu	Glu	Leu	Val	Ser	Leu
65					70				75						80
Pro	Phe	Phe	Ala	Asp	Glu	Lys	Ile	Val	Ile	Leu	Asp	Tyr	Phe	Met	Asp
				85					90					95	
Ile	Thr	Thr	Ala	Lys	Lys	Arg	Phe	Leu	Thr	Asp	Asp	Glu	Leu	Lys	Ser
			100					105					110		
Phe	Glu	Glu	Tyr	Leu	Asp	Asn	Ser	Ser	Pro	Thr	Thr	Lys	Leu	Ile	Ile
		115					120					125			
Phe	Ala	Glu	Gly	Lys	Leu	Asp	Ser	Lys	Arg	Arg	Leu	Val	Lys	Leu	Leu
		130				135					140				
Lys	Arg	Asp	Ala	Lys	Val	Phe	Asp	Ala	Val	Glu	Val	Lys	Glu	Gln	Glu
145					150					155					160
Leu	Arg	Gln	Tyr	Phe	Gln	Lys	Trp	Ser	Gln	Lys	Gln	Gly	Leu	Gln	Phe
				165				170						175	
Thr	Asn	His	Ser	Phe	Glu	Asn	Leu	Leu	Ile	Lys	Ser	Gly	Phe	Gln	Phe
			180					185					190		
Ser	Glu	Ile	Gln	Lys	Asn	Leu	Leu	Phe	Leu	Gln	Ser	Tyr	Lys	Ala	Asn
		195				200						205			
Ser	Val	Ile	Glu	Glu	Glu	Asp	Ile	Val	Asn	Ala	Ile	Pro	Lys	Thr	Leu
		210				215					220				
Gln	Asp	Asn	Ile	Phe	Asp	Leu	Thr	Gln	Phe	Ile	Leu	Thr	Lys	Lys	Met
225					230					235					240
Asp	Gln	Ala	Arg	Asp	Leu	Val	Arg	Asp	Leu	Thr	Leu	Gln	Gly	Glu	Asp
				245					250					255	
Glu	Ile	Lys	Leu	Ile	Ala	Val	Met	Leu	Gly	Gln	Phe	Arg	Thr	Phe	Thr
			260					265					270		
Gln	Val	Lys	Ile	Leu	Ala	Glu	Ser	Gly	Gln	Thr	Glu	Ser	Gln	Ile	Ala
			275					280					285		
Ser	Ser	Leu	Gly	Ser	Tyr	Leu	Gly	Arg	Asn	Pro	Asn	Pro	Tyr	Gln	Ile
		290				295					300				
Lys	Phe	Ala	Leu	Arg	Asp	Ser	Arg	Gly	Leu	Ser	Leu	Ser	Phe	Leu	Lys
305					310					315					320
Gln	Ala	Ile	Ser	Tyr	Leu	Ile	Glu	Thr	Asp	Tyr	Gln	Ile	Lys	Thr	Gly
				325					330					335	
Leu	Tyr	Glu	Lys	Gly	Phe	Leu	Phe	Glu	Lys	Ala	Leu	Leu	Gln	Ile	Ala
			340					345					350		
Ser	Gln	Val	Asn												
			355												

(2) INFORMATION FOR SEQ ID NO:3714:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...117

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3714:

```

Gln Phe Pro Lys Gly Ser Asn His Ser Phe Leu Phe Gln Leu Val Met
1           5           10           15
Ser Leu Ile Thr His Lys Arg Phe Ile Ser Cys Asn Glu Asn Ile Lys
          20           25           30
His Tyr Lys Arg Leu Ile Asp Lys Ala Glu Thr Cys Val Asn Asp Leu
          35           40           45
Met Ala Glu Phe Asn Ser Ile Ile Thr Thr Val Thr Gly Ile Gly Asn
          50           55           60
Arg Leu Gly Ala Val Ile Leu Ala Glu Ile Arg Asn Ile His Ala Phe
65           70           75           80
Asp Asn Pro Ala Gln Leu Gln Ala Phe Ala Gly Leu Asp Ser Ser Ile
          85           90           95
Tyr Gln Ser Gly Gln Ile Asp Leu Ala Gly Arg Met Val Lys Arg Gly
          100          105          110
Ser Pro His Leu Arg
          115
  
```

(2) INFORMATION FOR SEQ ID NO:3715:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 151 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...151

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3715:

```

Met Tyr Thr Lys Ser Arg Thr Ile Lys Ser Leu Ile Thr Gln Phe Thr
1           5           10           15
Ala Ile Leu Leu Tyr Glu Leu Pro Val Ala Leu Asp Ser Leu Val Phe
          20           25           30
Met Gly Phe Ser Met Lys Leu Ile His Asp Leu Asn Thr His Thr Thr
          35           40           45
His Ser Thr Ala Lys Met Leu Tyr Asn Val Lys Ala Lys Leu Phe Ser
          50           55           60
Gln Ala Ile Val Arg Ala Lys His Ile His Ser Asn Asn Phe Asp Ala
65           70           75           80
Thr Ser Asp Asn Ser Ile Val Ala Lys Lys Val Ile Ser Asn Asp Ser
  
```

				85					90					95					
Leu	Cys	Ser	Thr	Leu	Lys	Asn	Ser	Asp	Asp	Ile	Glu	Ile	Val	Lys	Ile				
				100				105					110						
Leu	Arg	Asn	Glu	Ala	His	Leu	Ser	Leu	Cys	Lys	Ser	Ile	Leu	Ile	Pro				
		115					120					125							
Arg	His	Asn	Leu	Arg	Lys	Thr	Arg	Lys	Ile	Met	Phe	Lys	Val	Lys	Ile				
	130					135					140								
Ile	Glu	Leu	Thr	Asn	Asn	Ser													
145					150														

(2) INFORMATION FOR SEQ ID NO:3716:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...189

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3716:

Leu	Ile	Thr	Lys	Glu	Arg	Arg	Ser	Ile	Met	Ala	Asn	Arg	Leu	Lys	Glu				
1				5				10					15						
Lys	Tyr	Leu	Asn	Glu	Val	Val	Pro	Ala	Leu	Thr	Glu	Gln	Phe	Asn	Tyr				
			20				25					30							
Ser	Ser	Val	Met	Ala	Val	Pro	Lys	Val	Asp	Lys	Ile	Val	Leu	Asn	Met				
		35				40					45								
Gly	Val	Gly	Glu	Ala	Val	Ser	Asn	Ala	Lys	Ser	Leu	Glu	Lys	Ala	Ala				
	50				55			60											
Glu	Glu	Leu	Ala	Leu	Ile	Ser	Gly	Gln	Lys	Pro	Leu	Ile	Thr	Lys	Ala				
65				70				75							80				
Lys	Lys	Ser	Ile	Ala	Gly	Phe	Arg	Leu	Arg	Glu	Gly	Val	Ala	Ile	Gly				
			85				90					95							
Ala	Lys	Val	Thr	Leu	Arg	Gly	Glu	Arg	Met	Tyr	Glu	Phe	Leu	Asp	Lys				
		100				105					110								
Leu	Val	Ser	Val	Ser	Leu	Pro	Arg	Val	Arg	Asp	Phe	His	Gly	Val	Pro				
		115				120				125									
Thr	Lys	Ser	Phe	Asp	Gly	Arg	Gly	Asn	Tyr	Thr	Leu	Gly	Val	Lys	Glu				
	130				135					140									
Gln	Leu	Ile	Phe	Pro	Glu	Ile	Asn	Phe	Asp	Asp	Val	Asp	Lys	Thr	Arg				
145				150				155						160					
Gly	Leu	Asp	Ile	Val	Ile	Val	Thr	Thr	Ala	Asn	Thr	Asp	Glu	Glu	Ser				
			165			170						175							
Arg	Ala	Leu	Leu	Thr	Gly	Leu	Gly	Met	Pro	Phe	Ala	Lys							

180

185

(2) INFORMATION FOR SEQ ID NO:3717:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...202

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3717:

Glu	Arg	Thr	Asn	Thr	Met	Tyr	Ala	Tyr	Leu	Lys	Gly	Ile	Ile	Thr	Lys
1			5						10					15	
Ile	Thr	Ala	Lys	Tyr	Ile	Val	Leu	Glu	Thr	Asn	Gly	Ile	Gly	Tyr	Ile
			20					25					30		
Leu	His	Val	Ala	Asn	Pro	Tyr	Ala	Tyr	Ser	Gly	Gln	Val	Asn	Gln	Glu
			35				40					45			
Ala	Gln	Ile	Tyr	Val	His	Gln	Val	Val	Arg	Glu	Asp	Ala	His	Leu	Leu
			50			55					60				
Tyr	Gly	Phe	Arg	Ser	Glu	Asp	Glu	Lys	Lys	Leu	Phe	Leu	Ser	Leu	Ile
65					70				75					80	
Ser	Val	Ser	Gly	Ile	Gly	Pro	Val	Ser	Ala	Leu	Ala	Ile	Ile	Ala	Ala
				85					90					95	
Asp	Asp	Asn	Ala	Gly	Leu	Val	Gln	Ala	Ile	Glu	Thr	Lys	Asn	Ile	Thr
			100					105					110		
Tyr	Leu	Thr	Lys	Phe	Pro	Lys	Ile	Gly	Lys	Lys	Thr	Ala	Gln	Gln	Met
			115				120					125			
Val	Leu	Asp	Leu	Glu	Gly	Lys	Val	Val	Val	Ala	Gly	Asp	Asp	Leu	Pro
			130			135					140				
Ala	Lys	Val	Ala	Val	Gln	Ala	Ser	Ala	Glu	Asn	Gln	Glu	Leu	Glu	Glu
145					150					155				160	
Ala	Met	Glu	Ala	Met	Leu	Ala	Leu	Gly	Tyr	Lys	Ala	Thr	Glu	Leu	Lys
				165					170					175	
Lys	Ile	Lys	Lys	Phe	Phe	Glu	Gly	Thr	Asp	Thr	Ala	Glu	Asn	Tyr	
			180				185					190			
Ile	Lys	Ser	Ala	Leu	Lys	Met	Leu	Val	Lys						
			195			200									

(2) INFORMATION FOR SEQ ID NO:3718:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...334

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3718:

```
Trp Met Thr Lys Ile Leu Leu Phe Gly Glu Pro Leu Ile Arg Ile Ser
1      5      10      15
Pro Leu Asp Ala Thr Ser Ile Gly Asp His Val Ala Ser Ser Thr Tyr
      20      25      30
Phe Gly Gly Ser Glu Ile Asn Ile Ala Cys Asn Leu Gln Ala Leu Gly
      35      40      45

Ile Ser Thr Lys Val Phe Thr Ala Leu Pro Ala Asn Glu Ile Gly Asp
50      55      60
Arg Phe Leu Thr Phe Leu Lys Gln His Gln Ile Asp Thr Ser Ser Ile
65      70      75      80
Cys Arg Leu Gly Asp Arg Ile Gly Leu Tyr Tyr Leu Glu Asn Gly Phe
      85      90      95
Gly Cys Arg Gln Ser Glu Val Phe Tyr Asp Arg Lys His Thr Ser Ile
      100      105      110
Ser Gln Ile Arg Pro Asn Met Leu Asp Met Asp Ser Leu Phe Gln Gly
      115      120      125
Ile Ser His Phe His Phe Ser Gly Ile Thr Val Ala Ile Gly Gln Glu
      130      135      140
Val Arg Ala Ile Leu Leu Leu Leu Leu Glu Glu Ala Lys Arg Arg Gly
145      150      155      160
Ile Val Val Ser Met Asp Leu Asn Leu Arg Thr Lys Met Ile Ser Val
      165      170      175
Leu Glu Ala Lys Tyr Glu Phe Ser Lys Phe Ala Arg Phe Thr Asp Tyr
      180      185      190
Cys Phe Gly Ile Asp Pro Leu Met Ile Asp Asp Gln Asn Leu Glu Met
      195      200      205
Phe Pro Arg Asp Ser Ala Ser Leu Glu Glu Val Glu Asn Arg Met Arg
      210      215      220
Leu Leu Lys Glu Ala Tyr Gly Phe Lys Ala Ile Phe His Thr Leu Arg
225      230      235      240
Ser Ser Asp Glu Gln Asp Lys Asn Val Tyr Gln Ala Tyr Ala Leu Glu
      245      250      255
Glu Arg Phe Glu Glu Ser Val Gln Leu Lys Thr Ala Val Tyr Gln Arg
      260      265      270
Ile Gly Ser Gly Asp Ala Phe Ile Ser Gly Ala Leu Tyr Gln Leu Leu
      275      280      285
His His Ser Ser Leu Lys Thr Thr Ile Asp Phe Ala Val Ala Ser Ala
      290      295      300
Thr Leu Lys Cys Thr Leu Pro Gly Asp His Leu Ser Thr Ser Ala Thr
305      310      315      320
Ser Ile Glu Asn Leu Leu Ala Asn Ala Gln Asp Ile Ile Arg
      325      330
```

(2) INFORMATION FOR SEQ ID NO:3719:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 324 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...324

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3719:

Leu	Phe	Ala	Asn	Ser	Ile	Gly	Glu	Glu	Val	Ser	Met	Val	Gln	Glu	Ile
1				5					10					15	
Ala	Gln	Glu	Ile	Ile	Arg	Ser	Ala	Arg	Lys	Lys	Gly	Thr	Gln	Asp	Ile
			20					25					30		
Tyr	Phe	Val	Pro	Lys	Leu	Asp	Ala	Tyr	Glu	Leu	His	Met	Arg	Val	Gly
		35					40					45			
Asp	Glu	Arg	Cys	Lys	Ile	Gly	Ser	Tyr	Asp	Phe	Glu	Lys	Phe	Ala	Ala
	50					55				60					
Val	Ile	Ser	His	Phe	Lys	Phe	Val	Ala	Gly	Met	Asn	Val	Gly	Glu	Lys
65					70					75					80
Arg	Arg	Ser	Gln	Leu	Gly	Ser	Cys	Asp	Tyr	Ala	Tyr	Asp	His	Lys	Ile
				85					90					95	
Ala	Ser	Leu	Arg	Leu	Ser	Thr	Val	Gly	Asp	Tyr	Arg	Gly	His	Glu	Ser
			100					105					110		
Leu	Val	Ile	Arg	Leu	Leu	His	Asp	Glu	Glu	Gln	Asp	Leu	His	Phe	Trp
		115					120					125			
Phe	Gln	Asp	Ile	Glu	Glu	Leu	Gly	Lys	Gln	Tyr	Arg	Gln	Arg	Gly	Leu
	130					135					140				
Tyr	Leu	Phe	Ala	Gly	Pro	Val	Gly	Ser	Gly	Lys	Thr	Thr	Leu	Met	His
145					150					155					160
Glu	Leu	Ser	Lys	Ser	Leu	Phe	Lys	Gly	Gln	Gln	Val	Met	Ser	Ile	Glu
			165						170					175	
Asp	Pro	Val	Glu	Ile	Lys	Gln	Asp	Asp	Met	Leu	Gln	Leu	Gln	Leu	Asn
			180					185					190		
Glu	Ala	Ile	Gly	Leu	Thr	Tyr	Glu	Asn	Leu	Ile	Lys	Leu	Ser	Leu	Arg
		195					200					205			
His	Arg	Pro	Asp	Leu	Leu	Ile	Ile	Gly	Glu	Ile	Arg	Asp	Ser	Glu	Thr
	210					215					220				
Ala	Arg	Ala	Val	Val	Arg	Ala	Ser	Leu	Thr	Gly	Ala	Thr	Val	Phe	Ser
225					230					235					240
Thr	Ile	His	Ala	Lys	Ser	Ile	Arg	Gly	Val	Tyr	Glu	Arg	Leu	Leu	Glu
			245						250					255	
Leu	Gly	Val	Ser	Glu	Glu	Glu	Leu	Ala	Val	Val	Leu	Gln	Gly	Val	Cys
		260						265					270		
Tyr	Gln	Arg	Leu	Ile	Gly	Gly	Gly	Gly	Ile	Val	Asp	Phe	Ala	Ser	Arg
		275					280					285			
Asp	Tyr	Gln	Glu	His	Gln	Ala	Ala	Lys	Trp	Asn	Glu	Gln	Ile	Asp	Gln
	290					295					300				
Leu	Leu	Lys	Asp	Gly	His	Ile	Thr	Ser	Leu	Gln	Ala	Glu	Thr	Glu	Lys
305					310					315					320

Ile Ser Tyr Ser

(2) INFORMATION FOR SEQ ID NO:3720:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 446 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...446

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3720:

Ile	Gly	Ala	Lys	Met	Lys	Arg	Thr	Gly	Leu	Phe	Ala	Lys	Ile	Phe	Ile
1				5					10					15	
Tyr	Thr	Phe	Ser	Ile	Phe	Ser	Val	Leu	Val	Ile	Cys	Leu	His	Leu	Ala
			20					25					30		
Ile	Tyr	Phe	Leu	Phe	Pro	Ser	Thr	Tyr	Leu	Ser	His	Arg	Gln	Glu	Thr
		35					40					45			
Ile	Gly	Gln	Lys	Ala	Thr	Ala	Ile	Ala	Gln	Ser	Leu	Glu	Gly	Lys	Asp
	50					55					60				
Arg	Gln	Ser	Ile	Glu	Gln	Val	Leu	Asp	Leu	Tyr	Ser	Gln	Thr	Ser	Asp
65					70					75				80	
Ile	Lys	Gly	Thr	Val	Lys	Gly	Glu	Met	Thr	Glu	Asp	Lys	Leu	Glu	Val
			85						90					95	
Lys	Asp	Ser	Leu	Pro	Leu	Asp	Thr	Asp	Arg	Gln	Thr	Thr	Ser	Leu	Phe
			100					105					110		
Ile	Glu	Glu	Arg	Glu	Val	Lys	Thr	Gln	Asp	Gly	Gly	Thr	Met	Ile	Leu
	115						120					125			
Gln	Phe	Leu	Ala	Ser	Met	Asp	Leu	Gln	Lys	Glu	Ala	Glu	Gln	Ile	Ser
	130					135					140				
Leu	Gln	Phe	Leu	Pro	Tyr	Thr	Leu	Leu	Ala	Ser	Phe	Leu	Ile	Ser	Leu
145					150					155				160	
Leu	Val	Ala	Tyr	Ile	Tyr	Ala	Arg	Thr	Ile	Val	Ala	Pro	Ile	Leu	Glu
			165						170					175	
Ile	Lys	Arg	Val	Thr	Arg	Arg	Met	Met	Asp	Leu	Asp	Ser	Gln	Val	Arg
			180					185					190		
Leu	Arg	Val	Asp	Ser	Lys	Asp	Glu	Ile	Gly	Asn	Leu	Lys	Glu	Gln	Ile
	195						200					205			
Asn	Ser	Leu	Tyr	Gln	His	Leu	Leu	Thr	Val	Ile	Ala	Asp	Leu	His	Glu
	210					215					220				
Lys	Asn	Glu	Ala	Ile	Leu	Gln	Leu	Glu	Lys	Met	Lys	Val	Glu	Phe	Leu
225					230					235				240	
Arg	Gly	Ala	Ser	His	Glu	Leu	Lys	Thr	Pro	Leu	Ala	Ser	Leu	Lys	Ile
			245						250					255	
Leu	Ile	Glu	Asn	Met	Arg	Glu	Asn	Ile	Gly	Arg	Tyr	Lys	Asp	Arg	Asp
			260					265					270		

Gln	Tyr	Leu	Gly	Val	Ala	Leu	Gly	Ile	Val	Asp	Glu	Leu	Asn	His	His
		275					280					285			
Val	Leu	Gln	Ile	Leu	Ser	Leu	Ser	Ser	Val	Gln	Glu	Leu	Arg	Asp	Asp
	290					295					300				
Arg	Glu	Thr	Ile	Asp	Leu	Leu	Gln	Met	Thr	Gln	Asn	Leu	Val	Lys	Asp
305					310					315					320
Tyr	Ala	Leu	Leu	Ala	Lys	Glu	Arg	Glu	Leu	Gln	Ile	Asp	Asn	Ser	Leu
				325					330					335	
Thr	His	Gln	Gln	Ala	Tyr	Leu	Asn	Pro	Ser	Val	Met	Lys	Leu	Ile	Leu
			340					345					350		
Ser	Asn	Leu	Ile	Ser	Asn	Ala	Ile	Lys	His	Ser	Val	Pro	Gly	Gly	Leu
	355					360						365			
Val	Arg	Ile	Gly	Glu	Arg	Glu	Gly	Glu	Leu	Phe	Ile	Glu	Asn	Ser	Cys
	370					375				380					
Ser	Ser	Glu	Glu	Gln	Glu	Lys	Leu	Ala	Gln	Ser	Phe	Ser	Asp	Asn	Ala
385					390				395						400
Ser	Arg	Lys	Val	Lys	Gly	Ser	Gly	Met	Gly	Leu	Phe	Val	Val	Lys	Ser
				405				410						415	
Leu	Leu	Glu	His	Glu	Lys	Leu	Ala	Tyr	Arg	Phe	Glu	Met	Glu	Glu	Asn
			420					425					430		
Arg	Leu	Thr	Phe	Phe	Ile	Asp	Phe	Pro	Lys	Val	Ala	Gln	Asp		
	435						440					445			

(2) INFORMATION FOR SEQ ID NO:3721:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 520 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...520

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3721:

Arg	Ser	Ala	Asn	Thr	Arg	Lys	Ala	Arg	Thr	Ala	Lys	Pro	Thr	Arg	Pro
1				5				10						15	
Ser	Arg	Arg	Ser	Arg	Arg	Ser	Ala	Ser	Gly	Cys	Ala	Arg	Val	Pro	Thr
		20					25					30			
Lys	Pro	Ala	Ile	Thr	His	Arg	Pro	Ala	Arg	Ser	Cys	Gly	Ala	Ser	Ala
		35				40					45				
His	Glu	Pro	Gly	Ala	Ala	Val	Ala	Arg	Pro	Thr	Pro	Ala	Pro	Gly	Pro
	50					55					60				
Gly	Arg	Ala	Arg	Pro	Gly	Pro	Pro	Ile	Ala	Thr	Gly	Ser	Arg	Arg	Gly
65				70				75						80	
Ala	Gly	Thr	His	Arg	Ala	Pro	Gly	Gly	Ala	Thr	Gly	Leu	Pro	Arg	Leu
			85					90					95		
Ala	Thr	Gly	Arg	Arg	Ala	Thr	Ala	Val	Ser	Arg	Leu	Pro	Gly	Gly	His
		100					105						110		

Ala	Arg	Pro	Pro	Ala	Pro	Gly	Ser	Leu	Ala	Ala	Ala	Gly	Arg	Thr	Ala	115	120	125
Ala	Gly	Lys	Gly	Ser	Arg	Pro	Gly	Thr	Gly	Leu	Arg	Arg	Asp	Arg	Ala	130	135	140
Ala	Pro	Arg	Arg	Gly	Ala	Arg	Ala	Pro	Ala	Ala	Val	Pro	Ala	Arg	Thr	145	150	155
Ala	Gly	Thr	Pro	Ala	Ala	Thr	Gly	Glu	Val	Arg	Arg	Thr	Gly	Ala	Pro	165	170	175
Arg	Arg	Arg	Arg	Ala	Pro	Gly	Ala	Ala	Arg	Thr	Gln	Arg	Gly	Arg	Arg	180	185	190
Thr	Gly	Arg	Ile	His	Pro	Pro	Arg	Asp	Leu	Ala	Met	Leu	Lys	Leu	Asn	195	200	205
Ala	Val	Asp	Thr	Ala	Pro	Leu	Val	Ser	Ser	Asp	Thr	Pro	Ala	Pro	Leu	210	215	220
Pro	Pro	Leu	Arg	Ala	Gln	Gln	Ile	Ala	Phe	Glu	Gln	Ala	Leu	Pro	Ala	225	230	235
His	Arg	Pro	Pro	Ala	Pro	Arg	Pro	Pro	Phe	Asp	Lys	Gly	Asp	Glu	Thr	245	250	255
Thr	Glu	Ala	Glu	Glu	Pro	Ala	Ala	Asn	Ser	Asp	Ala	Pro	Thr	Ser	Thr	260	265	270
Pro	Leu	Ala	Asp	Gln	Pro	Ala	Ala	Pro	Ala	Ala	Asp	Arg	Pro	Pro	Thr	275	280	285
Asn	Arg	Gln	Ala	Pro	Val	Pro	Val	Ala	Ala	Glu	Ala	Thr	Pro	Thr	Pro	290	295	300
Thr	Pro	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Val	305	310	315
Leu	Pro	Ser	Gly	Ser	Val	Ala	Arg	Gln	Ala	Pro	Ala	Val	Ser	Ala	Arg	325	330	335
Val	Ala	Ala	Ser	Thr	Gln	Ala	Arg	Glu	Pro	Ala	Ser	Val	Ser	Ala	Pro	340	345	350
Pro	Val	Asp	Glu	Pro	Pro	Leu	Val	Pro	Val	Ser	Ser	His	Pro	Gln	Ile	355	360	365
Ala	Gly	Arg	Thr	His	Glu	Arg	Pro	Gln	Pro	Gly	Pro	Gly	Phe	Pro	Ala	370	375	380
Lys	Thr	Ala	Ala	Glu	Val	Ala	Ser	Thr	Ala	Gln	Ala	Ser	Val	Gln	Val	385	390	395
Ser	Pro	Pro	Ala	Pro	Thr	Ala	Gly	Gly	Glu	Gly	Arg	Gly	Glu	Glu	Arg	405	410	415
Arg	Gln	Pro	Gly	Glu	Thr	Asp	Pro	Ser	Ala	Leu	Pro	Pro	Asp	Asp	Gln	420	425	430
Ala	Pro	Val	Pro	Leu	Pro	Ala	Met	Gln	Thr	Pro	Gly	Asp	Arg	Leu	Leu	435	440	445
Ala	Arg	Leu	Leu	Ala	Ser	Ser	Gly	Ser	Arg	Pro	Leu	Pro	Leu	Ala	Asp	450	455	460
Leu	Ala	Arg	Leu	Leu	Asp	Ala	Val	Gln	Gly	Arg	Ile	Gln	Val	Ala	Ser	465	470	475
Ala	Ala	Glu	Ser	His	Ala	Ala	Arg	Leu	Gln	Val	Arg	Leu	Pro	Gln	Leu	485	490	495
Gly	Ala	Val	Glu	Val	Gln	Val	Leu	His	Gly	His	Gly	Gln	Leu	Gln	Val	500	505	510
Val	Phe	Thr	Thr	Ser	Arg	Glu	Val									515	520	

(2) INFORMATION FOR SEQ ID NO:3722:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 461 amino acids

(B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...461

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3722:

```

Ile Asn Gln Asn Arg Lys Arg Ser Met Tyr Lys Thr Lys Cys Leu Arg
1      5      10      15
Glu Lys Leu Val Leu Phe Leu Lys Ile Phe Phe Pro Ile Leu Ile Tyr
      20      25      30
Gln Phe Ala Asn Tyr Ser Ala Ser Phe Val Asp Thr Ala Met Thr Gly
      35      40      45
Gln Tyr Asn Thr Met Asp Leu Ala Gly Val Ser Met Ala Thr Ser Ile
      50      55      60
Trp Asn Pro Phe Phe Thr Phe Leu Thr Gly Ile Val Ser Ala Leu Val
65      70      75      80
Pro Ile Ile Gly His His Leu Gly Arg Gly Lys Lys Glu Glu Val Ala
      85      90      95
Ser Asp Phe Tyr Gln Phe Ile Tyr Leu Ala Leu Gly Leu Ser Val Val
      100     105     110
Leu Leu Gly Met Val Leu Phe Leu Ala Pro Thr Ile Leu Asn His Ile
      115     120     125
Gly Leu Glu Ala Ala Val Ala Ala Val Ala Val Arg Tyr Leu Trp Phe
      130     135     140
Leu Ser Ile Gly Ile Ile Pro Leu Leu Leu Phe Ser Val Ile Arg Ser
145     150     155     160
Leu Leu Asp Ser Leu Gly Leu Thr Lys Leu Ser Met Tyr Leu Met Leu
      165     170     175
Leu Leu Leu Pro Leu Asn Ser Gly Phe Asn Tyr Leu Leu Ile Tyr Gly
      180     185     190
Ala Phe Gly Val Pro Glu Leu Gly Gly Ala Gly Ala Gly Leu Gly Thr
      195     200     205
Ser Leu Ala Tyr Trp Val Leu Leu Gly Ile Ser Val Leu Val Leu Phe
      210     215     220
Lys Gln Glu Lys Leu Lys Ala Leu His Leu Glu Lys Arg Ile Pro Leu
225     230     235     240
Asn Met Asp Lys Ile Lys Glu Gly Val Arg Leu Gly Leu Pro Ile Gly
      245     250     255
Gly Thr Val Phe Ala Glu Val Ala Val Phe Ser Val Val Gly Leu Ile
      260     265     270
Met Ala Lys Phe Ser Ser Leu Ile Ile Ala Ser His Gln Ser Ala Met
      275     280     285
Asn Phe Ser Ser Leu Met Tyr Ala Phe Pro Met Ser Ile Ser Ser Ala
      290     295     300
Met Ala Ile Val Val Ser Tyr Glu Val Gly Ala Lys Arg Phe Asp Asp
305     310     315     320

```

Ala	Lys	Thr	Tyr	Ile	Gly	Leu	Gly	Arg	Trp	Thr	Ala	Leu	Ile	Phe	Ala
				325					330					335	
Ala	Phe	Thr	Leu	Thr	Phe	Leu	Tyr	Ile	Phe	Arg	Gly	Asn	Val	Ala	Ser
			340					345					350		
Leu	Tyr	Gly	Asn	Asp	Pro	Lys	Phe	Ile	Asp	Leu	Thr	Ala	Arg	Phe	Leu
		355					360					365			
Thr	Tyr	Ser	Leu	Phe	Phe	Gln	Leu	Ala	Asp	Thr	Phe	Ala	Ala	Pro	Leu
		370				375					380				
Gln	Gly	Ile	Leu	Arg	Gly	Tyr	Lys	Asp	Thr	Val	Ile	Pro	Phe	Tyr	Leu
385					390					395					400
Gly	Leu	Leu	Gly	Tyr	Trp	Gly	Val	Ala	Ile	Pro	Val	Ala	Thr	Leu	Phe
			405					410					415		
Asp	Ser	Leu	Thr	Asp	Phe	Gly	Ala	Tyr	Ser	Tyr	Trp	Ile	Gly	Leu	Ile
			420				425					430			
Ile	Ser	Leu	Ile	Val	Ser	Gly	Ala	Leu	Tyr	Arg	Trp	Arg	Leu	Thr	Val
		435				440					445				
Ile	Met	Lys	Arg	Phe	Glu	Ser	Leu	Ala	Lys	Ser	Lys	Arg			
	450					455					460				

(2) INFORMATION FOR SEQ ID NO:3723:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 342 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...342

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3723:

Lys	Tyr	Gln	Lys	Thr	Arg	Arg	Ser	Ala	Asn	Ala	Ser	Val	Lys	Met	Val
1			5						10					15	
Leu	Phe	Ser	Ala	Gln	Glu	Gln	Leu	Tyr	Lys	Glu	Lys	Ile	Met	Thr	
			20					25				30			
Thr	Asn	Arg	Leu	Gln	Val	Ser	Leu	Pro	Gly	Leu	Asp	Leu	Lys	Asn	Pro
			35				40					45			
Ile	Ile	Pro	Ala	Ser	Gly	Cys	Phe	Gly	Phe	Gly	Gln	Lys	Tyr	Ala	Lys
	50					55				60					
Tyr	Tyr	Asp	Leu	Asp	Leu	Leu	Gly	Ser	Ile	Met	Ile	Lys	Ala	Thr	Thr
65					70					75				80	
Leu	Glu	Pro	Arg	Phe	Gly	Asn	Pro	Thr	Pro	Arg	Val	Ala	Glu	Thr	Pro
			85					90					95		
Ala	Gly	Met	Leu	Asn	Ala	Ile	Gly	Leu	Gln	Asn	Pro	Gly	Leu	Glu	Val
			100					105					110		
Val	Leu	Ala	Glu	Lys	Leu	Pro	Trp	Leu	Glu	Arg	Glu	Tyr	Pro	Asn	Leu
		115					120					125			
Pro	Ile	Ile	Ala	Asn	Val	Ala	Gly	Phe	Ser	Lys	Gln	Glu	Tyr	Ala	Ala
	130					135						140			

Val	Ser	His	Gly	Ile	Ser	Lys	Ala	Thr	Asn	Val	Lys	Ala	Ile	Glu	Leu
145					150					155					160
Asn	Ile	Ser	Cys	Pro	Asn	Val	Asp	His	Cys	Asn	His	Gly	Leu	Leu	Ile
			165						170						175
Gly	Gln	Asp	Pro	Asp	Leu	Ala	Tyr	Asp	Val	Val	Lys	Ala	Ala	Val	Glu
			180					185					190		
Ala	Ser	Glu	Val	Pro	Val	Tyr	Val	Lys	Leu	Thr	Pro	Ser	Val	Thr	Asp
		195					200					205			
Ile	Val	Thr	Val	Ala	Lys	Ala	Ala	Glu	Asp	Ala	Gly	Ala	Ser	Gly	Leu
	210					215					220				
Thr	Met	Ile	Asn	Thr	Leu	Val	Gly	Met	Arg	Phe	Asp	Leu	Lys	Thr	Arg
225					230					235					240
Lys	Pro	Ile	Leu	Ala	Asn	Gly	Thr	Gly	Gly	Met	Ser	Gly	Pro	Ala	Val
				245					250					255	
Phe	Pro	Val	Ala	Leu	Lys	Leu	Ile	Arg	Gln	Val	Ala	Gln	Thr	Thr	Asp
			260					265					270		
Leu	Pro	Ile	Ile	Gly	Met	Gly	Gly	Val	Asp	Ser	Thr	Glu	Ala	Ala	Leu
		275				280						285			
Glu	Met	Tyr	Leu	Ala	Gly	Ala	Ser	Ala	Ile	Gly	Val	Gly	Thr	Ala	Asn
	290					295					300				
Phe	Thr	Asn	Pro	Tyr	Ala	Cys	Pro	Asp	Ile	Ile	Glu	Asn	Leu	Pro	Lys
305					310					315					320
Val	Met	Asp	Lys	Tyr	Gly	Ile	Ser	Ser	Leu	Glu	Glu	Leu	Arg	Gln	Glu
			325						330					335	
Val	Lys	Glu	Ser	Leu	Arg										
			340												

(2) INFORMATION FOR SEQ ID NO:3724:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...72

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3724:

Phe	Asn	Gln	Lys	Ser	Val	Asp	Thr	Ala	Ser	Arg	Asn	Pro	Leu	Ile	Gly
1			5						10					15	
Leu	Asp	Asn	Ala	Ile	Trp	His	Asn	Ser	Ser	Thr	Leu	Asn	Ile	Pro	Thr
			20					25					30		
Asn	Ile	Asp	Leu	Thr	Ser	Ile	Pro	Pro	Tyr	Thr	Pro	Glu	Met	Asn	Pro
		35					40					45			
Leu	Asn	Lys	Cys	Gly	Lys	Arg	Phe	Val	Asn	Val	Asp	Leu	Arg	Ile	Lys
	50					55					60				
Pro	Phe	Glu	Leu	Trp	Lys	Ile	Ser								
65					70										

(2) INFORMATION FOR SEQ ID NO:3725:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 434 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...434

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3725:

Trp	Leu	Gln	Lys	Ser	Arg	Lys	Lys	Asn	Val	Met	Asn	Glu	Ile	Lys	Cys	
1			5					10					15			
Ser	Asn	Cys	Gly	Val	Xaa	Thr	Val	Asn	Glu	Ser	Gln	Tyr	Ser	Glu		
		20					25					30				
Leu	Leu	Ser	Gln	Val	Arg	Thr	Ala	Glu	Phe	Asp	Lys	Glu	Leu	His	Asp	
		35					40					45				
Arg	Met	Arg	Gln	Glu	Leu	Ala	Leu	Ala	Glu	Gln	Lys	Ala	Met	Asn	Glu	
	50					55					60					
Gln	Gln	Thr	Lys	Leu	Ala	Gln	Lys	Asp	Gln	Glu	Ile	Ala	Gln	Leu	Gln	
65				70					75					80		
Ser	Gln	Ile	Gln	Asn	Phe	Asp	Thr	Glu	Lys	Glu	Leu	Ala	Lys	Lys	Glu	
			85					90						95		
Val	Glu	Gln	Thr	Ser	His	Gln	Ala	Leu	Leu	Ala	Lys	Asp	Lys	Glu	Val	
			100					105					110			
Gln	Ala	Leu	Glu	Asn	Gln	Leu	Ala	Thr	Leu	Arg	Leu	Glu	His	Glu	Asn	
	115						120					125				
Gln	Leu	Gln	Lys	Thr	Leu	Ser	Asp	Leu	Glu	Lys	Glu	Arg	Asn	Gln	Val	
	130					135					140					
Lys	Asn	Gln	Leu	Leu	Leu	Gln	Glu	Lys	Glu	Asn	Glu	Leu	Ser	Leu	Ala	
145				150					155					160		
Ser	Val	Lys	Gln	Asn	Tyr	Glu	Ala	Gln	Leu	Lys	Ala	Ala	Ser	Glu	Gln	
			165					170						175		
Val	Glu	Phe	Tyr	Lys	Asn	Phe	Lys	Ala	Gln	Gln	Ser	Thr	Lys	Ala	Ile	
		180					185						190			
Gly	Glu	Ser	Leu	Glu	Gln	Tyr	Ala	Glu	Ser	Glu	Phe	Asn	Lys	Val	Arg	
	195						200					205				
Ser	Phe	Ala	Phe	Pro	Asn	Ala	Tyr	Phe	Glu	Lys	Asp	Asn	Lys	Val	Ser	
	210					215					220					
Ser	Arg	Gly	Ser	Lys	Gly	Asp	Phe	Ile	Phe	Arg	Glu	Cys	Asp	Glu	Asn	
225				230					235					240		
Gly	Val	Glu	Ile	Ile	Ser	Ile	Met	Phe	Glu	Met	Lys	Asn	Glu	Ala	Asp	
			245					250					255			
Gly	Thr	Glu	Lys	Lys	His	Lys	Asn	Ala	Asp	Phe	Tyr	Lys	Glu	Leu	Asp	
	260						265						270			
Lys	Asp	Arg	Arg	Glu	Lys	Asn	Cys	Glu	Tyr	Ala	Val	Leu	Val	Thr	Met	
	275					280						285				

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Leu Glu Ala Asp Asn Asp Tyr Phe Asn Thr Gly Ile Val Asp Val Ser
290                295                300
His Glu Tyr Glu Lys Met Tyr Val Val Arg Pro Gln Phe Phe Ile Gln
305                310                315                320
Leu Ile Gly Leu Leu Arg Asn Ala Ala Leu Asn Ser Leu Lys Tyr Lys
                325                330                335
Gln Glu Leu Ala Leu Val Arg Glu Gln Asn Ile Asp Ile Thr His Phe
                340                345                350
Glu Glu Asp Leu Asp Ala Phe Lys Leu Ala Phe Ala Lys Asn Tyr Asn
                355                360                365
Ser Ala Ser Thr Asn Phe Gly Lys Ala Ile Asp Glu Ile Asp Lys Ala
                370                375                380
Ile Lys Arg Met Glu Glu Val Lys Lys Phe Leu Thr Thr Ser Glu Asn
385                390                395                400
Gln Leu Arg Leu Ala Asn Asn Lys Leu Glu Asp Val Ser Val Lys Lys
                405                410                415
Leu Thr Arg Lys Asn Pro Thr Met Lys Ala Lys Phe Glu Ala Leu Lys
                420                425                430
Gly Glu

```

(2) INFORMATION FOR SEQ ID NO:3726:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 219 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...219

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3726:

```

Lys Asn Lys Lys Ile Val Ala Ile Asn Asn Gly Ile Asn Val Ser Asn
1          5          10          15
Ser Asp Leu Asp Val Val Gly Val Gln Asp Phe Lys Lys Glu Phe Cys
20          25          30
Ile Pro Asn Asn Lys Lys Ile Ile Cys Tyr Val Gly Arg Leu Asp Pro
35          40          45
Glu Lys Arg Pro Asp Arg Phe Leu Glu Phe Ala Glu Lys Leu Phe Leu
50          55          60
Val Arg Glu Asp Val Ile Phe Ile Met Ala Gly Asn Gly Ser Met Trp
65          70          75          80
Ala Ala Leu Lys Glu Lys Ile Cys His Leu Lys Cys Arg Asp Asn Phe
85          90          95
Arg Leu Leu Gly Glu Ile Tyr Pro Ala Thr Ile Val Tyr Gln Ile Ser
100         105         110
Asp Leu Leu Tyr Ile Pro Tyr Asp Thr Glu Gly Ile Pro Met Cys Val
115         120         125

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Leu	Glu	Ser	Met	Ser	Gln	Gly	Thr	Pro	Val	Leu	Ala	Ser	Asn	Val	Gly
130						135					140				
Gly	Leu	Ser	Glu	Ile	Ile	Glu	His	Arg	Val	Asp	Gly	Phe	Leu	Phe	Glu
145					150					155					160
Lys	Glu	Asp	Val	Glu	Gly	Val	Cys	Ala	Cys	Ala	Asn	Phe	Leu	Leu	Asn
				165					170					175	
Asp	Ser	Glu	Tyr	Leu	Lys	Tyr	Ile	Gly	Glu	Asn	Ser	Lys	Ser	Lys	Ile
			180					185					190		
Arg	Lys	His	Phe	Ser	Val	Gln	Lys	Met	Phe	Val	Glu	Thr	Met	Arg	Val
		195					200						205		
Tyr	Asp	Glu	Leu	Leu	Glu	Lys	Ser	Ser	His	Gly					
210						215									

(2) INFORMATION FOR SEQ ID NO:3727:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 102 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...102
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3727:

Met	Asn	Lys	Lys	Lys	Met	Ile	Leu	Thr	Ser	Leu	Ala	Ser	Val	Ala	Ile
1				5					10					15	
Leu	Gly	Ala	Gly	Phe	Val	Thr	Ser	Gln	Pro	Thr	Val	Val	Arg	Ala	Glu
		20						25					30		
Glu	Ser	Pro	Val	Ala	Ser	Gln	Ser	Lys	Ala	Glu	Lys	Asp	Tyr	Asp	Ala
		35					40					45			
Ala	Val	Lys	Asn	Ala	Thr	Ala	Ala	Lys	Lys	Ala	Ala	Glu	Asp	Ala	Gln
	50					55					60				
Arg	Ala	Leu	Asp	Glu	Ala	Lys	Ala	Ala	Gln	Lys	Lys	Tyr	Asp	Glu	Asp
65					70					75					80
Gln	Lys	Lys	Thr	Glu	Glu	Lys	Ala	Lys	Glu	Val	Lys	Lys	Ala	Ser	Glu
			85						90					95	
Glu	Asn	Lys	Leu	Gln	Ile										
			100												

(2) INFORMATION FOR SEQ ID NO:3728:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2123 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2123

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3728:

Arg	Gly	Lys	Lys	Met	Asp	Ala	Leu	Thr	Arg	Arg	Gln	Phe	Asp	Arg	Ala
1				5					10					15	
Met	Phe	Ala	Lys	Glu	Arg	Thr	Leu	Ala	Ile	Arg	Val	Gly	Glu	Tyr	Ala
			20					25					30		
Ser	Arg	Asp	Ile	Lys	Glu	Ala	Ser	Phe	Glu	Tyr	Gly	Tyr	Ile	Lys	Gly
		35					40					45			
Asp	Thr	Tyr	Lys	Pro	Gly	Gly	Thr	Cys	Ala	Gly	Ser	Gly	Lys	Ile	Thr
	50					55				60					
Phe	Thr	Ser	Ile	Ile	Thr	Thr	Phe	Asn	Lys	Leu	Asp	Thr	Leu	His	Pro
65					70				75					80	
Glu	Ile	Gly	Leu	Leu	Val	Gly	Asp	Thr	Tyr	Gln	Trp	Val	Lys	Met	Gly
			85						90					95	
Glu	Tyr	Phe	Ile	Asn	Asp	Ile	Glu	Ile	Asp	Arg	Asn	Arg	Asn	Thr	Thr
			100					105					110		
Thr	Leu	Glu	Leu	Met	Asp	Gly	Met	Phe	Lys	Leu	Asn	Arg	Glu	Tyr	Val
		115					120					125			
Thr	Asp	Leu	His	Phe	Pro	Ala	Glu	Val	Arg	Glu	Val	Ile	Gln	Glu	Ile
	130					135					140				
Cys	Leu	Lys	Thr	Gly	Ile	Glu	Leu	Ala	Asn	Asp	Tyr	Phe	Gly	Ile	Ser
145					150					155				160	
Ala	Met	Arg	Tyr	His	Ile	Glu	Gln	Val	Pro	Glu	Gly	Lys	Lys	Leu	Ser
			165						170					175	
Phe	Arg	Asp	Met	Leu	Ser	Ala	Met	Thr	Gln	Met	Ile	Gly	Met	Ser	Cys
		180					185						190		
Phe	Phe	Asn	Arg	Glu	Gly	Lys	Met	Glu	Ile	Arg	Asp	Leu	Thr	Glu	Ser
	195					200					205				
Asn	Ile	Thr	Ile	Asn	Ala	Asp	Ser	Tyr	Phe	Leu	His	Gly	Leu	Thr	Lys
	210					215					220				
Ser	Glu	Ile	Glu	Tyr	Gln	Ile	Ala	Gly	Ile	Thr	Cys	Lys	Thr	Asp	Lys
225					230					235				240	
Lys	Ser	Leu	Thr	Val	Gly	Met	Thr	Thr	Gly	Arg	Ser	Leu	Glu	Leu	Asp
			245						250					255	
Asn	Val	Phe	Ile	Thr	Gln	Ser	Ala	Leu	Asn	Asp	Leu	Tyr	Tyr	Lys	Leu
		260						265					270		
Lys	Asn	Leu	Thr	Tyr	Tyr	Pro	Tyr	Asn	Leu	Asn	Tyr	Gln	Gly	His	Leu
	275						280					285			
Leu	Leu	Glu	Val	Gly	Gln	Trp	Val	Thr	Ile	Gln	Thr	Asn	Lys	Lys	Glu
	290					295					300				
Thr	Phe	Lys	Val	Pro	Val	Leu	Ser	Gln	Ser	Phe	Ile	Phe	Lys	Gly	Gly
305					310					315				320	
Leu	Arg	Gly	Arg	Ile	Ser	Ala	Asp	Ser	Lys	Ala	Gly	Asn	Asp	Thr	Gln
			325						330				335		
Tyr	Ser	Tyr	Glu	Gly	Thr	Ile	Thr	Lys	Gln	Ile	Lys	Gln	Gln	Asp	Gly
		340					345					350			
Phe	Glu	Ala	Lys	Ile	Gln	Ala	Gln	Ile	Glu	Ala	Ala	Asp	Lys	Asp	Phe

		355				360				365					
Asp	Gln	Lys	Val	Asp	Lys	Ile	Lys	Lys	Asp	Phe	Asn	Asp	Gln	Val	Glu
	370					375				380					
Leu	Ala	Lys	Ala	Arg	Ala	Glu	Glu	Val	Lys	Arg	Glu	Leu	Ser	Asp	Thr
385					390					395					400
Ile	Asn	Gln	Arg	Phe	Asn	Ser	Phe	Asp	Asn	Gly	Pro	Leu	Lys	Glu	Ala
				405					410					415	
Lys	Arg	Lys	Ala	Glu	Glu	Ala	Leu	Arg	Asn	Ala	Gly	Ala	Ser	Ser	Ser
			420					425					430		
Leu	Ala	Gln	Glu	Ser	Lys	Arg	Ile	Gly	Leu	Asp	Ser	Val	Ala	Arg	Leu
	435						440					445			
Glu	Ala	Phe	Lys	Ser	Gln	Thr	Thr	Ser	Ala	Gln	Thr	Ala	Leu	Ser	Gly
450						455				460					
Asp	Leu	Asp	Val	Leu	Lys	Arg	Thr	Ile	Ala	Asn	Asp	Ile	Arg	Pro	Lys
465					470					475					480
Gln	Ala	Gln	Ala	Glu	Ala	Glu	Ile	Ala	Lys	Gln	Val	Glu	Ala	Leu	Ser
				485					490					495	
Arg	Thr	Lys	Asn	Glu	Leu	Asp	Gly	Ala	Ser	Thr	Leu	Leu	Ala	Gln	Glu
			500					505					510		
Ala	Lys	Arg	Ile	Glu	Leu	Asp	Ser	Val	Ala	Arg	Leu	Glu	Ala	Phe	Lys
	515						520					525			
Ser	Gln	Thr	Thr	Ser	Ala	Gln	Thr	Ala	Leu	Ser	Gly	Asp	Leu	Asp	Val
530						535					540				
Leu	Lys	Arg	Thr	Ile	Ala	Asn	Asp	Ile	Arg	Pro	Lys	Gln	Ala	Gln	Ala
545					550					555					560
Glu	Ala	Glu	Ile	Ala	Lys	Gln	Val	Glu	Ala	Leu	Ser	Arg	Thr	Lys	Asn
				565				570						575	
Glu	Leu	Ala	Gly	Val	Lys	Ser	Ala	Gln	Ala	Thr	Tyr	Glu	Glu	Thr	Thr
			580					585					590		
Thr	Arg	Arg	Leu	Ser	Glu	Leu	Thr	Asn	Leu	Ala	Asn	Gly	Lys	Ala	Ser
			595				600					605			
Lys	Ser	Glu	Leu	Thr	Gln	Thr	Ala	Glu	Glu	Leu	Ala	Ser	Arg	Ile	Ala
610						615					620				
Ser	Val	Gln	Ala	Gly	Ser	Ser	Arg	Asn	Tyr	Phe	Arg	Asn	Ser	Arg	Ser
625					630					635					640
Arg	Thr	Phe	Thr	Thr	Gly	Gly	Gln	Ala	Val	Tyr	Asp	Tyr	Arg	Thr	Phe
				645					650					655	
Ile	Val	Pro	Asp	Phe	Trp	Lys	Asn	Ser	Asp	Arg	Phe	Lys	Arg	Asp	Tyr
			660					665					670		
Val	Arg	Ile	Ser	Phe	Asp	Val	Thr	Phe	Pro	Val	Ala	Leu	Val	Asn	Asp
	675						680					685			
Met	Pro	Ala	Met	Val	His	Phe	Ser	Ala	His	Pro	Trp	Tyr	Ala	Tyr	Arg
690						695					700				
Asn	Leu	Ile	Phe	Lys	Gly	Gly	Thr	Val	Glu	Arg	Gln	His	Phe	Glu	Phe
705					710					715					720
Thr	Ile	Asp	Leu	Ser	Ser	Ser	Ser	Glu	Thr	Tyr	Gln	Thr	Asn	Asn	Val
				725					730					735	
Phe	Ile	Arg	Phe	Gly	Thr	Asn	Tyr	Gly	Phe	Pro	Ala	Gly	Leu	Gln	Val
			740					745					750		
Val	Ile	Glu	Asn	Ala	Met	Leu	Ser	Val	Gly	Asn	Tyr	Phe	Pro	Ala	Tyr
	755						760					765			
Gln	Pro	Ala	Tyr	Glu	Asp	Gln	Asp	Glu	Arg	Val	Ser	Ala	Val	Glu	Ser
770						775					780				
Asn	Phe	Lys	Gln	Arg	Ala	Asp	Ser	Leu	Asp	Ala	Gly	Val	Ser	Arg	Leu
785					790					795					800
Thr	Glu	Gly	Leu	Arg	Thr	Lys	Val	Asp	Ile	Ser	Ser	Leu	Asn	Val	Thr
				805					810					815	

Ala	Glu	Asn	Ile	Arg	Gln	Ser	Val	Lys	Ser	Leu	Glu	Thr	Asp	Thr	Gln	
			820					825					830			
Asn	Lys	Leu	Asn	Gln	Lys	Leu	Ser	Gln	Ala	Glu	Phe	Glu	Val	Arg	Ala	
		835						840					845			
Gly	Ser	Ile	Arg	Gln	Glu	Ile	Leu	Asn	Ala	Thr	Lys	Asp	Lys	Ala	Ser	
	850					855						860				
Lys	Ser	Glu	Leu	Thr	Gln	Thr	Ala	Glu	Glu	Leu	Ala	Ser	Lys	Ile	Ala	
865					870						875				880	
Ser	Val	His	Leu	Gly	Arg	Arg	Asn	Leu	Leu	Lys	Gly	Thr	Lys	Glu	Leu	
			885						890					895		
Ala	Arg	Tyr	Lys	Pro	Val	Ser	Glu	Tyr	Asn	Gly	Phe	Lys	Val	Ile	Arg	
		900						905					910			
Thr	Val	Ala	Gly	Ala	Thr	Arg	Tyr	Gln	Asp	Ser	Tyr	Val	Glu	Arg	Thr	
	915						920						925			
Val	Ile	Pro	Thr	Ala	Gly	Thr	Glu	Tyr	Ile	Ala	Ile	Phe	Tyr	Ala	Arg	
	930					935					940					
Ala	Ser	Glu	Asn	Asp	Tyr	Pro	Val	Arg	Cys	His	Phe	Tyr	Asn	Pro	Asn	
945					950					955					960	
Thr	Val	Val	Ser	Ser	Glu	Asn	Ser	Ser	Gly	Tyr	Lys	Ser	Arg	Ser	Ser	
			965						970					975		
Asp	Gly	Leu	Ser	Ile	Ile	Arg	Leu	Ser	Thr	Asp	Trp	Gln	Leu	Cys	Trp	
		980						985					990			
Val	Lys	Trp	Thr	Gln	Thr	Ala	Thr	Asp	Gln	Ala	Lys	Thr	Val	Ile	Ile	
	995						1000						1005			
Gly	Arg	His	Gly	Pro	Gln	Val	Gly	Gly	Lys	Glu	Gly	Val	Trp	Val	Glu	
	1010					1015					1020					
Ile	Cys	Ala	Pro	Ala	Ile	Phe	Glu	Gly	Asn	Leu	Ala	Gly	Asp	Trp	Ser	
1025					1030					1035					1040	
Pro	Ala	Tyr	Glu	Asp	Gln	Asp	Glu	Arg	Val	Ser	Val	Val	Glu	Ser	Asn	
			1045						1050					1055		
Phe	Lys	Gln	Arg	Ala	Asp	Ser	Leu	Asp	Ala	Gly	Val	Ser	Arg	Leu	Thr	
		1060						1065					1070			
Glu	Gly	Leu	Arg	Thr	Lys	Ala	Asp	Ile	Ser	Ser	Leu	Asn	Val	Thr	Ala	
	1075						1080					1085				
Glu	Asn	Ile	Arg	Gln	Ser	Val	Lys	Ser	Leu	Glu	Thr	Asp	Thr	Gln	Asn	
	1090					1095					1100					
Lys	Leu	Asn	Gln	Lys	Leu	Ser	Gln	Ala	Glu	Phe	Glu	Val	Arg	Ala	Gly	
1105					1110					1115					1120	
Ser	Ile	Arg	Gln	Glu	Ile	Leu	Asn	Ala	Thr	Lys	Asp	Lys	Ala	Asp	Lys	
			1125						1130					1135		
Thr	Leu	Val	Val	Thr	Glu	Ala	Gly	Lys	Leu	Arg	Glu	Glu	Phe	Ser	Lys	
		1140						1145					1150			
Met	Lys	Val	Gly	Gly	Arg	Asn	Leu	Trp	Ile	Lys	Ser	Lys	Thr	Val	Gly	
	1155						1160					1165				
Ala	Val	Ile	Glu	Lys	Leu	Pro	Glu	Asn	His	Val	Thr	Gly	Gln	Lys	Glu	
	1170					1175					1180					
Cys	Tyr	Arg	Leu	Glu	Asn	Asn	Ser	Thr	Leu	Thr	Phe	Asn	Leu	Glu	Pro	
1185					1190					1195					1200	
Asp	Phe	Ser	Ser	Arg	Leu	Tyr	Gln	Lys	Val	Thr	Phe	Ser	Ala	Trp	Ile	
			1205						1210					1215		
Lys	Tyr	Glu	Asn	Val	Val	Gln	Gly	Arg	Asn	Phe	Trp	Asn	Val	Phe	Asn	
		1220					1225						1230			
Cys	Phe	Lys	His	Tyr	Leu	Phe	Arg	Lys	Asn	Ser	Glu	Thr	Gly	Val	Gln	
	1235						1240					1245				
Ser	Gly	Pro	Asp	Tyr	Ala	Thr	Leu	Gly	Met	Tyr	Lys	Gly	Ser	Ala	Asp	
	1250					1255					1260					
Trp	Lys	Tyr	Ile	Thr	Phe	Thr	Tyr	Asp	Tyr	Ser	Glu	Lys	Thr	Asn	Phe	

Tyr	Lys	Gly	Tyr	Lys	Pro	Arg	Thr	Trp	Gln	Pro	His	Pro	Glu	Asp	Ala		
1730						1735					1740						
Val	Ala	Asp	Ala	Asn	Lys	Lys	Leu	Glu	Ala	Thr	Gln	Thr	Lys	Met	Thr		
1745					1750					1755					1760		
Gln	Leu	Ala	Gly	Ser	Trp	Val	Val	Glu	Asn	Ile	Asn	Ser	Ala	Gly	Asp		
				1765					1770					1775			
Ile	Ile	Ser	Gly	Ile	Asn	Leu	Gly	Ala	Asn	Gly	His	Asn	Arg	Leu	Val		
			1780					1785					1790				
Gly	Lys	Leu	Thr	His	Ile	Thr	Gly	Glu	Thr	Leu	Ile	Asp	Arg	Ala	Val		
			1795					1800					1805				
Ile	Lys	Ser	Ala	Met	Val	Asp	Lys	Leu	Lys	Thr	Ala	Asn	Phe	Glu	Ala		
	1810					1815					1820						
Gly	Ser	Val	Thr	Thr	Thr	Ile	Leu	Glu	Ala	Glu	Ala	Val	Thr	Ala	Glu		
1825					1830					1835					1840		
Lys	Leu	Lys	Val	Asp	Asn	Ala	Leu	Ile	Lys	Lys	Leu	Thr	Ala	Thr	Asp		
				1845					1850					1855			
Ala	Phe	Ile	Asp	Gln	Leu	Ile	Ser	Lys	Arg	Ile	Phe	Ser	Thr	Lys	Val		
			1860					1865					1870				
Glu	Ser	Val	Ile	Ser	Ser	Ser	Thr	Phe	Leu	Glu	Ala	Tyr	Gln	Gly	Arg		
		1875					1880						1885				
Ile	Gly	Gly	Phe	Thr	Leu	Gly	Gln	Phe	Asp	Gln	Gly	Gly	Gly	Arg	Trp		
	1890					1895					1900						
Ile	Ser	Gly	Val	Asn	Gln	Phe	Ser	Val	Gly	Met	Gly	Asn	Gly	Ala	Gly		
1905					1910					1915					1920		
Tyr	Gly	Val	Arg	Thr	Ala	Phe	Trp	Ala	Asn	Trp	Gly	Asn	Asn	Trp	Asn		
				1925					1930					1935			
Tyr	Ala	Gly	Pro	Lys	Ala	Trp	Asn	Val	Asn	Thr	Asp	Gly	Lys	Met	Tyr		
			1940					1945					1950				
Cys	Arg	Asn	Glu	Val	Gly	Phe	Tyr	Asp	Gln	Val	Asp	Phe	Ser	Asn	Ser		
		1955					1960					1965					
Ser	Arg	Ala	Asn	Phe	Tyr	Gly	Asn	Thr	Thr	Phe	Ser	Arg	Ser	Pro	Val		
	1970					1975					1980						
Phe	Ser	Asn	Gly	Ile	Glu	Leu	Gly	Ser	Lys	Asp	Val	Leu	Gly	Asp	Gly		
1985					1990					1995					2000		
Trp	Asn	Pro	Lys	Gly	Gly	Arg	Asn	Ala	Val	Val	Trp	Trp	Asn	Gln	Val		
				2005					2010					2015			
Gly	Ser	Gly	Ser	Leu	Lys	Tyr	Trp	Met	Glu	Gln	Lys	Ser	Asp	Arg	Arg		
			2020					2025					2030				
Leu	Lys	Glu	Asn	Ile	Thr	Asp	Thr	Ala	Val	Lys	Ala	Leu	Asp	Lys	Ile		
		2035				2040					2045						
Asn	Arg	Leu	Arg	Met	Val	Ala	Phe	Asp	Phe	Ile	Glu	Asn	Lys	Lys	His		
	2050					2055					2060						
Glu	Glu	Ile	Gly	Leu	Ile	Ala	Gln	Glu	Ala	Glu	Thr	Ile	Val	Pro	Lys		
2065					2070					2075					2080		
Ile	Val	Ser	Arg	Asp	Pro	Glu	Asn	Pro	Asp	Gly	Tyr	Leu	His	Ile	Asp		
			2085						2090					2095			
Tyr	Thr	Ala	Leu	Val	Pro	Tyr	Leu	Ile	Lys	Ala	Ile	Gln	Glu	Leu	Asn		
		2100					2105						2110				
Gln	Lys	Ile	Glu	Lys	Met	Glu	Lys	Thr	Ile	Ala							
	2115						2120										

(2) INFORMATION FOR SEQ ID NO:3729:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 326 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...326

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3729:

Lys	Gly	Lys	Lys	Met	Ser	Thr	Leu	Asp	Lys	Asn	Leu	Leu	Leu	Glu	Met
1				5					10					15	
Phe	Arg	Lys	Met	Glu	Glu	Ile	Arg	Arg	Met	Asp	Leu	Lys	Ile	Ala	Gln
		20						25					30		
Leu	Val	Lys	Lys	Gly	Lys	Val	Pro	Gly	Met	Thr	His	Phe	Ser	Val	Gly
		35					40					45			
Glu	Glu	Ala	Ala	Asn	Val	Gly	Ala	Met	Leu	Ala	Leu	Asn	Pro	Asp	Asp
	50					55					60				
Leu	Ile	Thr	Ser	Asn	His	Arg	Gly	His	Gly	Gln	Ala	Ile	Ala	Lys	Gly
65					70				75					80	
Ile	Asp	Leu	Asn	Gly	Met	Met	Ala	Glu	Ile	Leu	Gly	Lys	Tyr	Thr	Gly
				85					90					95	
Thr	Cys	Lys	Gly	Lys	Gly	Gly	Ser	Met	His	Ile	Ala	Asp	Leu	Asp	Ala
			100					105					110		
Gly	Asn	Leu	Gly	Ala	Asn	Gly	Ile	Val	Gly	Gly	Gly	Met	Gly	Ile	Ala
		115					120					125			
Val	Gly	Ala	Ala	Leu	Ser	Gln	Gln	Met	Gln	Asn	Thr	Gly	Lys	Ile	Val
		130				135					140				
Val	Cys	Phe	Phe	Gly	Asp	Gly	Ala	Thr	Asn	Glu	Gly	Val	Phe	His	Glu
145					150					155					160
Ala	Val	Asn	Met	Ala	Ser	Ile	Trp	Asn	Leu	Pro	Val	Ile	Phe	Tyr	Cys
			165					170						175	
Ile	Asn	Asn	Gly	Tyr	Gly	Ile	Ser	Ala	Asp	Ile	Lys	Lys	Met	Thr	Asn
			180				185						190		
Ile	Glu	His	Ile	His	Gln	Arg	Ser	Ala	Ala	Tyr	Gly	Ile	Pro	Gly	Met
	195					200						205			
Phe	Ile	Glu	Asp	Gly	Asn	Asn	Val	Ile	Asp	Val	Tyr	Glu	Gly	Phe	Gln
	210					215					220				
Lys	Ala	Val	Asp	His	Val	Arg	Ser	Gly	Asn	Gly	Pro	Val	Leu	Ile	Glu
225					230					235					240
Ser	Val	Thr	Tyr	Arg	Trp	Leu	Gly	His	Ser	Ser	Ser	Asp	Pro	Gly	Lys
			245						250					255	
Tyr	Arg	Thr	Arg	Glu	Glu	Val	Glu	Leu	Trp	Lys	Gln	Lys	Asp	Pro	Ile
		260					265						270		
Glu	Asn	Leu	Arg	Asn	Tyr	Leu	Ile	Glu	Asn	Asn	Ile	Ala	Ser	Ala	Glu
	275						280					285			
Glu	Leu	Glu	Glu	Ile	Gln	Ala	Gln	Val	Lys	Glu	Ala	Val	Glu	Ala	Ser
	290					295						300			
Val	Lys	Phe	Ala	Glu	Glu	Ser	Pro	Phe	Pro	Ser	Leu	Glu	Ser	Ala	Phe
305					310					315					320
Glu	Asp	Ile	Tyr	Ala	Asp										
				325											

(2) INFORMATION FOR SEQ ID NO:3730:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...316

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3730:

Met	Gly	Lys	Lys	Arg	Trp	Ala	Arg	Asn	Gly	Ser	Glu	Ser	Asn	Asp	Ala
1				5					10					15	
Ser	Tyr	Ala	Gln	Val	Val	Ser	Leu	Tyr	Asp	Asp	Thr	Ser	Ile	Ser	Val
			20					25					30		
Ser	Asn	Asn	Glu	Thr	Asp	Lys	Val	Leu	Thr	Gly	Ser	Leu	Tyr	Thr	Glu
		35					40					45			
Thr	Asn	Glu	Gln	Gly	Leu	Thr	Ile	Pro	Ser	Ser	Leu	Leu	Lys	Asn	Trp
	50					55					60				
Asn	Glu	Gln	Thr	Gly	Lys	Asn	Leu	Thr	Thr	Asn	Asp	Leu	Ile	Gly	Lys
65					70					75					80
Ser	Val	Ser	Ala	Ser	Ile	Val	Glu	Ser	Ala	Ala	Glu	Thr	Ser	Lys	Ile
			85						90					95	
Ala	Gln	Phe	Gln	Thr	Lys	Ile	Val	Arg	Val	Ile	Asn	Asp	Glu	Asp	Asp
			100					105					110		
Met	Glu	Asp	Ser	Asn	Ser	Phe	Met	Leu	Ser	His	Gln	Met	Glu	Thr	Ile
	115						120					125			
Leu	Lys	Glu	Ala	Gly	Phe	Thr	Lys	Ala	Val	Ser	Tyr	Phe	Ile	Leu	Glu
	130					135					140				
Leu	Lys	Asp	Pro	Ser	Gln	Thr	Lys	Val	Val	Thr	Glu	Glu	Leu	Gln	Lys
145					150					155					160
Asn	Lys	Lys	Tyr	Thr	Val	Leu	Ser	Gln	Gln	Arg	Val	Leu	Asp	Ile	Val
			165					170						175	
Ile	Thr	Phe	Ile	Arg	Val	Ile	Gln	Gly	Leu	Leu	Ile	Val	Leu	Ser	Ser
		180						185					190		
Gln	Ala	Ile	Val	Val	Ala	Ala	Val	Met	Ile	Gly	Ile	Ile	Ile	Tyr	Ile
	195						200					205			
Asn	Ile	Met	Gln	Arg	Ser	Lys	Glu	Ile	Gly	Val	Met	Lys	Ala	Val	Gly
	210					215					220				
Tyr	Gln	Asn	Arg	Gly	Val	Lys	Gly	Ile	Phe	Ile	Tyr	Glu	Ala	Ile	Trp
225				230					235					240	
Ile	Val	Gly	Ile	Ala	Leu	Leu	Leu	Ala	Phe	Leu	Val	Ala	Gln	Gly	Val
			245					250					255		
Gly	Ser	Leu	Ala	Asn	Ala	Ile	Val	Ser	His	Phe	Tyr	Pro	Ser	Ile	Thr
		260					265					270			
Lys	Val	Phe	Glu	Leu	Asn	Leu	Leu	Ser	Val	Leu	Gly	Thr	Leu	Val	Phe
	275						280					285			

Ala	Leu	Leu	Gly	Tyr	Val	Ser	Ala	Tyr	Phe	Pro	Ala	Arg	Lys	Ile
290					295					300				
Ser	Lys	Met	Asp	Pro	Val	Glu	Ser	Leu	Arg	Tyr	Glu			
305				310					315					

(2) INFORMATION FOR SEQ ID NO:3731:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...128

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3731:

Pro	Leu	Lys	Lys	Thr	Thr	Gly	Thr	Cys	His	Leu	Gln	Ile	Ser	His	Leu
1				5				10					15		
Ser	Gly	Val	Met	Ala	Val	Ser	Ser	Arg	Pro	Arg	Phe	Leu	Gln	Lys	Ile
			20					25				30			
Thr	Asp	Ala	Tyr	Asn	Arg	Asp	Ala	Asp	Leu	Ala	His	Leu	Leu	Leu	Asp
			35				40					45			
Glu	Tyr	Phe	Leu	Asp	Val	Thr	Ala	Lys	Tyr	Gln	Gln	Ala	Val	Arg	Asp
			50			55				60					
Ile	Val	Ala	Leu	Ala	Val	Gln	Ala	Gly	Val	Pro	Val	Pro	Thr	Phe	Ser
65					70					75				80	
Ala	Ala	Ile	Thr	Tyr	Phe	Asp	Ser	Tyr	Arg	Ser	Ala	Asp	Leu	Pro	Ala
				85				90					95		
Asn	Leu	Ile	Gln	Ala	Gln	Arg	Asp	Tyr	Phe	Gly	Ala	His	Thr	Tyr	Gln
			100					105					110		
Arg	Lys	Asp	Lys	Glu	Gly	Thr	Phe	His	Tyr	Ser	Trp	Tyr	Asp	Glu	Lys
			115				120					125			

(2) INFORMATION FOR SEQ ID NO:3732:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 504 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...504

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3732:

Lys	Leu	Lys	Lys	Arg	Glu	Asp	Met	Ile	Thr	Gly	Glu	Leu	Lys	Asn	Lys
1				5					10					15	
Ile	Asp	Gln	Leu	Trp	Glu	Ile	Leu	Trp	Thr	Glu	Gly	Asn	Ala	Asn	Pro
			20					25					30		
Leu	Thr	Asn	Ile	Glu	Gln	Leu	Thr	Tyr	Leu	Leu	Phe	Met	Lys	Asp	Leu
		35					40					45			
Asp	Ser	Val	Glu	Leu	Gly	Arg	Glu	Ser	Asp	Ala	Glu	Phe	Leu	Gly	Ile
	50					55				60					
Pro	Tyr	Glu	Gly	Val	Phe	Pro	Lys	Asp	Lys	Pro	Glu	Tyr	Arg	Trp	Ser
65					70				75					80	
Thr	Phe	Lys	Asn	Ile	Gly	Asp	Ala	Gln	Glu	Val	Tyr	Arg	Leu	Met	Thr
			85						90					95	
Gln	Glu	Ile	Phe	Pro	Phe	Ile	Lys	Asn	Leu	Lys	Gly	Asp	Thr	Asp	Asp
			100					105					110		
Thr	Ala	Phe	Ser	Arg	Tyr	Met	Arg	Glu	Ala	Ile	Phe	Gln	Ile	Asn	Lys
		115					120					125			
Pro	Ala	Thr	Leu	Gln	Lys	Ala	Ile	Ser	Ile	Leu	Asp	Val	Phe	Pro	Thr
		130				135					140				
Arg	Gly	Leu	Asp	Val	Asp	Phe	Asp	Asn	Asp	Lys	Gln	Ser	Ile	Thr	Asp
145					150					155					160
Ile	Gly	Asp	Ile	Tyr	Glu	Tyr	Leu	Leu	Ser	Lys	Leu	Ser	Thr	Ala	Gly
				165					170					175	
Lys	Asn	Gly	Gln	Phe	Arg	Thr	Pro	Arg	His	Ile	Ile	Asp	Met	Met	Val
			180					185					190		
Glu	Leu	Met	Gln	Pro	Thr	Ile	Lys	Asp	Ile	Ile	Ser	Asp	Pro	Ala	Met
		195					200					205			
Gly	Ser	Ala	Gly	Phe	Leu	Val	Ser	Ala	Ser	Arg	Tyr	Leu	Lys	Arg	Lys
		210				215					220				
Lys	Asp	Glu	Trp	Glu	Thr	Asn	Thr	Asp	Asn	Ile	Asn	His	Phe	His	Asn
225					230					235					240
Gln	Met	Phe	His	Gly	Asn	Asp	Thr	Asp	Thr	Thr	Met	Leu	Arg	Leu	Gly
				245					250					255	
Ala	Met	Asn	Met	Met	Leu	His	Gly	Val	Glu	Asn	Pro	Gln	Ile	Ser	Tyr
			260				265						270		
Leu	Asp	Ser	Leu	Ser	Gln	Asp	Asn	Glu	Glu	Ala	Asp	Lys	Tyr	Thr	Leu
		275					280					285			
Val	Leu	Ala	Asn	Pro	Pro	Phe	Lys	Gly	Ser	Leu	Asp	Tyr	Asn	Ser	Thr
		290				295					300				
Ser	Asn	Asp	Leu	Leu	Ala	Thr	Val	Lys	Thr	Lys	Lys	Thr	Glu	Leu	Leu
305					310					315					320
Phe	Leu	Ser	Leu	Phe	Leu	Arg	Thr	Leu	Lys	Pro	Gly	Gly	Arg	Ala	Ala
				325					330					335	
Val	Ile	Val	Pro	Asp	Gly	Val	Leu	Phe	Gly	Ser	Ser	Lys	Ala	His	Lys
			340					345					350		
Gly	Ile	Arg	Gln	Glu	Ile	Val	Glu	Asn	His	Lys	Leu	Asp	Ala	Val	Ile
		355					360					365			
Ser	Met	Pro	Ser	Gly	Val	Phe	Lys	Pro	Tyr	Ala	Gly	Val	Ser	Thr	Ala
		370				375					380				
Ile	Leu	Ile	Phe	Thr	Lys	Thr	Gly	Asn	Gly	Gly	Thr	Asp	Lys	Val	Trp
385					390					395					400

Phe	Tyr	Asp	Met	Lys	Ala	Asp	Gly	Leu	Ser	Leu	Asp	Asp	Lys	Arg	Gln
				405					410					415	
Pro	Ile	Arg	Asp	Asn	Asp	Ile	Pro	Asp	Ile	Ile	Glu	Arg	Phe	His	His
			420					425					430		
Leu	Glu	Lys	Glu	Ala	Glu	Arg	Gln	Arg	Thr	Asp	Gln	Ser	Phe	Phe	Val
		435					440				445				
Pro	Val	Ala	Glu	Ile	Lys	Glu	Asn	Asp	Tyr	Asp	Leu	Ser	Ile	Asn	Lys
	450					455					460				
Tyr	Lys	Glu	Ile	Glu	Tyr	Glu	Lys	Val	Glu	Tyr	Glu	Pro	Thr	Glu	Val
465					470					475					480
Ile	Leu	Lys	Lys	Ile	Asn	Asp	Leu	Glu	Lys	Glu	Ile	Gln	Ala	Gly	Leu
			485					490						495	
Ala	Glu	Leu	Glu	Lys	Leu	Leu	Lys								
			500												

(2) INFORMATION FOR SEQ ID NO:3733:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 714 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...714

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3733:

Leu	Leu	Lys	Lys	Thr	Val	Glu	Lys	Ala	Val	Ala	Asp	Asn	Val	Lys	Asp
1			5						10					15	
Ser	Ile	Asp	Val	Pro	Ala	Ala	Tyr	Leu	Glu	Lys	Ala	Lys	Gly	Glu	Gly
		20					25					30			
Pro	Phe	Thr	Ala	Gly	Val	Asn	His	Val	Ile	Pro	Tyr	Glu	Leu	Phe	Ala
	35				40						45				
Gly	Asp	Gly	Met	Leu	Thr	Arg	Leu	Leu	Leu	Lys	Ala	Ser	Asp	Lys	Ala
	50				55				60						
Pro	Trp	Ser	Asp	Asn	Gly	Asp	Ala	Lys	Asn	Pro	Ala	Leu	Ser	Pro	Leu
65				70					75					80	
Gly	Glu	Asn	Val	Lys	Thr	Lys	Gly	Gln	Tyr	Phe	Tyr	Gln	Val	Ala	Leu
		85					90						95		
Asp	Gly	Asn	Val	Ala	Gly	Lys	Glu	Lys	Gln	Ala	Leu	Ile	Asp	Gln	Phe
	100					105						110			
Arg	Ala	Asn	Gly	Thr	Gln	Thr	Tyr	Ser	Ala	Thr	Val	Asn	Val	Tyr	Gly
	115				120						125				
Asn	Lys	Asp	Gly	Lys	Pro	Asp	Leu	Asp	Asn	Ile	Val	Ala	Thr	Lys	Lys
	130			135						140					
Val	Thr	Ile	Asn	Ile	Asn	Gly	Leu	Ile	Ser	Lys	Glu	Thr	Val	Gln	Lys
145				150					155					160	
Ala	Val	Ala	Asp	Asn	Val	Lys	Asp	Ser	Ile	Asp	Val	Pro	Ala	Ala	Tyr

				165					170				175			
Leu	Glu	Lys	Ala	Lys	Gly	Glu	Gly	Pro	Phe	Thr	Ala	Gly	Val	Asn	His	
			180					185					190			
Val	Ile	Pro	Tyr	Glu	Leu	Phe	Ala	Gly	Asp	Gly	Met	Leu	Thr	Arg	Leu	
		195					200					205				
Leu	Leu	Lys	Ala	Ser	Asp	Lys	Ala	Pro	Trp	Ser	Asp	Asn	Gly	Asp	Ala	
	210				215						220					
Lys	Asn	Pro	Ala	Leu	Ser	Pro	Leu	Gly	Glu	Asn	Val	Lys	Thr	Lys	Gly	
225				230						235					240	
Gln	Tyr	Phe	Tyr	Gln	Val	Ala	Leu	Asp	Gly	Asn	Val	Ala	Gly	Lys	Glu	
				245					250						255	
Lys	Gln	Ala	Leu	Ile	Asp	Gln	Phe	Arg	Ala	Asn	Gly	Thr	Gln	Thr	Tyr	
			260					265					270			
Ser	Ala	Thr	Val	Asn	Val	Tyr	Gly	Asn	Lys	Asp	Gly	Lys	Pro	Asp	Leu	
	275						280					285				
Asp	Asn	Ile	Val	Ala	Thr	Lys	Lys	Val	Thr	Ile	Asn	Ile	Asn	Gly	Leu	
	290					295					300					
Ile	Ser	Lys	Glu	Thr	Val	Gln	Lys	Ala	Val	Ala	Asp	Asn	Val	Lys	Asp	
305				310						315					320	
Ser	Ile	Asp	Val	Pro	Ala	Ala	Tyr	Leu	Glu	Lys	Ala	Lys	Gly	Glu	Gly	
			325					330						335		
Pro	Phe	Thr	Ala	Gly	Val	Asn	His	Val	Ile	Pro	Tyr	Glu	Leu	Phe	Ala	
		340						345					350			
Gly	Asp	Gly	Met	Leu	Thr	Arg	Leu	Leu	Lys	Ala	Ser	Asp	Lys	Ala		
	355						360				365					
Pro	Trp	Ser	Asp	Asn	Gly	Asp	Ala	Lys	Asn	Pro	Ala	Leu	Ser	Pro	Leu	
	370				375						380					
Gly	Glu	Asn	Val	Lys	Thr	Lys	Gly	Gln	Tyr	Phe	Tyr	Gln	Val	Ala	Leu	
385				390						395					400	
Asp	Gly	Asn	Val	Ala	Gly	Lys	Glu	Lys	Gln	Ala	Leu	Ile	Asp	Gln	Phe	
			405					410						415		
Arg	Ala	Asn	Gly	Thr	Gln	Thr	Tyr	Ser	Ala	Thr	Val	Asn	Val	Tyr	Gly	
		420						425				430				
Asn	Lys	Asp	Gly	Lys	Pro	Asp	Leu	Asp	Asn	Ile	Val	Ala	Thr	Lys	Lys	
	435					440					445					
Val	Thr	Ile	Asn	Ile	Asn	Gly	Leu	Ile	Ser	Lys	Glu	Thr	Val	Gln	Lys	
	450				455						460					
Ala	Val	Ala	Asp	Asn	Val	Lys	Asp	Ser	Ile	Asp	Val	Pro	Ala	Ala	Tyr	
465				470						475				480		
Leu	Glu	Lys	Ala	Lys	Gly	Glu	Gly	Pro	Phe	Thr	Ala	Gly	Val	Asn	His	
			485					490						495		
Val	Ile	Pro	Tyr	Glu	Leu	Phe	Ala	Gly	Asp	Gly	Met	Leu	Thr	Arg	Leu	
		500						505				510				
Leu	Leu	Lys	Ala	Ser	Asp	Lys	Ala	Pro	Trp	Ser	Asp	Asn	Gly	Asp	Ala	
	515					520						525				
Lys	Asn	Pro	Ala	Leu	Ser	Pro	Leu	Gly	Glu	Asn	Val	Lys	Thr	Lys	Gly	
	530					535					540					
Gln	Tyr	Phe	Tyr	Gln	Leu	Ala	Leu	Asp	Gly	Asn	Val	Ala	Gly	Lys	Glu	
545				550						555					560	
Lys	Gln	Ala	Leu	Ile	Asp	Gln	Phe	Arg	Ala	Asn	Gly	Thr	Gln	Thr	Tyr	
			565					570						575		
Ser	Ala	Thr	Val	Asn	Val	Tyr	Gly	Asn	Lys	Asp	Gly	Lys	Pro	Asp	Leu	
		580						585				590				
Asp	Asn	Ile	Val	Ala	Thr	Lys	Lys	Val	Thr	Ile	Lys	Ile	Asn	Val	Lys	
	595					600					605					
Glu	Thr	Ser	Asp	Thr	Ala	Asn	Gly	Ser	Leu	Ser	Pro	Ser	Asn	Ser	Gly	
	610					615					620					

```

Ser Gly Val Thr Pro Met Asn His Asn His Ala Thr Gly Thr Thr Asp
625                               630                               635                               640
Ser Met Pro Ala Asp Thr Met Thr Ser Ser Thr Asn Thr Met Ala Gly
                               645                               650                               655
Glu Asn Met Ala Ala Ser Ala Asn Lys Met Ser Asp Thr Met Met Ser
                               660                               665                               670
Glu Asp Lys Ala Met Leu Pro Asn Thr Gly Glu Thr Gln Thr Ser Met
                               675                               680                               685
Ala Ser Ile Gly Phe Leu Gly Leu Ala Leu Ala Gly Leu Leu Gly Gly
690                               695                               700
Leu Gly Leu Lys Asn Lys Lys Glu Glu Asn
705                               710

```

(2) INFORMATION FOR SEQ ID NO:3734:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 130 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...130
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3734:

```

Ser Ser Lys Asn Thr Ser Thr Ser Asn Asp Glu Lys Thr Val Ala Thr
1                               5                               10                               15
Ser Asn Ser Ser Lys Glu Thr Ile Thr Phe Asp Thr Pro Val Val Thr
20                               25                               30
Asp Asp Ala Ile Glu Ser Ile Arg Thr Tyr Ala Asp Tyr Ile Asp Leu
35                               40                               45
Tyr Lys Asn Ile Phe Asp Asp Tyr Phe Thr Lys Ala Glu Glu Gly Phe
50                               55                               60

Lys Gly Thr Ala Met Glu Asn Asn Asp Ser Phe Thr Lys Leu Lys Glu
65                               70                               75                               80
Ser Thr Gln Lys Leu Phe Asp Ala Gln Lys Lys Arg Leu Asn Asn Glu
85                               90                               95
Asp Arg Ile Glu Thr Thr Lys Asn Asn Val Ile Ala Lys His Cys Gln
100                              105                              110
Thr Val Leu Ser Phe Leu Val Leu Thr Ser Phe Phe Val Lys Asn Cys
115                              120                              125
Val Lys
130

```

(2) INFORMATION FOR SEQ ID NO:3735:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 158 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...158

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3735:

Thr	Gln	Lys	Lys	Ser	Phe	Trp	Tyr	Asn	Lys	Ser	Met	Tyr	Thr	Lys	Asn
1				5				10						15	
Glu	Glu	Glu	Leu	Gln	Ala	Leu	Gly	Glu	Arg	Leu	Gly	His	Leu	Leu	Ala
			20				25					30			
Lys	Asn	Asp	Val	Leu	Ile	Leu	Thr	Gly	Glu	Leu	Gly	Ala	Gly	Lys	Thr
	35					40					45				
Thr	Phe	Thr	Lys	Gly	Leu	Ala	Lys	Gly	Leu	Gln	Ile	Ser	Gln	Met	Ile
50					55					60					
Lys	Ser	Pro	Thr	Tyr	Thr	Ile	Val	Arg	Glu	Tyr	Glu	Gly	Arg	Leu	Pro
65				70				75						80	
Leu	Tyr	His	Leu	Asp	Val	Tyr	Arg	Ile	Glu	Gly	Asp	Ala	Asp	Ser	Ile
			85					90					95		
Asp	Leu	Asp	Glu	Phe	Ile	Phe	Gly	Gly	Gly	Val	Thr	Val	Ile	Glu	Trp
	100						105					110			
Gly	Asn	Leu	Leu	Gly	Asp	Ala	Leu	Pro	Asp	Ala	Tyr	Leu	Glu	Leu	Glu
	115						120					125			
Ile	Leu	Lys	Glu	Ala	Asp	Gly	Arg	Arg	Leu	Asn	Phe	Gln	Ala	Lys	Gly
	130						135				140				
Leu	Arg	Ala	Glu	Lys	Leu	Leu	Glu	Glu	Leu	Gln	Tyr	Gly	Val		
145					150					155					

(2) INFORMATION FOR SEQ ID NO:3736:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 573 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3736:

Asn	Lys	Lys	Asn	Cys	Cys	Asp	Ile	Asn	Arg	Phe	Gly	Gly	Phe	Phe	Asn
1			5					10					15		
Met	Val	Leu	Asp	Lys	Ala	Ser	Cys	Asp	Leu	Leu	Gln	Tyr	Leu	Met	Asp
		20					25						30		
Gln	Glu	Thr	Ser	Lys	Thr	Ile	Met	Ala	Ile	Ser	Lys	Asp	Leu	Lys	Glu
		35				40						45			
Ser	Arg	Arg	Lys	Ile	Tyr	Tyr	His	Ile	Asp	Lys	Ile	Asn	Ala	Ala	Leu
	50				55						60				
Val	Asp	Glu	Ala	Leu	His	Ile	Ile	Ser	Ile	Pro	Arg	Ile	Gly	Ile	His
65				70					75					80	
Leu	Thr	Glu	Glu	Gln	Arg	Asp	Ala	Cys	Cys	Lys	Leu	Leu	Ser	Glu	Val
			85					90						95	
Asp	Ser	Tyr	Asp	Tyr	Ile	Met	Ser	Ala	His	Glu	Arg	Met	Met	Ile	Met
		100					105						110		
Leu	Leu	Trp	Ile	Gly	Ile	Ser	Lys	Glu	Arg	Ile	Thr	Ile	Glu	Lys	Leu
		115					120					125			
Ile	Glu	Leu	Thr	Glu	Val	Ser	Arg	Asn	Thr	Val	Leu	Asn	Asp	Leu	Asn
	130				135						140				
Ser	Ile	Arg	Tyr	Gln	Leu	Thr	Leu	Glu	Gln	Tyr	Gln	Val	Thr	Leu	Gln
145				150					155					160	
Val	Ser	Lys	Ser	Gln	Gly	Tyr	His	Leu	His	Ala	His	Pro	Leu	Asn	Lys
			165					170						175	
Ile	Gln	Tyr	Leu	Gln	Ser	Leu	Leu	Tyr	His	Ile	Phe	Met	Glu	Glu	Asn
		180					185					190			
Ala	Thr	Phe	Val	Ser	Ile	Leu	Glu	Asp	Lys	Met	Lys	Glu	Arg	Leu	Asp
		195				200						205			
Asp	Glu	Cys	Leu	Leu	Ser	Val	Glu	Met	Asn	Gln	Phe	Phe	Lys	Glu	Gln
	210				215						220				
Val	Pro	Leu	Val	Glu	Gln	Asp	Leu	Gly	Lys	Lys	Ile	Asn	His	His	Glu
225				230					235					240	
Ile	Thr	Phe	Met	Leu	Gln	Val	Leu	Pro	Tyr	Leu	Leu	Leu	Ser	Cys	His
			245					250						255	
Asn	Val	Glu	Gln	Tyr	Gln	Glu	Arg	His	Gln	Asp	Ile	Glu	Lys	Glu	Phe
		260					265					270			
Ser	Leu	Ile	Arg	Lys	Arg	Ile	Glu	Tyr	Gln	Val	Ser	Lys	Lys	Leu	Gly
	275					280						285			
Glu	Arg	Leu	Phe	Gln	Lys	Phe	Glu	Ile	Ser	Leu	Ser	Gly	Leu	Glu	Val
	290				295						300				
Ser	Leu	Val	Ala	Val	Leu	Leu	Ser	Tyr	Arg	Lys	Asp	Leu	Asp	Ile	
305				310					315					320	
His	Ala	Glu	Ser	Asp	Phe	Arg	Gln	Leu	Lys	Leu	Ala	Leu	Glu	Glu	
			325				330						335		
Phe	Ile	Trp	Tyr	Phe	Glu	Ser	Gln	Ile	Arg	Met	Glu	Ile	Glu	Asn	Lys
		340					345						350		
Asp	Asp	Leu	Leu	Arg	Asn	Leu	Met	Ile	His	Cys	Lys	Ala	Leu	Leu	Phe
	355				360							365			
Arg	Lys	Thr	Tyr	Gly	Ile	Phe	Ser	Lys	Asn	Pro	Leu	Thr	Lys	Gln	Ile
	370				375							380			
Arg	Ser	Lys	Tyr	Gly	Glu	Leu	Phe	Leu	Val	Thr	Arg	Lys	Ser	Ala	Glu
385				390					395					400	
Ile	Leu	Glu	Gly	Ala	Trp	Phe	Ile	Arg	Leu	Thr	Asp	Asp	Asp	Ile	Ala
			405				410							415	
Tyr	Leu	Thr	Ile	His	Ile	Gly	Gly	Phe	Leu	Lys	Tyr	Thr	Pro	Ser	Ser
		420				425							430		
Gln	Lys	Asn	Met	Lys	Lys	Val	Tyr	Leu	Val	Cys	Asp	Glu	Gly	Val	Ala
		435				440						445			

Val	Ser	Arg	Leu	Leu	Leu	Lys	Gln	Cys	Lys	Leu	Tyr	Phe	Pro	Asn	Glu
	450					455				460					
Gln	Ile	Asp	Thr	Val	Phe	Thr	Thr	Glu	Gln	Phe	Lys	Ser	Val	Glu	Asp
465				470						475					480
Ile	Ala	Gln	Val	Asp	Val	Val	Ile	Thr	Thr	Asn	Asp	Asp	Leu	Asp	Ser
			485						490					495	
Arg	Phe	Pro	Ile	Leu	Arg	Val	Asn	Pro	Ile	Leu	Glu	Ala	Glu	Asp	Ile
		500						505					510		
Leu	Lys	Met	Leu	Asp	Tyr	Leu	Lys	His	Asn	Ile	Phe	Arg	Asn	Lys	Ser
		515					520					525			
Lys	Ser	Phe	Ser	Glu	Asn	Leu	Ser	Ser	Leu	Ile	Ser	Ser	Tyr	Ile	Val
	530					535					540				
Asp	Ser	Lys	Leu	Ala	Ser	Lys	Phe	Gln	Glu	Glu	Val	Gln	Thr	Leu	Ile
545				550					555						560
Asn	Gln	Glu	Ile	Val	Val	Gln	Ala	Phe	Leu	Glu	Asp	Ile			
			565						570						

(2) INFORMATION FOR SEQ ID NO:3737:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...93

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3737:

Ser	Lys	Lys	Asn	Phe	Ser	Asp	Ser	Leu	Arg	Tyr	Tyr	Pro	Tyr	Arg	Ser
1			5					10					15		
Leu	Lys	Glu	Arg	Asn	Arg	Lys	Met	Glu	Glu	Trp	Lys	Glu	Arg	Phe	Lys
		20					25					30			
Lys	Glu	Tyr	Tyr	Glu	Leu	Lys	Glu	Arg	Phe	Gln	Lys	Leu	Asp	Met	Met
		35				40					45				
Ile	Gly	Lys	Tyr	Glu	Lys	Gly	Gln	Leu	Glu	Phe	Glu	Ser	Lys	Cys	Pro
	50					55				60					
Ile	Asp	Ser	Leu	Lys	Gly	Gln	Arg	Ser	Thr	Met	Trp	Asn	Tyr	Leu	Arg
65				70					75						80
Ile	Leu	Glu	Gln	Arg	Ala	Lys	Ile	Glu	Glu	Ile	Lys	Leu			
			85					90							

(2) INFORMATION FOR SEQ ID NO:3738:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...303

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3738:

```

Leu Arg Lys Lys Glu Glu Arg Lys Ile Met Arg Ala Lys Lys Leu Asp
1      5      10      15
Lys Leu Ala Thr Ala Val Leu Tyr Thr Ile Ala Ser Ile Ile Val Thr
      20      25      30
Ile Leu Ala Ser Leu Ile Leu Tyr Ile Leu Val Arg Gly Leu Pro His
      35      40      45
Ile Ser Trp Ser Phe Leu Thr Gly Arg Ser Ser Ala Phe Gln Ala Gly
      50      55      60
Gly Gly Ile Gly Ile Gln Leu Tyr Asn Ser Phe Phe Leu Leu Val Ile
65      70      75      80
Thr Leu Ile Ile Ser Val Pro Leu Ser Met Gly Ala Gly Ile Tyr Leu
      85      90      95
Ala Glu Tyr Ala Lys Lys Gly Pro Val Thr Asn Phe Val Arg Thr Cys
      100     105     110
Ile Glu Ile Leu Ser Ser Leu Pro Ser Val Val Val Gly Leu Phe Gly
      115     120     125
Tyr Leu Ile Phe Val Val Gln Phe Glu Tyr Gly Phe Ser Ile Ile Ser
      130     135     140
Gly Ala Leu Ala Leu Thr Val Phe Asn Leu Pro Gln Met Thr Arg Asn
145     150     155     160
Val Glu Asp Ser Leu Lys His Val His His Thr Gln Arg Glu Ala Gly
      165     170     175
Leu Ala Leu Gly Ile Ser Arg Trp Glu Thr Val Val His Val Val Ile
      180     185     190
Pro Glu Ala Leu Pro Gly Ile Val Thr Gly Val Val Leu Ala Ser Gly
      195     200     205
Arg Ile Phe Gly Glu Ala Ala Ala Leu Ile Tyr Thr Ala Gly Gln Ser
      210     215     220
Ala Pro Ala Leu Asp Trp Ser Asn Trp Asn Ile Leu Ser Val Thr Ser
225     230     235     240
Pro Ile Ser Ile Phe Arg Gln Ala Glu Thr Leu Ala Val His Ile Trp
      245     250     255
Lys Val Asn Ser Glu Gly Thr Ile Pro Asp Gly Thr Ile Val Ser Ala
      260     265     270
Gly Ser Ala Ala Val Leu Leu Ile Phe Ile Leu Ile Phe Asn Phe Gly
      275     280     285
Ala Arg Lys Phe Gly Ser Tyr Leu His Lys Lys Leu Thr Ala Ala
      290     295     300

```

(2) INFORMATION FOR SEQ ID NO:3739:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 124 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3739:

Val	Leu	Lys	Lys	Asn	Phe	Arg	Val	Lys	Arg	Glu	Lys	Asp	Phe	Lys	Ala
1				5					10					15	
Ile	Phe	Lys	Glu	Gly	Thr	Ser	Phe	Ala	Asn	Arg	Lys	Phe	Val	Ile	Tyr
			20					25					30		
Gln	Leu	Glu	Asn	Gln	Lys	Asn	His	Phe	Arg	Val	Gly	Leu	Ser	Val	Ser
		35				40						45			
Lys	Lys	Leu	Gly	Asn	Ala	Val	Thr	Arg	Asn	Gln	Ile	Lys	Arg	Arg	Ile
		50				55					60				
Arg	His	Ile	Ile	Gln	Asn	Ala	Lys	Gly	Ser	Leu	Val	Glu	Asp	Val	Asp
65					70					75					80
Phe	Val	Val	Ile	Ala	Arg	Lys	Gly	Val	Glu	Ala	Leu	Gly	Tyr	Ala	Glu
				85					90					95	
Met	Glu	Lys	Asn	Leu	Leu	His	Val	Leu	Lys	Leu	Ser	Lys	Ile	Tyr	Gln
			100					105					110		
Glu	Gly	Asn	Gly	Ser	Glu	Lys	Glu	Thr	Lys	Val	Asp				
			115					120							

(2) INFORMATION FOR SEQ ID NO:3740:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 249 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...249

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3740:

Leu	Leu	Lys	Lys	Arg	Leu	Ile	Cys	Gln	Ile	Leu	Lys	Phe	Cys	Lys	Arg
1					5				10					15	
Val	Thr	Met	Ser	Arg	Ile	Glu	Phe	Ser	Pro	Ser	Leu	Met	Thr	Met	Asp

			20					25				30			
Leu	Asp	Lys	Phe	Lys	Glu	Gln	Ile	Thr	Phe	Leu	Asn	Asp	Lys	Val	Ala
	35						40				45				
Ser	Tyr	His	Ile	Asp	Ile	Met	Asp	Gly	His	Phe	Val	Pro	Asn	Ile	Thr
	50					55					60				
Leu	Ser	Pro	Trp	Phe	Ile	Gln	Glu	Val	Gln	Lys	Ile	Ser	Asp	Thr	Pro
65					70					75				80	
Leu	Ser	Val	His	Leu	Met	Val	Thr	Asp	Pro	Thr	Phe	Trp	Val	Asp	Gln
			85					90					95		
Val	Leu	Asp	Leu	Gln	Cys	Glu	Tyr	Ile	Cys	Ile	His	Ala	Glu	Val	Leu
	100							105					110		
Asn	Gly	Leu	Ala	Phe	Arg	Leu	Ile	Asp	Lys	Ile	His	Asp	Ala	Gly	Leu
	115						120					125			
Lys	Ala	Gly	Val	Val	Leu	Asn	Pro	Glu	Thr	Pro	Val	Ser	Thr	Ile	Phe
	130					135					140				
Pro	Tyr	Ile	Asp	Leu	Leu	Asp	Lys	Val	Thr	Ile	Met	Thr	Val	Asp	Pro
145					150					155				160	
Gly	Phe	Ala	Gly	Gln	Arg	Phe	Leu	Glu	Ser	Thr	Leu	Tyr	Lys	Ile	Gln
			165					170					175		
Glu	Leu	Arg	Gln	Leu	Arg	Val	Gln	Asn	Gly	Tyr	His	Tyr	Ile	Ile	Glu
	180							185					190		
Met	Asp	Gly	Ser	Ser	Ser	Arg	Lys	Thr	Phe	Lys	Gln	Ile	Asp	Val	Ala
	195						200					205			
Gly	Pro	Asp	Ile	Tyr	Val	Ile	Gly	Arg	Ser	Gly	Leu	Phe	Gly	Leu	Asp
	210					215					220				
Asp	Asp	Ile	Ala	Lys	Ala	Trp	Asp	Ile	Cys	Ser	Arg	Asp	Tyr	Glu	Glu
225					230					235				240	
Met	Thr	Gly	Lys	Thr	Met	Pro	Ile	Lys							
				245											

(2) INFORMATION FOR SEQ ID NO:3741:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...154

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3741:

Thr	Met	Lys	Lys	Met	Lys	Tyr	Tyr	Glu	Glu	Thr	Ser	Ala	Leu	Leu	His
1				5				10					15		
Glu	Phe	Ser	Glu	Glu	Asn	Gln	Lys	Tyr	Phe	Glu	Glu	Leu	Trp	Glu	Ser
			20				25					30			
Phe	Asn	Leu	Ala	Gly	Phe	Leu	Tyr	Asp	Glu	Asp	Tyr	Leu	Arg	Glu	Gln
	35					40					45				
Ile	Tyr	Leu	Met	Met	Leu	Asp	Phe	Ser	Glu	Ala	Glu	Arg	Asp	Gly	Met

50		55		60											
Ser	Ala	Glu	Asp	Tyr	Leu	Gly	Lys	Asn	Pro	Lys	Lys	Ile	Met	Lys	Glu
65					70					75					80
Ile	Leu	Lys	Gly	Ala	Pro	Arg	Ser	Ser	Ile	Lys	Glu	Ser	Leu	Leu	Thr
					85					90					95
Pro	Ile	Leu	Val	Leu	Val	Val	Leu	Arg	Tyr	Tyr	Gln	Leu	Leu	Ser	Asp
					100					105					110
Phe	Ser	Lys	Gly	Pro	Leu	Leu	Thr	Val	Asn	Leu	Leu	Thr	Phe	Leu	Gly
					115					120					125
Gln	Leu	Leu	Ile	Phe	Leu	Ile	Gly	Phe	Gly	Leu	Val	Ala	Thr	Ile	Leu
					130					135					140
Arg	Arg	Ser	Leu	Val	Lys	Ile	Leu	Leu	Lys						
145					150										

(2) INFORMATION FOR SEQ ID NO:3742:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 98 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...98

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3742:

Glu	Met	Lys	Lys	Thr	Ser	Ser	Lys	Leu	Phe	Val	Val	Pro	Tyr	Met	Leu
1				5					10					15	
Trp	Ile	Ala	Leu	Phe	Val	Leu	Ala	Pro	Leu	Val	Leu	Ile	Phe	Gly	Gln
				20				25					30		
Ser	Phe	Phe	Asn	Ile	Glu	Gly	Gln	Phe	Ser	Leu	Glu	Asn	Tyr	Lys	Ser
				35			40					45			
Tyr	Phe	Ala	Ser	Gln	His	Leu	Thr	Tyr	Leu	Ile	Asn	Glu	Phe	Gln	Leu
				50		55					60				
Ser	Ala	Leu	Cys	Arg	Asp	Cys	Asp	Leu	Cys	Asp	Leu	Ser	Tyr	Gln	Leu
65				70					75						80
Ser	Asn	Ser	Pro	Leu	Phe	Asp	Pro	Ser	Gln	Ala	Arg	Val	Asn	Ser	Gly
				85					90						95
Ser	Cys														

(2) INFORMATION FOR SEQ ID NO:3743:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 468 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...468

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3743:

Arg	Met	Lys	Asn	Gln	Glu	Tyr	Trp	Ala	Lys	Arg	Lys	Ala	Asn	Leu	Ile
1			5					10					15		
Tyr	Gln	Gln	Met	Asp	Lys	Ala	Glu	Lys	Gln	Ala	Asp	Gln	Phe	Asp	Lys
			20				25					30			
Val	Tyr	Gln	Glu	Ala	Lys	Thr	Tyr	Leu	Asp	Lys	Glu	Ile	Asn	Lys	Ile
		35				40					45				
Phe	Asp	Lys	Phe	Gln	Arg	Asp	Tyr	Gly	Leu	Ser	Gln	Val	Glu	Ala	Arg
	50				55					60					
Gln	Val	Leu	Lys	Asn	Met	Lys	Asp	Lys	Lys	Asn	Leu	Asn	Glu	Leu	Arg
65				70					75					80	
Lys	Val	Leu	Glu	Ala	Arg	Pro	Asn	Asp	Pro	Asn	Ile	Gln	Arg	Leu	Leu
			85				90						95		
Ala	Asp	Leu	Asp	Ser	Pro	Ala	Tyr	Ser	Phe	Arg	Met	Lys	Arg	Leu	Glu
		100					105					110			
Arg	Leu	Ser	Asp	Asp	Leu	Asp	Arg	Met	Arg	Glu	Ser	Ile	Tyr	His	Ser
	115					120						125			
Glu	Lys	Thr	Gly	Ser	Asp	Ala	Phe	Tyr	Ser	Asp	Leu	Met	Lys	Asp	Ser
	130					135					140				
Tyr	Tyr	Lys	Ala	Thr	Phe	Asp	Leu	Gln	Gln	Gln	Thr	Gly	Leu	Ala	Tyr
145				150					155					160	
Gly	Phe	Ser	Gly	Leu	Pro	Glu	Asn	Glu	Ile	Lys	His	Leu	Gln	Ser	Phe
			165				170						175		
Ser	Trp	Val	Gly	Asp	Gly	Ser	Thr	Tyr	Ser	Thr	Asp	Ile	Trp	Lys	Asn
		180					185					190			
Thr	Gly	Lys	Leu	Thr	Ser	Ser	Ile	Lys	Asp	Glu	Leu	Leu	Ile	Ser	Leu
	195					200						205			
Met	Thr	Gly	Arg	Asp	Thr	Arg	Glu	Thr	Ala	Gln	Ala	Ile	Ala	Glu	Arg
	210				215						220				
Phe	Asn	Val	Gly	Gln	Asn	Asp	Ala	Arg	Arg	Leu	Val	Arg	Thr	Glu	Ser
225				230						235				240	
Ala	Phe	Phe	His	Asn	Gln	Met	Glu	Leu	Leu	Ser	Tyr	Glu	Glu	Ala	Asp
			245				250							255	
Ile	Glu	Lys	Tyr	Ile	Phe	Val	Ala	Val	Leu	Asp	Lys	Arg	Thr	Ser	Arg
		260				265						270			
Ile	Cys	Gln	Glu	His	Asp	Asn	Gln	Val	Tyr	Asp	Arg	Asp	Lys	Ala	Val
	275					280					285				
Pro	Gly	Val	Asn	Cys	Pro	Pro	Met	His	Pro	Trp	Cys	Arg	Ser	Thr	Thr
	290				295						300				
Val	Gly	Tyr	Asp	Glu	Asp	Ala	Asp	Tyr	Ser	Lys	Leu	Lys	Arg	Arg	Ala
305				310					315					320	
Arg	Asn	Pro	Glu	Thr	Gly	Lys	Val	Glu	Tyr	Val	Pro	Ala	Asp	Met	Thr
			325						330				335		
Tyr	Lys	Glu	Trp	Tyr	Ser	Lys	Tyr	Val	Asp	Gly	Asn	Arg	Glu	Ser	Ile
		340					345						350		

```

Lys Arg Lys Ala Phe Asp Lys Thr Ile Lys Asp Gly Ile Ile Val Ser
      355                      360                      365
Val Ser Gly Thr Thr Ile Gly His Thr Pro Pro Gly Lys Ile Gly Leu
      370                      375                      380
Pro Asn Ser Val Val Gln His Asn Ala Thr Asn Gly Asp Val Leu Gly
      385                      390                      395                      400
Arg Thr Tyr Tyr Asp Ala Arg Gly Phe Lys Thr Lys Asp Val His Phe
      405                      410                      415
Thr Asn His Lys Gln Pro Ala Arg His Pro Tyr Gly Lys Ile Gly Glu
      420                      425                      430
His Ala His Asp Phe Val Phe Asp Asp Glu Gly Lys Phe Val Ser Arg
      435                      440                      445
Ser Thr Arg Glu Leu Thr Asp Asp Glu Arg Lys Glu Asn Gln Asp Ile
      450                      455                      460
Leu Trp Arg Tyr
      465

```

(2) INFORMATION FOR SEQ ID NO:3744:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...76

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3744:

```

Asn Gln Lys Lys Leu Glu Arg Ile Pro Leu Ser Ile Leu Thr Phe Tyr
1      5      10      15
Ile Pro Lys Val Pro Ser Tyr Ser Ile Lys Glu Lys Gln Ser Lys Trp
      20      25      30
Leu Gln Ser Gly Tyr Lys Ser Ile Lys Thr Asp Lys Ala Ile Leu Ser
      35      40      45
Ser Ser Pro Ile Gln Thr Ile Leu Ser Val Val Glu Ser His His Ile
      50      55      60
Ser Leu Arg Ser Arg Thr Ser Leu Lys Arg Arg Lys
65      70      75

```

(2) INFORMATION FOR SEQ ID NO:3745:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3745:

Arg	Glu	Lys	Lys	Met	Gln	Asn	Lys	Gln	Glu	Gln	Trp	Thr	Val	Leu	Lys
1				5					10					15	
Arg	Leu	Met	Ser	Tyr	Leu	Lys	Pro	Tyr	Gly	Leu	Leu	Thr	Phe	Leu	Ala
			20					25					30		
Leu	Ser	Phe	Leu	Leu	Ala	Thr	Thr	Val	Ile	Lys	Ser	Val	Ile	Pro	Leu
		35					40					45			
Val	Ala	Ser	His	Phe	Ile	Asp	Gln	Tyr	Leu	Ser	Asn	Leu	Asn	Gln	Leu
	50					55					60				
Ala	Val	Thr	Val	Leu	Leu	Val	Tyr	Tyr	Gly	Leu	Tyr	Ile	Leu	Gln	Thr
65					70					75				80	
Val	Val	Gln	Tyr	Val	Gly	Asn	Leu	Leu	Phe	Ala	Arg	Val	Ser	Tyr	Ser
			85						90					95	
Ile	Val	Arg	Asp	Ile	Arg	Arg	Asp	Ala	Phe	Ala	Asn	Met	Glu	Lys	Leu
			100					105					110		
Gly	Met	Ser	Tyr	Phe	Asp	Lys	Thr	Pro	Ala	Gly	Ser	Ile	Val	Ser	Arg
		115					120						125		
Leu	Thr	Asn	Asp	Thr	Glu	Thr	Ile	Ser	Asp	Met	Phe	Ser	Gly	Ile	Leu
	130						135				140				
Ser	Ser	Phe	Ile	Ser	Ala	Val	Phe	Ile	Phe	Leu	Thr	Thr	Leu	Tyr	Thr
145					150					155				160	
Met	Leu	Val	Leu	Asp	Phe	Arg	Leu	Thr	Ala	Leu	Val	Leu	Leu	Phe	Leu
			165						170					175	
Pro	Leu	Ile	Phe	Leu	Leu	Val	Asn	Leu	Tyr	Arg	Lys	Lys	Ser	Val	Lys
			180					185					190		
Ile	Ile	Glu	Lys	Thr	Arg	Ser	Leu	Leu	Ser	Asp	Ile	Asn	Ser	Lys	Leu
		195					200					205			
Ala	Glu	Asn	Ile	Glu	Gly	Ile	Arg	Ile	Ile	Gln	Ala	Phe	Asn	Gln	Glu
	210					215					220				
Lys	Arg	Leu	Gln	Ala	Glu	Phe	Asp	Glu	Ile	Asn	Gln	Glu	His	Leu	Ala
225					230					235				240	
Tyr	Ala	Asn	Arg	Ser	Val	Ala	Leu	Asp	Ala	Leu	Phe	Leu	Arg	Pro	Ala
			245						250					255	
Met	Ser	Leu	Leu	Lys	Leu	Leu	Gly	Tyr	Ala	Val	Leu	Met	Thr	Tyr	Phe
		260						265					270		
Gly	Tyr	Arg	Gly	Leu	Ser	Ile	Gly	Ile	Thr	Ala	Gly	Thr	Met	Tyr	Ala
	275						280					285			
Phe	Ile	Gln	Tyr	Ile	Asn	Arg	Pro	Leu							
	290					295									

(2) INFORMATION FOR SEQ ID NO:3746:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 82 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...82
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3746:

```

Ile Phe Glu Lys Thr Leu Arg Pro Ser Ser Thr Ala Thr Ile Ile Val
1           5           10           15
Ala Lys Leu Ser Ser Ala Arg Ile Ile Ser Glu Ala Pro Leu Glu Thr
          20           25           30
Ser Val Pro Val Ile Pro Ile Pro Ile Pro Met Ser Ala Val Phe Arg
          35           40           45
Ala Gly Ala Ser Leu Thr Pro Ser Pro Val Met Ala Thr Thr Leu Pro
          50           55           60
Cys Phe Cys Gln Ala Leu Thr Ile Arg Thr Leu Cys Ser Gly Asp Thr
65           70           75           80
Arg Ala

```

(2) INFORMATION FOR SEQ ID NO:3747:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 404 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...404
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3747:

```

Phe Gly Glu Lys Gly Phe Ile Leu Lys Ser Ile Gly Phe Ile Glu Lys
1           5           10           15
Leu Lys Gly Leu Ser Ser Lys Glu Leu Ile Leu Leu Gly Ile Ile Leu
          20           25           30
Ser Ile Phe Leu Pro Phe Tyr Leu Phe Val Val Val Leu Cys Leu Tyr
          35           40           45
Ile Ile Ser Leu Ile Phe Thr Gly Asp Met Lys Ser Ile Leu Gln Lys
          50           55           60
Met Gly Glu His Pro Met Leu Leu Leu Phe Leu Ser Tyr Ser Thr Val
65           70           75           80
Ile Ser Ile Leu Ala Gln Asn Trp Met Gly Leu Val Ala Ser Val Gly

```

				85				90					95				
Met	Phe	Leu	Phe	Thr	Ile	Phe	Phe	Leu	His	Tyr	Gln	Ser	Ile	Leu	Ser		
			100					105					110				
His	Lys	Phe	Phe	Arg	Leu	Ile	Leu	Gln	Phe	Val	Leu	Phe	Gly	Ser	Val		
		115					120					125					
Leu	Ser	Ala	Val	Phe	Ala	Ser	Leu	Glu	His	Phe	Gln	Ile	Val	Lys	Lys		
		130				135					140						
Phe	Asn	Tyr	Ala	Phe	Leu	Ser	Pro	Asn	Met	Gln	Val	Trp	His	Gln	Asn		
145					150					155					160		
Arg	Ala	Glu	Val	Thr	Phe	Phe	Asn	Pro	Asn	Tyr	Tyr	Gly	Ile	Ile	Cys		
				165					170					175			
Cys	Phe	Cys	Ile	Met	Ile	Ala	Phe	Tyr	Leu	Phe	Thr	Thr	Thr	Lys	Leu		
		180						185					190				
Asn	Trp	Leu	Lys	Val	Phe	Cys	Val	Ile	Ala	Gly	Phe	Val	Asn	Leu	Phe		
	195						200					205					
Gly	Leu	Asn	Phe	Thr	Gln	Asn	Arg	Thr	Ala	Phe	Pro	Ala	Ile	Ile	Ala		
	210					215					220						
Gly	Ala	Ile	Ile	Tyr	Leu	Phe	Thr	Thr	Ile	Lys	Asn	Trp	Lys	Ala	Phe		
225					230					235					240		
Trp	Leu	Ser	Ile	Gly	Val	Phe	Ala	Ile	Gly	Leu	Ser	Phe	Leu	Phe	Ser		
			245						250					255			
Ser	Asp	Leu	Gly	Val	Arg	Met	Gly	Thr	Leu	Asp	Ser	Ser	Met	Glu	Glu		
		260					265						270				
Arg	Ile	Ser	Ile	Trp	Asp	Ala	Gly	Met	Ala	Leu	Phe	Lys	Gln	Asn	Pro		
	275					280						285					
Phe	Trp	Gly	Glu	Gly	Pro	Leu	Thr	Tyr	Met	His	Ser	Tyr	Pro	Arg	Ile		
	290					295					300						
His	Ala	Pro	Tyr	His	Glu	His	Ala	His	Ser	Leu	Tyr	Ile	Asp	Thr	Ile		
305					310					315					320		
Leu	Ser	Tyr	Gly	Ile	Val	Gly	Thr	Ile	Leu	Leu	Val	Leu	Ser	Ser	Val		
			325						330					335			
Ala	Pro	Val	Arg	Leu	Met	Met	Asp	Met	Ser	Gln	Glu	Ser	Gly	Lys	Arg		
		340					345						350				
Pro	Ile	Ile	Gly	Leu	Tyr	Leu	Ser	Phe	Leu	Thr	Val	Val	Ala	Val	His		
	355					360						365					
Gly	Ile	Phe	Asp	Leu	Ala	Leu	Phe	Trp	Ile	Gln	Ser	Gly	Phe	Ile	Phe		
	370					375					380						
Leu	Leu	Val	Met	Cys	Ser	Ile	Pro	Leu	Glu	His	Arg	Met	Leu	Val	Ser		
385					390					395					400		
Asp	Met	Thr	Asp														

(2) INFORMATION FOR SEQ ID NO:3748:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3748:

Asn	Leu	Glu	Lys	Ile	Phe	Met	Glu	Pro	Asp	Ile	Phe	Ile	Ile	Thr	Lys
1			5						10					15	
Leu	Leu	Ser	Asp	Pro	Ser	Arg	Met	His	Ile	Leu	Asp	Ile	Leu	Met	Asp
			20					25					30		
Gly	Lys	Ala	His	Thr	Val	Asn	Glu	Ile	Ala	Ser	Phe	Thr	Lys	Ile	Lys
		35					40					45			
Gln	His	Thr	Val	Ser	Tyr	His	Leu	Lys	Leu	Leu	Thr	Glu	Ala	Gln	Val
	50					55					60				
Thr	Thr	Leu	Gln	Thr	Tyr	Gly	Arg	Phe	His	Tyr	Tyr	Ser	Leu	Lys	Ser
65					70					75					80
Ala	Ala	Ile	Ala	Glu	Met	Leu	Glu	Phe	Leu	Ser	Phe	Tyr	Ser	Pro	Gln
				85					90					95	
Arg	Asp	Val	Lys	Ser	Tyr	Lys	Gln	His	Ile	His	Lys	Lys	Glu	Leu	Lys
			100					105					110		
Val	Ala	Arg	Thr	Cys	Tyr	Asp	His	Ile	Ala	Gly	Glu	Leu	Gly	Ile	Ser
		115					120					125			
Ile	Thr	Asn	Tyr	Leu	Leu	Gln	Glu	Asn	Leu	Leu	Ser	Glu	Ser	Glu	Lys
	130					135					140				
Asp	Phe	Gln	Leu	Thr	Glu	Ala	Gly	Lys	Ser	Tyr	Phe	Gln	Arg	Lys	Leu
145					150					155					160
His	Ile	Asp	Thr	Asp	Glu	Leu	Lys	Lys	Lys	Lys	Arg	Lys	Phe	Cys	Pro
				165					170					175	
Lys	Cys	Leu	Asp	Trp	Ser	Glu	Arg	Lys	Asn	His	Val	Gly	Gly	Ala	Leu
			180					185					190		
Gly	Asn	Ala	Leu	Leu	Glu	Phe	Phe	Ser	Glu	Lys	Gln	Leu	Val	Ile	Pro
		195					200					205			
Ala	Gln	Thr	Pro	Arg	Ser	Leu	Thr	Ile	Thr	Glu	Lys	Gly	Lys	Glu	Phe
	210					215					220				
Leu	Glu	Lys	Glu	Trp	Gly	Ile									
225					230										

(2) INFORMATION FOR SEQ ID NO:3749:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...286

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3749:

Tyr	Lys	Glu	Lys	Tyr	Met	Tyr	Leu	Ile	Glu	Ile	Leu	Lys	Ser	Ile	Phe
1				5					10					15	
Phe	Gly	Ile	Val	Glu	Gly	Ile	Thr	Glu	Trp	Leu	Pro	Ile	Ser	Ser	Thr
			20					25					30		
Gly	His	Leu	Ile	Leu	Ala	Glu	Glu	Phe	Ile	Gln	Tyr	Gln	Asn	Gln	Asn
		35					40					45			
Glu	Ala	Phe	Met	Ser	Met	Phe	Asn	Val	Val	Ile	Gln	Leu	Gly	Ala	Ile
	50					55					60				
Leu	Ala	Val	Met	Val	Ile	Tyr	Phe	Asn	Lys	Leu	Asn	Pro	Phe	Lys	Pro
65					70					75					80
Thr	Lys	Asp	Lys	Gln	Glu	Val	Arg	Lys	Thr	Trp	Arg	Leu	Trp	Leu	Lys
			85						90					95	
Val	Leu	Ile	Ala	Thr	Leu	Pro	Leu	Leu	Gly	Val	Phe	Lys	Phe	Asp	Asp
			100					105					110		
Trp	Phe	Asp	Thr	His	Phe	His	Asn	Met	Val	Ser	Val	Ala	Leu	Met	Leu
		115					120					125			
Ile	Ile	Tyr	Gly	Val	Ala	Phe	Ile	Tyr	Leu	Glu	Lys	Arg	Asn	Lys	Ala
	130					135						140			
Arg	Ala	Ile	Glu	Pro	Ser	Val	Thr	Glu	Leu	Asp	Lys	Leu	Pro	Tyr	Thr
145					150					155					160
Thr	Ala	Phe	Tyr	Ile	Gly	Leu	Phe	Gln	Val	Leu	Ala	Leu	Leu	Pro	Gly
			165						170					175	
Thr	Ser	Arg	Ser	Gly	Ala	Thr	Ile	Val	Gly	Gly	Leu	Leu	Asn	Gly	Thr
			180					185					190		
Ser	Arg	Ser	Val	Val	Thr	Glu	Phe	Thr	Phe	Tyr	Leu	Gly	Ile	Pro	Val
		195					200					205			
Met	Phe	Gly	Ala	Ser	Ala	Leu	Lys	Ile	Phe	Lys	Phe	Val	Lys	Ala	Gly
	210					215					220				
Glu	Leu	Leu	Ser	Phe	Gly	Gln	Leu	Phe	Leu	Leu	Leu	Val	Ala	Met	Gly
225					230					235					240
Val	Ala	Phe	Ala	Val	Ser	Met	Val	Ala	Ile	Arg	Phe	Leu	Thr	Ser	Tyr
			245						250					255	
Val	Lys	Lys	His	Asp	Phe	Thr	Leu	Phe	Gly	Lys	Tyr	Arg	Ile	Val	Leu
			260					265					270		
Gly	Ser	Val	Leu	Leu	Leu	Tyr	Ser	Phe	Val	Arg	Leu	Phe	Val		
		275					280					285			

(2) INFORMATION FOR SEQ ID NO:3750:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 301 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...301
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3750:

Tyr	Lys	Glu	Lys	Lys	Met	Thr	Lys	Lys	Gln	Leu	His	Leu	Val	Ile	Val
1				5					10					15	
Thr	Gly	Met	Ser	Gly	Ala	Gly	Lys	Thr	Val	Ala	Ile	Gln	Ser	Phe	Glu
			20					25					30		
Asp	Leu	Gly	Tyr	Phe	Thr	Ile	Asp	Asn	Met	Pro	Pro	Ala	Leu	Leu	Pro
	35						40					45			
Lys	Phe	Leu	Gln	Leu	Val	Glu	Ile	Lys	Glu	Asp	Asn	Pro	Lys	Leu	Ala
	50					55					60				
Leu	Val	Val	Asp	Met	Arg	Ser	Arg	Ser	Phe	Phe	Ser	Glu	Ile	Gln	Ala
65					70					75					80
Val	Leu	Asp	Glu	Leu	Glu	Asn	Gln	Asp	Gly	Leu	Asp	Phe	Lys	Ile	Leu
				85					90					95	
Phe	Leu	Asp	Ala	Ala	Asp	Lys	Glu	Leu	Val	Ala	Arg	Tyr	Lys	Glu	Thr
			100					105					110		
Arg	Arg	Ser	His	Pro	Leu	Ala	Ala	Asp	Gly	Arg	Ile	Leu	Asp	Gly	Ile
		115					120					125			
Lys	Leu	Glu	Arg	Glu	Leu	Leu	Ala	Pro	Leu	Lys	Asn	Met	Ser	Gln	Asn
	130					135					140				
Val	Val	Asp	Thr	Thr	Glu	Leu	Thr	Pro	Arg	Glu	Leu	Arg	Lys	Thr	Leu
145					150					155					160
Ala	Glu	Gln	Phe	Ser	Asp	Gln	Glu	Gln	Ala	Gln	Ser	Phe	Arg	Ile	Glu
				165					170					175	
Val	Met	Ser	Phe	Gly	Phe	Lys	Tyr	Gly	Ile	Pro	Ile	Asp	Ala	Asp	Leu
			180					185					190		
Val	Phe	Asp	Val	Arg	Phe	Leu	Pro	Asn	Pro	Tyr	Tyr	Leu	Pro	Glu	Leu
	195						200					205			
Arg	Asn	Gln	Thr	Gly	Val	Asp	Glu	Pro	Val	Tyr	Asp	Tyr	Val	Met	Asn
	210					215					220				
His	Pro	Glu	Ser	Glu	Asp	Phe	Tyr	Gln	His	Leu	Leu	Ala	Leu	Ile	Glu
225					230					235					240
Pro	Ile	Leu	Pro	Ser	Tyr	Gln	Lys	Glu	Gly	Lys	Ser	Val	Leu	Thr	Ile
				245					250					255	
Ala	Met	Gly	Cys	Thr	Gly	Gly	Gln	His	Arg	Ser	Val	Ala	Phe	Ala	Lys
			260					265					270		
Arg	Leu	Val	Gln	Asp	Leu	Ser	Lys	Asn	Trp	Ser	Val	Asn	Glu	Gly	His
	275						280					285			
Arg	Asp	Lys	Asp	Arg	Arg	Lys	Glu	Thr	Val	Asn	Arg	Ser			
	290					295					300				

(2) INFORMATION FOR SEQ ID NO:3751:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...236

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3751:

Asn	Lys	Glu	Lys	Ala	Met	Pro	Val	Asn	Glu	Tyr	Gly	Gln	Met	Ile	Gly	
1				5				10						15		
Glu	Ser	Met	Glu	Gly	Tyr	Thr	Pro	Gly	Ala	Leu	Pro	Ser	Ile	Asp	Phe	
			20					25					30			
Leu	Glu	Gly	Arg	Tyr	Ala	Arg	Ile	Glu	Ala	Leu	Ser	Val	Glu	Lys	His	
		35					40					45				
Ala	Glu	Asp	Leu	Leu	Ala	Val	Tyr	Gly	Pro	Asp	Thr	Pro	Arg	Glu	Met	
	50					55					60					
Trp	Thr	Tyr	Leu	Phe	Gln	Glu	Pro	Val	Ala	Asp	Met	Gly	Glu	Leu	Val	
65					70					75					80	
Ser	Leu	Leu	Asn	Gln	Met	Leu	Ala	Arg	Lys	Asp	Arg	Phe	Tyr	Tyr	Ala	
			85						90					95		
Ile	Ile	Asp	Lys	Ala	Thr	Gly	Lys	Ala	Leu	Gly	Thr	Phe	Ser	Leu	Met	
		100						105					110			
Arg	Ile	Asp	Gln	Asn	Asn	Arg	Val	Ile	Glu	Val	Gly	Ala	Val	Thr	Phe	
		115					120					125				
Ser	Pro	Glu	Leu	Arg	Gly	Thr	Arg	Ile	Gly	Thr	Glu	Ala	Gln	Tyr	Leu	
	130					135					140					
Leu	Ala	Arg	Tyr	Ile	Phe	Glu	Glu	Leu	Asn	Tyr	Arg	Arg	Tyr	Glu	Trp	
145					150					155					160	
Lys	Cys	Asp	Ala	Leu	Asn	Leu	Pro	Ser	Arg	Arg	Val	Ala	Glu	Arg	Leu	
			165						170					175		
Gly	Phe	Val	Tyr	Glu	Gly	Thr	Phe	Arg	Gln	Ala	Val	Val	Tyr	Lys	Gly	
		180						185					190			
Arg	Thr	Arg	Asp	Thr	Asp	Trp	Leu	Ser	Met	Ile	Asp	Met	Asp	Trp	Pro	
		195					200					205				
Gln	Val	Lys	Asp	Arg	Leu	Glu	Thr	Trp	Leu	Arg	Pro	Glu	Asn	Phe	Asp	
	210					215					220					
Lys	Asn	Gly	Gln	Gln	Tyr	Lys	Ser	Leu	Arg	Glu	Leu					
225					230					235						

(2) INFORMATION FOR SEQ ID NO:3752:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...350

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3752:

Thr	Lys	Glu	Lys	Lys	Ile	Met	Phe	Glu	His	Tyr	Ser	Val	Ala	Asp	Leu	
1			5					10						15		
Phe	Ala	Asn	Leu	Tyr	Lys	Lys	Arg	Lys	Ala	Asn	Ile	Leu	Ala	Leu	Ile	

(A) NAME/KEY: misc_feature
(B) LOCATION 1...181

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3753:

```
Lys Lys Glu Lys Asn Arg Asn Met Arg Lys His Gln Leu Gln Val His
1      5      10      15
Lys Leu Thr Ile Leu Ser Met Met Ile Ala Leu Asp Val Val Leu Thr
20      25      30
Pro Ile Phe Arg Ile Glu Gly Met Ala Pro Met Ser Ser Val Val Asn
35      40      45
Ile Leu Ala Gly Ile Met Met Gly Pro Val Tyr Ala Leu Ala Met Ala
50      55      60
Thr Val Thr Ala Phe Ile Arg Met Thr Thr Gln Gly Ile Pro Pro Leu
65      70      75      80
Ala Leu Thr Gly Ala Thr Phe Gly Ala Leu Leu Ala Gly Leu Phe Tyr
85      90      95
Lys Tyr Gly Arg Lys Phe Tyr Phe Ser Ala Leu Gly Glu Ile Val Gly
100     105     110
Thr Gly Ile Ile Gly Ser Ile Val Ser Tyr Pro Val Met Val Leu Phe
115     120     125
Thr Gly Ser Ala Ala Lys Leu Ser Trp Phe Ile Tyr Thr Pro Arg Phe
130     135     140
Phe Gly Ala Thr Leu Ile Gly Thr Ala Ile Ser Phe Ile Ala Phe Arg
145     150     155     160
Phe Leu Ile Lys Gln Glu Phe Phe Lys Lys Val Gln Gly Tyr Phe Phe
165     170     175
Ala Glu Arg Ile Glu
180
```

(2) INFORMATION FOR SEQ ID NO:3754:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 216 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3754:

```
Lys Lys Glu Asn Glu Val Val Val Gln Leu Leu Glu Asn Trp Leu Leu
1      5      10      15
Lys Glu Gln Glu Lys Ile Gln Thr Lys Tyr Arg His Leu Asn His Ile
20      25      30
Ser Val Val Glu Pro Asn Ile Leu Phe Ile Gly Asp Ser Ile Val Glu
35      40      45
Tyr Tyr Pro Leu Gln Glu Leu Phe Gly Thr Ser Lys Thr Ile Val Asn
```

50		55		60
Arg Gly Ile Arg Gly Tyr Gln Thr Gly Leu Leu Leu Glu Asn Leu Asp				
65		70		75
Ala His Leu Tyr Gly Gly Ala Val Asp Lys Ile Phe Leu Leu Ile Gly				80
	85		90	
Thr Asn Asp Ile Gly Lys Asp Val Pro Val Asn Glu Val Leu Asn Asn				95
	100		105	
Leu Glu Ala Ile Ile Gln Ser Val Ala Arg Asp Tyr Pro Leu Thr Glu				110
	115		120	
Ile Lys Leu Leu Ser Ile Leu Pro Val Asn Glu Gly Glu Lys Tyr Gln				125
	130		135	
Gln Ala Val Tyr Ile Arg Ser Asn Glu Lys Ile Gln Asn Trp Asn Gln				140
145		150		155
Ala Tyr Gln Glu Leu Ala Ser Ala Tyr Met Gln Val Glu Phe Val Pro				160
	165		170	
Val Phe Asp Cys Leu Thr Asp Gln Ala Gly Gln Leu Lys Lys Glu Tyr				175
	180		185	
Thr Thr Asp Gly Leu His Leu Ser Ile Ala Gly Tyr Gln Ala Leu Ser				190
	195		200	
Lys Ser Leu Lys Asp Tyr Leu Tyr				205
	210		215	

(2) INFORMATION FOR SEQ ID NO:3755:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...210

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3755:

Glu Lys Glu Lys Cys Met Gly Trp Trp Arg Glu Thr Ile Asp Ile Val				
1	5	10	15	
Lys Glu Asn Asp Pro Ala Ala Arg Thr Thr Leu Glu Val Leu Leu Thr				
	20	25	30	
Tyr Pro Gly Val Lys Ala Leu Ala Ala His Arg Leu Ser His Phe Leu				
	35	40	45	
Trp Lys Tyr Asp Phe Lys Leu Leu Ala Arg Met His Ser Gln Phe Trp				
50	55	60		
Arg Phe Trp Thr Gln Ile Glu Ile His Pro Gly Ala Gln Ile Asp Ser				
65	70	75		80
Gly Val Phe Ile Asp His Gly Ser Gly Leu Val Ile Gly Glu Thr Ala				
	85	90		95
Ile Val Glu Lys Gly Val Leu Leu Tyr His Gly Val Thr Leu Gly Gly				
	100	105		110
Thr Gly Lys Asp Cys Gly Lys Arg His Pro Thr Val Arg Lys Gly Ala				

```

      115              120              125
Leu Ile Ser Ala His Ala Gln Val Ile Gly Pro Val Glu Ile Gly Glu
  130              135              140
Asn Ala Lys Val Gly Ala Ala Val Val Val Ala Asp Val Pro Ser
145              150              155              160
Asp Val Thr Val Val Gly Ile Pro Ala Lys Ile Val Arg Leu His Gly
      165              170              175
Lys Lys Asp Glu Pro Val Ile His Glu Val Glu Glu Lys Arg Glu Tyr
      180              185              190
Tyr Val Asn Lys Leu Glu Gln Ala Lys Asp Ala Ser His Arg Ser Ser
      195              200              205
Gly Leu
  210

```

(2) INFORMATION FOR SEQ ID NO:3756:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 265 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...265
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3756:

```

Ile His Trp Lys Thr Ser Met Ala Thr Ile Lys Glu Ile Lys Glu Leu
1      5      10      15
Leu Val Thr Val Lys Glu Leu Glu Ser Pro Ile Phe Leu Asp Leu Glu
      20      25      30
Lys Asp Asn Arg Ser Gly Val Gln Lys Glu Ile Ser Lys Arg Lys Arg
      35      40      45
Ala Ile Gln Ala Glu Leu Asp Glu Asn Leu Arg Leu Glu Ser Met Leu
      50      55      60
Ser Tyr Glu Lys Glu Leu Tyr Lys Gln Gly Leu Thr Leu Ile Ala Gly
65      70      75      80
Ile Asp Glu Val Gly Arg Gly Pro Leu Ala Gly Pro Val Val Ala Ala
      85      90      95
Ala Val Ile Leu Pro Lys Asn Cys Lys Ile Lys Gly Leu Asn Asp Ser
      100     105     110
Lys Lys Ile Pro Lys Lys Lys His Leu Glu Ile Phe Gln Ala Val Gln
      115     120     125
Asp Gln Ala Leu Ser Ile Gly Ile Gly Ile Ile Asp Asn Gln Val Ile
      130     135     140
Asp Gln Val Asn Ile Tyr Glu Ala Thr Lys Leu Ala Met Gln Glu Ala
145     150     155     160
Ile Ser Gln Leu Ser Pro Gln Pro Glu His Leu Leu Ile Asp Ala Met
      165     170     175
Lys Leu Asp Leu Pro Ile Ser Gln Thr Ser Ile Ile Lys Gly Asp Ala

```

		180						185					190				
Asn	Ser	Leu	Ser	Ile	Ala	Ala	Ala	Ser	Ile	Val	Ala	Lys	Val	Thr	Arg		
		195						200					205				
Asp	Glu	Leu	Met	Lys	Glu	Tyr	Asp	Gln	Gln	Phe	Pro	Gly	Tyr	Asp	Phe		
		210						215					220				
Ala	Thr	Asn	Ala	Gly	Tyr	Gly	Thr	Ala	Lys	His	Leu	Glu	Gly	Leu	Thr		
225						230					235				240		
Lys	Leu	Gly	Val	Thr	Pro	Ile	His	Arg	Thr	Ser	Phe	Glu	Pro	Val	Lys		
				245					250						255		
Ser	Leu	Val	Leu	Gly	Lys	Lys	Glu	Ser									
			260					265									

(2) INFORMATION FOR SEQ ID NO:3757:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 131 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3757:

Leu	Xaa	Trp	Asn	Xaa	Xaa	Gly	Glu	Ala	Gly	Pro	Arg	Trp	Cys	Val	Gly		
1				5					10					15			
Gly	Ser	Gly	Trp	Leu	Gly	Phe	Leu	Ser	Leu	Trp	Gly	Ala	Gly	Gly	Arg		
			20					25					30				
Gly	Ala	Gly	Ala	Arg	Gly	Ser	Arg	Ala	Gly	Arg	Gly	Trp	Leu	Val	Ala		
			35				40					45					
Leu	Leu	Ser	Val	Leu	Gly	Cys	Val	Ala	Arg	Ser	Gly	Leu	Trp	Arg	Val		
		50				55				60							
Gly	Xaa	Gly	Arg	Gly	Gly	Gly	Cys	Val	Cys	Gly	Gly	Xaa	Leu	Xaa			
65				70				75					80				
Arg	Leu	Val	Ala	Ala	Asp	Leu	Gly	Arg	Leu	Arg	Pro	Ala	Ala	Leu	Gly		
				85				90					95				
Gly	Ala	Ala	Gly	Arg	Ala	Pro	Arg	Ala	Arg	Val	Gly	Thr	Gly	Glu	Val		
			100					105					110				
Gly	Arg	Ser	Thr	Gly	Leu	Glu	Asp	Gly	Val	Leu	Met	Leu	Ser	Gly	Ala		
		115					120					125					
Pro	Ala	Xaa															
		130															

(2) INFORMATION FOR SEQ ID NO:3758:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 119 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3758:

Gly	Arg	Trp	Asn	Gln	Arg	His	Ser	Ser	Ser	Leu	Arg	Lys	Glu	Lys	Glu
1			5					10					15		
Met	Ile	Glu	Ala	Gln	Gly	Phe	Leu	Val	Asp	Lys	Gln	Thr	Arg	Cys	Ile
		20					25				30				
His	Tyr	His	Ser	Lys	Leu	Asp	Ile	Ile	Ala	Leu	Gln	Cys	Tyr	Asp	Cys
	35				40						45				
Lys	Lys	Tyr	Tyr	Ala	Cys	Tyr	Arg	Cys	His	Asp	Ser	Leu	Glu	Asn	His
	50				55					60					
Pro	Phe	Glu	Pro	Tyr	Pro	Leu	Ser	Leu	Ile	Gln	Asp	Lys	Pro	Ile	Leu
65				70					75					80	
Cys	Gly	Val	Cys	Leu	Lys	Leu	Leu	Thr	Tyr	Lys	Gln	Tyr	Lys	Glu	Ser
			85					90						95	
Leu	Ser	Cys	Pro	Phe	Cys	Phe	Ser	Arg	Phe	Asn	Pro	Gly	Cys	Gln	Asn
		100					105						110		
His	Lys	Glu	Arg	Tyr	Phe	Lys									
		115													

(2) INFORMATION FOR SEQ ID NO:3759:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 62 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...62

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3759:

Ser	Val	Trp	Lys	Phe	His	Gln	Thr	His	Thr	His	Ser	Thr	Leu	Asp	Val
1			5					10					15		
Lys	Ser	Ser	Leu	Lys	Gln	Met	Asp	Ala	Trp	Ile	Val	Ser	Thr	Lys	Asn
		20					25				30				
Thr	Val	Ser	Asn	Asn	Asp	Lys	Arg	Thr	Val	Ser	Ala	Val	Leu	Phe	Cys

	35		40		45								
Phe	Leu	Lys	Ser	Thr	Ala	Val	Phe	Met	Phe	Gln	Thr	His	Leu
	50					55					60		

(2) INFORMATION FOR SEQ ID NO:3760:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...248

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3760:

Phe	Arg	Arg	Asn	Ile	Tyr	Lys	Gly	Lys	Asp	Arg	Ile	Pro	Ala	Gly	Glu
1			5					10						15	
Thr	Phe	Val	His	Glu	Leu	Gln	Lys	Arg	Asp	Ile	Pro	Ile	Leu	Phe	Val
			20					25					30		
Thr	Asn	Asn	Thr	Thr	Arg	Thr	Pro	Glu	Ser	Val	Lys	Glu	Met	Leu	Ala
			35				40					45			
Gln	Asn	Phe	Asn	Ile	Asp	Thr	Pro	Ile	Ser	Thr	Val	Tyr	Thr	Ala	Thr
			50			55					60				
Leu	Ala	Thr	Ile	Asp	Tyr	Met	Asn	Asp	Leu	Gly	Leu	Glu	Lys	Thr	Val
65					70				75					80	
Tyr	Val	Val	Gly	Glu	Ala	Gly	Leu	Lys	Glu	Ala	Ile	Lys	Ala	Ala	Gly
				85					90					95	
Tyr	Val	Glu	Asp	Lys	Glu	Lys	Pro	Ala	Tyr	Val	Val	Val	Gly	Leu	Asp
			100					105					110		
Trp	Gln	Val	Asp	Tyr	Glu	Lys	Phe	Ala	Thr	Ala	Thr	Leu	Ala	Ile	Gln
			115				120					125			
Lys	Gly	Ala	His	Phe	Ile	Gly	Thr	Asn	Pro	Asp	Leu	Asn	Ile	Pro	Thr
			130			135					140				
Glu	Arg	Gly	Leu	Leu	Pro	Gly	Ala	Gly	Ser	Leu	Ile	Thr	Leu	Leu	Glu
145					150				155					160	
Val	Ala	Thr	Arg	Val	Lys	Pro	Val	Tyr	Ile	Gly	Lys	Pro	Asn	Ala	Ile
				165					170					175	
Ile	Met	Asp	Lys	Ala	Val	Glu	His	Leu	Gly	Leu	Glu	Arg	Glu	Glu	Leu
			180				185						190		
Ile	Met	Val	Gly	Asp	Asn	Tyr	Leu	Thr	Asp	Ile	Arg	Ala	Gly	Ile	Asp
			195				200					205			
Asn	Gly	Ile	Pro	Thr	Leu	Leu	Val	Thr	Thr	Gly	Phe	Thr	Lys	Ala	Glu
			210			215					220				
Glu	Val	Ala	Gly	Leu	Pro	Ile	Ala	Pro	Thr	His	Val	Val	Ser	Ser	Ile
225					230					235					240
Ala	Glu	Trp	Asp	Phe	Asp	Glu	Asn								
				245											

(2) INFORMATION FOR SEQ ID NO:3761:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...71

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3761:

Gln	Thr	Arg	Lys	Leu	Ala	Ala	Gly	Cys	Ser	Lys	His	Cys	Phe	Lys	Val
1			5					10					15		
Val	Asp	Gly	Thr	Asp	Glu	Val	Ser	Ser	Lys	His	Cys	Phe	Glu	Val	Val
		20					25					30			
Asp	Arg	Thr	Asp	Glu	Val	Ser	Asn	His	Thr	Tyr	Gly	Lys	Ala	Thr	Leu
		35				40					45				
Thr	Trp	Phe	Glu	Glu	Ile	Phe	Glu	Glu	Tyr	Lys	Ser	Leu	His	Asn	Lys
	50				55					60					
Thr	His	Ile	Thr	Lys	Val	Val									
65				70											

(2) INFORMATION FOR SEQ ID NO:3762:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...324

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3762:

Gly	Ser	Arg	Lys	Ser	Met	Tyr	Pro	Asp	Asp	Ser	Leu	Thr	Leu	His	Thr
1			5					10					15		
Asp	Leu	Tyr	Gln	Ile	Asn	Met	Met	Gln	Val	Tyr	Phe	Asp	Gln	Gly	Ile
		20					25				30				
His	Asn	Lys	Lys	Ala	Val	Phe	Glu	Val	Tyr	Phe	Arg	Gln	Gln	Pro	Phe
		35				40					45				

```

Lys Asn Gly Tyr Ala Val Phe Ala Gly Leu Glu Arg Ile Val Asn Tyr
 50          55          60
Leu Glu Asp Leu Arg Phe Ser Asp Ser Asp Ile Ala Tyr Leu Glu Ser
 65          70          75          80
Leu Gly Tyr His Gly Ala Phe Leu Asp Tyr Leu Arg Asn Phe Lys Leu
          85          90          95
Glu Leu Thr Val Arg Ser Ala Gln Glu Gly Asp Leu Val Phe Ala Asn
          100          105          110
Glu Pro Ile Val Gln Val Glu Gly Pro Leu Ala Gln Cys Gln Leu Val
          115          120          125
Glu Thr Ala Leu Leu Asn Ile Val Asn Tyr Gln Thr Leu Val Ala Thr
          130          135          140
Lys Ala Ala Arg Ile Arg Ser Val Ile Glu Asp Glu Pro Leu Met Glu
145          150          155          160
Phe Gly Thr Arg Arg Ala Gln Glu Thr Asp Ala Ala Ile Trp Gly Thr
          165          170          175
Arg Ala Ala Val Ile Gly Gly Ala Asn Gly Thr Ser Asn Val Arg Ala
          180          185          190
Gly Lys Leu Phe Asp Ile Pro Val Leu Gly Thr His Ala His Ala Leu
          195          200          205
Val Gln Val Tyr Gly Asn Asp Tyr Glu Ala Phe Lys Ala Tyr Ala Ala
          210          215          220
Thr His Lys Asn Cys Val Phe Leu Val Asp Thr Tyr Asp Thr Leu Arg
225          230          235          240
Ile Gly Val Pro Ala Ala Ile Gln Val Ala Arg Glu Leu Gly Asp Gln
          245          250          255
Ile Asn Phe Met Gly Val Arg Ile Asp Ser Gly Asp Ile Ala Tyr Ile
          260          265          270
Ser Lys Lys Val Arg Gln Gln Leu Asp Glu Ala Gly Phe Thr Glu Ala
          275          280          285
Lys Ile Tyr Ala Ser Asn Asp Leu Asp Glu Asn Thr Ile Leu Asn Leu
          290          295          300
Lys Met Gln Lys Ala Lys Ile Asp Val Trp Gly Val Gly Thr Thr Ala
305          310          315          320
Asp Tyr Ser Leu

```

(2) INFORMATION FOR SEQ ID NO:3763:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 749 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...749
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3763:

Asn	Gly	Arg	Lys	Asn	Trp	Arg	Val	Glu	Met	Pro	Lys	Glu	Val	Asn	Leu
1			5					10						15	
Thr	Gly	Glu	Glu	Val	Val	Ala	Leu	Thr	Lys	Glu	Tyr	Leu	Thr	Glu	Glu
		20						25					30		
Asp	Val	His	Phe	Val	His	Lys	Ala	Leu	Val	Tyr	Ala	Val	Glu	Cys	His
		35					40					45			
Ser	Gly	Gln	Tyr	Arg	Lys	Ser	Gly	Glu	Pro	Tyr	Ile	Ile	His	Pro	Ile
	50					55					60				
Gln	Val	Ala	Gly	Ile	Leu	Ala	Lys	Leu	Lys	Leu	Asp	Ala	Val	Thr	Val
65					70					75					80
Ala	Cys	Gly	Phe	Leu	His	Asp	Val	Val	Glu	Asp	Thr	Asp	Ala	Thr	Leu
				85					90					95	
Asp	Asp	Leu	Glu	Arg	Glu	Phe	Gly	Pro	Asp	Val	Arg	Val	Ile	Val	Asp
		100						105					110		
Gly	Val	Thr	Lys	Leu	Gly	Lys	Val	Glu	Tyr	Lys	Ser	Ile	Glu	Glu	Gln
		115					120					125			
Leu	Ala	Glu	Asn	His	Arg	Lys	Met	Leu	Met	Ala	Met	Ser	Glu	Asp	Ile
	130					135						140			
Arg	Val	Ile	Leu	Val	Lys	Leu	Ser	Asp	Arg	Leu	His	Asn	Met	Arg	Thr
145					150					155					160
Leu	Lys	His	Leu	Arg	Lys	Asp	Lys	Gln	Glu	Arg	Ile	Ser	Lys	Glu	Thr
			165						170					175	
Met	Glu	Ile	Tyr	Ala	Pro	Leu	Ala	His	Arg	Leu	Gly	Ile	Ser	Ser	Val
		180						185					190		
Lys	Trp	Glu	Leu	Glu	Asp	Leu	Ser	Phe	Arg	Tyr	Leu	Asn	Pro	Thr	Glu
	195					200						205			
Phe	Tyr	Lys	Ile	Thr	His	Met	Met	Lys	Glu	Lys	Arg	Arg	Glu	Arg	Glu
	210					215						220			
Ala	Leu	Val	Asp	Glu	Val	Val	Thr	Lys	Leu	Glu	Glu	Tyr	Thr	Thr	Glu
225					230					235					240
Arg	His	Leu	Lys	Gly	Lys	Ile	Tyr	Gly	Arg	Pro	Lys	His	Ile	Tyr	Ser
			245						250					255	
Ile	Phe	Arg	Lys	Met	Gln	Asp	Lys	Arg	Lys	Arg	Phe	Glu	Glu	Ile	Tyr
		260						265					270		
Asp	Leu	Ile	Ala	Ile	Arg	Cys	Ile	Leu	Asp	Thr	Gln	Ser	Asp	Val	Tyr
	275					280						285			
Ala	Met	Leu	Gly	Tyr	Val	His	Glu	Phe	Trp	Lys	Pro	Met	Pro	Gly	Arg
	290					295					300				
Phe	Lys	Asp	Tyr	Ile	Ala	Asn	Arg	Lys	Ala	Asn	Gly	Tyr	Gln	Ser	Ile
305					310					315					320
His	Thr	Thr	Val	Tyr	Gly	Pro	Lys	Gly	Pro	Ile	Glu	Phe	Gln	Ile	Arg
			325						330					335	
Thr	Lys	Glu	Met	His	Glu	Val	Ala	Glu	Tyr	Gly	Val	Ala	Ala	His	Trp
		340						345					350		
Ala	Tyr	Lys	Lys	Gly	Ile	Lys	Gly	Gln	Val	Asn	Ser	Lys	Glu	Ser	Ala
	355						360						365		
Ile	Gly	Met	Asn	Trp	Ile	Lys	Glu	Met	Met	Glu	Leu	Gln	Asp	Gln	Ala
	370					375					380				
Asp	Asp	Ala	Lys	Glu	Phe	Val	Asp	Ser	Val	Lys	Glu	Asn	Tyr	Leu	Ala
385					390					395					400
Glu	Glu	Ile	Tyr	Val	Phe	Thr	Pro	Asp	Gly	Ala	Val	Arg	Ser	Leu	Pro
			405						410					415	
Lys	Asp	Ser	Gly	Pro	Ile	Asp	Phe	Ala	Tyr	Glu	Ile	His	Thr	Lys	Val
		420						425					430		
Gly	Glu	Lys	Ala	Thr	Gly	Ala	Lys	Val	Asn	Gly	Arg	Met	Val	Pro	Leu
		435					440					445			
Thr	Thr	Lys	Leu	Lys	Thr	Gly	Asp	Gln	Val	Glu	Ile	Ile	Ala	Asn	Pro

450	Asn Ser Phe Gly Pro Ser Arg Asp Trp Leu Asn Met Val Lys Thr Ser	455	460
465	Lys Ala Arg Asn Lys Ile Arg Gln Phe Phe Lys Asn Gln Asp Lys Glu	470	475
		485	490
	Leu Ser Val Asn Lys Gly Arg Glu Met Leu Met Ala Gln Phe Gln Glu		495
		500	505
	Asn Gly Tyr Val Ala Asn Lys Phe Met Asp Lys Arg His Met Asp Gln		510
		515	520
	Val Leu Gln Lys Thr Ser Tyr Lys Thr Glu Asp Ser Leu Phe Ala Ala		525
		530	535
	Ile Gly Phe Gly Glu Ile Gly Ala Ile Thr Val Phe Asn Arg Leu Thr		540
		545	550
	Glu Lys Glu Arg Arg Glu Glu Glu Arg Ala Lys Ala Lys Ala Glu Ala		555
		565	570
	Glu Glu Leu Val Lys Gly Gly Glu Val Lys Val Glu Asn Lys Glu Thr		575
		580	585
	Leu Lys Val Lys His Glu Gly Gly Val Val Ile Glu Gly Ala Ser Gly		590
		595	600
	Leu Leu Val Arg Ile Ala Lys Cys Cys Asn Pro Val Pro Gly Asp Asp		605
		610	615
	Ile Val Gly Tyr Ile Thr Lys Gly Arg Gly Val Ala Ile His Arg Val		620
		625	630
	Asp Cys Met Asn Leu Arg Ala Gln Glu Asn Tyr Glu Gln Arg Leu Leu		635
		645	650
	Asp Val Glu Trp Glu Asp Gln Tyr Ser Ser Ser Asn Lys Glu Tyr Leu		655
		660	665
	Ala His Ile Asp Ile Tyr Gly Leu Asn Arg Thr Gly Leu Leu Asn Asp		670
		675	680
	Val Leu Gln Val Leu Ser Asn Thr Thr Lys Asn Ile Ser Thr Val Asn		685
		690	695
	Ala Gln Pro Thr Lys Asp Met Lys Phe Ala Asn Ile His Val Ser Phe		700
		705	710
	Gly Ile Ala Asn Leu Ser Thr Leu Thr Thr Val Val Asp Lys Ile Lys		715
		725	730
	Ser Val Pro Glu Val Tyr Ser Val Lys Arg Thr Asn Gly		735
		740	745

(2) INFORMATION FOR SEQ ID NO:3764:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 188 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...188

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3764:

Ile	Tyr	Arg	Lys	Leu	Gly	Trp	Arg	Thr	Ser	Leu	Phe	Leu	Lys	Ile	Arg
1				5					10					15	
Arg	Asn	Met	Asn	Lys	Lys	Thr	Arg	Gln	Thr	Leu	Ile	Gly	Leu	Leu	Val
			20					25					30		
Leu	Leu	Leu	Leu	Ser	Thr	Gly	Ser	Tyr	Tyr	Ile	Lys	Gln	Met	Pro	Ser
			35				40					45			
Ala	Pro	Asn	Ser	Pro	Lys	Thr	Asn	Leu	Ser	Gln	Lys	Lys	Gln	Ala	Ser
			50			55					60				
Glu	Ala	Pro	Ser	Gln	Ala	Leu	Ala	Glu	Ser	Val	Leu	Thr	Asp	Ala	Val
65					70					75					80
Lys	Ser	Gln	Ile	Lys	Gly	Ser	Leu	Glu	Trp	Asn	Gly	Ser	Gly	Ala	Phe
				85					90					95	
Ile	Val	Asn	Gly	Asn	Lys	Thr	Asn	Leu	Asp	Ala	Lys	Val	Ser	Ser	Lys
			100					105					110		
Pro	Tyr	Ala	Asp	Asn	Lys	Thr	Lys	Thr	Val	Gly	Lys	Glu	Thr	Val	Pro
			115				120					125			
Thr	Val	Ala	Asn	Ala	Leu	Leu	Ser	Lys	Ala	Thr	Arg	Gln	Tyr	Lys	Asn
					135						140				
Arg	Lys	Glu	Thr	Gly	Asn	Gly	Ser	Thr	Ser	Trp	Thr	Pro	Pro	Gly	Trp
145					150					155					160
His	Gln	Val	Lys	Asn	Leu	Lys	Gly	Ser	Tyr	Thr	His	Ala	Val	Asp	Arg
				165					170					175	
Val	Ile	Trp	Gln	Ser	Ser	Pro	Arg	Val	Val	Asp	Gly				
			180					185							

(2) INFORMATION FOR SEQ ID NO:3765:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3765:

Phe	Cys	Arg	Lys	Ser	Asn	Lys	Glu	Thr	Ser	Lys	Val	Met	Pro	Tyr	Phe
1				5					10					15	
Ile	Gly	Gly	His	Pro	Gly	Phe	Asn	Cys	Pro	Leu	Leu	Asp	Asp	Gly	Val
			20					25					30		
Tyr	Glu	Asp	Tyr	Tyr	Leu	Glu	Ser	Glu	Lys	Glu	Glu	Thr	Cys	Ser	Val
			35				40					45			
Pro	Arg	Pro	Phe	Pro	Glu	Thr	Gly	Met	Leu	Asp	Phe	Gln	Asp	Arg	Ser
			50			55					60				
Pro	Trp	Leu	Glu	Gly	Gln	Lys	Glu	Ile	Asp	Leu	Ser	Tyr	Asp	Leu	Phe
65					70					75					80
Ser	Thr	Asp	Ala	Val	Thr	Leu	Asp	Glu	Leu	Gln	Ser	Arg	Thr	Ile	Ala

				85					90					95			
Leu	Arg	Ser	Leu	Lys	His	Asp	Lys	Gly	Leu	Lys	Val	His	Phe	Ala	Glu		
			100					105					110				
Phe	Pro	Asn	Leu	Ile	Ile	Trp	Ser	Thr	Leu	Asn	Lys	Gly	Pro	Phe	Ile		
		115					120					125					
Thr	Phe	Glu	Pro	Trp	Ser	Gly	Leu	Ser	Thr	Phe	Leu	Glu	Glu	Gly	Asp		
	130					135					140						
His	Leu	Glu	Asp	Lys	Lys	Asn	Val	Cys	Leu	Leu	Glu	Ala	Asn	Gln	Val		
145					150					155					160		
Glu	Glu	Leu	Gly	Phe	Glu	Ile	Glu	Val	Leu								
				165					170								

(2) INFORMATION FOR SEQ ID NO:3766:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 469 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...469

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3766:

Ala	Ser	Arg	Asn	Ser	Tyr	Gly	Gln	Asp	Cys	Thr	His	Thr	Gly	Ser	Glu		
1				5					10					15			
Trp	Leu	Arg	Ser	Asp	Trp	Ile	Arg	Leu	Met	Thr	Asp	Glu	Arg	Ile	His		
		20						25				30					
Val	Leu	Arg	Asp	Ile	Leu	Leu	Glu	Leu	His	Asn	Gly	Ala	Ser	Pro	Glu		
		35				40					45						
Ser	Val	Gln	Asp	Arg	Phe	Asp	Ala	Thr	Phe	Thr	Gly	Val	Ser	Ala	Ile		
	50				55					60							
Glu	Ile	Ser	Leu	Met	Glu	His	Glu	Leu	Met	Asn	Ser	Asp	Ser	Gly	Val		
65				70					75					80			
Thr	Phe	Glu	Asp	Val	Met	Glu	Leu	Cys	Asp	Val	His	Ala	Asn	Leu	Phe		
			85					90					95				
Lys	Asn	Ala	Ile	Lys	Gly	Val	Glu	Val	Ser	Asp	Thr	Glu	His	Pro	Gly		
		100					105					110					
His	Pro	Val	Arg	Val	Phe	Lys	Glu	Glu	Asn	Leu	Ala	Leu	Arg	Ala	Ala		
	115					120						125					
Leu	Ile	Arg	Ile	Arg	Arg	Leu	Leu	Asp	Thr	Tyr	Glu	Ser	Met	Glu	Asp		
	130					135					140						
Glu	Glu	Met	Leu	Ala	Glu	Met	Arg	Lys	Gly	Leu	Val	Arg	Gln	Met	Gly		
145				150					155					160			
Leu	Val	Gly	Gln	Phe	Asp	Ile	His	Tyr	Gln	Arg	Lys	Glu	Glu	Leu	Phe		
			165					170					175				
Phe	Pro	Ile	Met	Glu	Arg	Tyr	Gly	His	Asp	Ser	Pro	Pro	Lys	Val	Met		
	180						185					190					
Trp	Gly	Val	Asp	Asp	Gln	Ile	Arg	Glu	Leu	Phe	Gln	Thr	Ala	Leu	Thr		

	195		200		205										
Thr	Ala	Lys	Ser	Leu	Pro	Glu	Val	Ser	Ile	Ser	Ser	Val	Lys	Glu	Ala
	210					215					220				
Phe	Glu	Ala	Phe	Ala	Thr	Glu	Phe	Glu	Ser	Met	Ile	Phe	Lys	Glu	Glu
225					230					235					240
Ser	Ile	Leu	Leu	Met	Ile	Leu	Leu	Glu	Ser	Phe	Thr	Gln	Asp	Asp	Trp
				245					250					255	
Leu	Gln	Ile	Ala	Glu	Glu	Ser	Asp	Ala	Tyr	Gly	Tyr	Ala	Ile	Ile	Arg
		260						265					270		
Pro	Ser	Glu	Lys	Trp	Val	Pro	Glu	Arg	Gln	Ile	Phe	Ile	Glu	Glu	Lys
		275					280					285			
Ile	Ala	Glu	Glu	Pro	Val	Gln	Leu	Asp	Thr	Ala	Glu	Gly	Gln	Val	Gln
	290					295				300					
Gln	Val	Ile	Asp	Thr	Pro	Glu	Gly	His	Phe	Thr	Ile	Thr	Phe	Thr	Pro
305					310					315					320
Lys	Glu	Lys	Glu	Ala	Val	Leu	Asp	Arg	His	Ser	Gln	Gln	Ala	Phe	Gly
				325					330					335	
Asn	Gly	Tyr	Leu	Ser	Val	Glu	Gln	Ala	Asn	Leu	Ile	Leu	Asn	His	Leu
			340					345					350		
Pro	Met	Glu	Ile	Thr	Phe	Val	Asn	Lys	Glu	Asp	Ile	Phe	Gln	Tyr	Tyr
		355					360					365			
Asn	Asp	Asn	Thr	Pro	Ala	Asp	Glu	Met	Ile	Phe	Lys	Arg	Thr	Pro	Ser
	370					375					380				
Gln	Val	Gly	Arg	Asn	Val	Glu	Leu	Cys	His	Pro	Pro	Lys	Tyr	Leu	Asp
385					390					395					400
Lys	Val	Lys	Ala	Ile	Met	Lys	Gly	Leu	Arg	Glu	Gly	Thr	Lys	Asp	Lys
				405					410					415	
Tyr	Glu	Met	Trp	Phe	Lys	Ser	Glu	Ser	Arg	Gly	Lys	Phe	Val	His	Ile
				420					425				430		
Thr	Tyr	Ala	Ala	Val	His	Asp	Glu	Asn	Gly	Glu	Phe	Gln	Gly	Val	Leu
		435					440					445			
Glu	Tyr	Val	Gln	Asp	Ile	Gln	Pro	Tyr	Arg	Glu	Ile	Asp	Thr	Asp	Tyr
	450					455					460				
Phe	Arg	Gly	Leu	Glu											
465															

(2) INFORMATION FOR SEQ ID NO:3767:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...164

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3767:

Arg Thr Arg Asn Val Ala Phe Tyr Gly Leu Thr Ser Val Ser Asn Trp

```

1           5           10           15
Ser Leu Ser Ser Asn Ile Ser Thr Arg Leu Ile Glu Val Phe Leu Ile
                20           25           30
His His Leu His Tyr Thr Ser Asp Gln Ile His Glu Glu Ala Asp Val
                35           40           45
Leu Asp Asn Thr Val Ser Asp Leu Phe Val Glu Arg Leu Asp Lys Leu
                50           55           60
Leu Gly Phe Pro Lys Thr Cys Pro His Gly Gly Thr Ile Pro Ala Lys
65           70           75           80
Gly Glu Leu Leu Val Glu Ile Asn Asn Leu Pro Leu Ala Asp Ile Lys
                85           90           95
Glu Ala Gly Ala Tyr Arg Leu Thr Arg Val His Asp Ser Phe Asp Ile
                100           105           110
Leu His Tyr Leu Asp Lys His Ser Leu His Ile Cys Asp Gln Leu Gln
                115           120           125
Val Lys Gln Phe Asp Gly Phe Ser Asn Thr Ser Thr Ile Leu Ser Asn
                130           135           140
Asp Glu Asp Leu Xaa Val Asn Met Asp Ile Ala Lys Gln Leu Tyr Val
145           150           155           160
Glu Lys Ile Asn

```

(2) INFORMATION FOR SEQ ID NO:3768:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...107

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3768:

```

Asp Glu Arg Asn Phe Arg Asn Leu Met Met Asn Met Gln Asn Met Met
1           5           10           15
Arg Gln Ala Gln Lys Leu Gln Lys Gln Met Glu Gln Ser Gln Ala Glu
                20           25           30
Leu Ala Ala Met Gln Phe Val Gly Lys Ser Ala Gln Asp Leu Val Gln
                35           40           45
Ala Thr Leu Thr Gly Asp Lys Lys Val Val Ser Ile Asp Phe Asn Pro
50           55           60
Ala Val Val Asp Pro Glu Asp Leu Glu Thr Leu Ser Asp Met Thr Val
65           70           75           80
Gln Ala Ile Asn Ser Ala Leu Glu Gln Ile Asp Glu Thr Thr Lys Lys
                85           90           95
Lys Leu Gly Ala Phe Ala Gly Lys Leu Pro Phe
                100           105

```

(2) INFORMATION FOR SEQ ID NO:3769:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 82 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...82
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3769:

Ile	Glu	Arg	Asn	Tyr	Met	Ile	Tyr	Lys	Val	Phe	Tyr	Gln	Glu	Thr	Lys
1			5					10					15		
Glu	Arg	Ser	Pro	Arg	Arg	Glu	Thr	Thr	Arg	Ala	Leu	Tyr	Leu	Asp	Ile
			20					25					30		
Asp	Thr	Ser	Ser	Glu	Leu	Glu	Gly	Arg	Ile	Thr	Ala	Arg	Gln	Leu	Val
			35				40					45			
Glu	Glu	Asn	Arg	Pro	Glu	Tyr	Asn	Ile	Glu	Tyr	Ile	Glu	Leu	Leu	Ser
			50				55				60				
Asp	Lys	Leu	Leu	Asp	Tyr	Glu	Lys	Glu	Thr	Gly	Ala	Phe	Glu	Ile	Thr
65					70					75					80
Glu	Phe														

(2) INFORMATION FOR SEQ ID NO:3770:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 385 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...385
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3770:

Lys	Arg	Arg	Asn	Leu	Tyr	Gln	Leu	Lys	Lys	Pro	Ile	Ile	Glu	Phe	Lys
1			5					10					15		
Asn	Val	Ser	Lys	Val	Phe	Glu	Asp	Ser	Asn	Thr	Lys	Val	Leu	Lys	Asp

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...332

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3771:

Arg	Val	Arg	Lys	Ser	Arg	Val	Asn	Asn	Ser	Gln	Gln	Met	Leu	Gln	Ala
1				5					10					15	
Leu	Glu	Glu	Gln	Asp	Leu	Thr	Lys	Ala	Glu	His	Tyr	Phe	Ala	Lys	Ala
			20					25					30		
Leu	Glu	Asn	Asp	Ser	Ser	Asp	Leu	Leu	Tyr	Glu	Leu	Ala	Thr	Tyr	Leu
		35					40					45			
Glu	Gly	Ile	Gly	Phe	Tyr	Pro	Gln	Ala	Lys	Glu	Ile	Tyr	Leu	Lys	Ile
	50				55					60					
Val	Glu	Asp	Phe	Pro	Glu	Val	His	Leu	Asn	Leu	Ala	Ala	Ile	Ala	Ser
65				70					75					80	
Glu	Asp	Gly	Gln	Ile	Glu	Glu	Ala	Phe	Thr	Tyr	Leu	Glu	Glu	Ile	Gln
			85					90						95	
Ala	Asp	Ser	Asp	Trp	Tyr	Val	Ser	Ser	Leu	Ala	Leu	Lys	Ala	Asp	Leu
			100					105					110		
Tyr	Gln	Leu	Glu	Gly	Leu	Thr	Asp	Val	Ala	Arg	Glu	Lys	Leu	Leu	Glu
		115					120					125			
Ala	Leu	Thr	Tyr	Ser	Glu	Asp	Ser	Leu	Leu	Ile	Leu	Gly	Leu	Ala	Glu
	130					135					140				
Leu	Asp	Ser	Glu	Leu	Glu	Asn	Tyr	Gln	Ala	Ala	Ile	Gln	Ala	Tyr	Ala
145				150					155					160	
Gln	Leu	Asp	Asn	Arg	Ser	Ile	Tyr	Glu	Gln	Thr	Gly	Ile	Ser	Thr	Tyr
			165					170						175	
Gln	Arg	Ile	Gly	Phe	Ala	Tyr	Ala	Gln	Leu	Gly	Lys	Phe	Glu	Thr	Ala
		180						185					190		
Thr	Glu	Phe	Leu	Glu	Lys	Ala	Leu	Glu	Leu	Glu	Tyr	Asp	Asp	Leu	Thr
	195					200						205			
Ala	Phe	Glu	Leu	Ala	Ser	Leu	Tyr	Phe	Asp	Gln	Glu	Glu	Tyr	Gln	Lys
	210				215					220					
Ala	Thr	Leu	Tyr	Phe	Lys	Gln	Leu	Asp	Thr	Ile	Ser	Pro	Asp	Phe	Glu
225				230					235					240	
Gly	Tyr	Glu	Tyr	Gly	Tyr	Ser	Gln	Ala	Leu	His	Lys	Glu	His	Gln	Val
			245					250						255	
Gln	Glu	Ala	Leu	Arg	Ile	Ala	Lys	Gln	Gly	Leu	Glu	Lys	Asn	Pro	Phe
		260					265						270		
Glu	Thr	Arg	Leu	Leu	Leu	Ala	Ala	Ser	Gln	Phe	Ser	Tyr	Glu	Leu	His
		275					280						285		
Asp	Ala	Ser	Gly	Ala	Glu	Asn	Tyr	Leu	Leu	Thr	Ala	Lys	Glu	Asp	Ala
	290					295					300				
Glu	Asp	Thr	Glu	Glu	Ile	Leu	Leu	Arg	Leu	Ala	Thr	Ile	Tyr	Leu	Glu
305				310						315				320	
Gln	Glu	Arg	Tyr	Glu	Asp	Ile	Leu	Glu	Leu	Gln	Ser				
			325					330							

(2) INFORMATION FOR SEQ ID NO:3772:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 393 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...393
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3772:

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Lys Lys Arg Asn Ser Met Leu His Tyr Thr Lys Glu Asp Leu Leu Glu
1      5      10      15
Leu Gly Ala Glu Ile Thr Thr Arg Glu Ile Tyr Gln Gln Pro Asp Val
20      25      30
Trp Arg Glu Ala Phe Glu Phe Tyr Gln Ala Lys Arg Glu Glu Ile Ala
35      40      45
Ala Phe Leu Gln Glu Ile Ala Asp Lys His Asp Tyr Ile Lys Val Ile
50      55      60
Leu Thr Gly Ala Gly Thr Ser Ala Tyr Val Gly Asp Thr Leu Leu Pro
65      70      75      80
Tyr Phe Lys Glu Val Tyr Asp Glu Arg Lys Trp Asn Phe Asn Ala Ile
85      90      95
Ala Thr Thr Asp Ile Val Ala Asn Pro Ala Thr Tyr Leu Lys Lys Asp
100     105     110
Val Ala Thr Val Leu Val Ser Phe Ala Arg Ser Gly Asn Ser Pro Glu
115     120     125
Ser Val Ala Thr Val Asp Leu Ala Lys Ser Leu Val Asp Glu Leu Tyr
130     135     140
Gln Val Thr Ile Thr Cys Ala Ala Asp Gly Lys Leu Ala Leu Gln Ala
145     150     155     160
His Gly Asp Asp Arg Asn Leu Leu Leu Leu Gln Pro Ala Val Ser Asn
165     170     175
Asp Ala Gly Phe Ala Met Thr Ser Ser Phe Thr Ser Met Met Leu Thr
180     185     190
Thr Leu Leu Val Phe Asp Pro Thr Glu Phe Ala Val Lys Ser Glu Arg
195     200     205
Phe Glu Val Val Ser Ser Leu Ala Arg Lys Val Leu Asp Lys Ala Glu
210     215     220
Asp Val Lys Glu Leu Val Asp Leu Asp Phe Asn Arg Val Ile Tyr Leu
225     230     235     240
Gly Ala Gly Pro Phe Phe Gly Leu Ala His Glu Ala Gln Leu Lys Ile
245     250     255
Leu Glu Leu Thr Ala Gly Gln Val Ala Thr Met Tyr Glu Ser Pro Val
260     265     270
Gly Phe Arg His Gly Pro Lys Ser Leu Ile Asn Glu Asn Thr Val Val
275     280     285
Leu Val Phe Gly Thr Arg Thr Asp Tyr Thr Arg Lys Tyr Asp Leu Asp
290     295     300
Leu Val Arg Glu Val Ala Gly Asp Gln Ile Ala Arg Arg Val Val Leu

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305		310		315		320
Leu	Ser	Asp	Gln	Ala	Phe	Gly
		325		330		335
Gly	Cys	Gly	Gly	Val	Leu	Asn
		340		345		350
Val	Tyr	Ala	Gln	Leu	Phe	Ala
		355		360		365
Lys	Pro	Asp	Thr	Pro	Ser	Pro
		370		375		380
Gly	Val	Ile	Ile	His	Glu	Tyr
385				390		

(2) INFORMATION FOR SEQ ID NO:3773:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 61 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...61
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3773:

Phe	Trp	Arg	Lys	Ile	Leu	Ser	Leu	Leu	Phe	Ile	Ile	Leu	Asn	Leu	Phe
1			5				10					15			
Ile	Leu	Tyr	Lys	Ile	Tyr	Ser	Leu	Arg	Arg	Glu	Lys	Ser	Lys	Tyr	Leu
		20				25						30			
Ile	Tyr	Thr	Ala	Tyr	Ile	Ile	Phe	Gly	Val	Asn	Val	Val	Tyr	Gly	Ile
		35				40						45			
Gln	Trp	Leu	Leu	Lys	Glu	Leu	Ile	Ser	Thr	Ile	Ser	Pro			
50				55				60							

(2) INFORMATION FOR SEQ ID NO:3774:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 334 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature

(B) LOCATION 1...334

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3774:

Ile	Arg	Arg	Asn	Leu	Val	Met	Val	Val	Phe	Thr	Gly	Ser	Thr	Val	Glu
1			5						10					15	
Glu	Ala	Ile	Gln	Lys	Gly	Leu	Lys	Glu	Leu	Asp	Ile	Pro	Arg	Met	Lys
			20					25					30		
Ala	His	Ile	Lys	Val	Ile	Ser	Arg	Glu	Lys	Lys	Gly	Phe	Leu	Gly	Leu
			35				40					45			
Phe	Gly	Lys	Lys	Pro	Ala	Gln	Val	Asp	Ile	Glu	Ala	Ile	Ser	Glu	Thr
	50					55					60				
Thr	Val	Val	Lys	Ala	Asn	Gln	Gln	Val	Val	Lys	Gly	Val	Pro	Lys	Lys
65					70					75					80
Ile	Asn	Asp	Leu	Asn	Glu	Pro	Val	Lys	Thr	Val	Ser	Glu	Glu	Thr	Val
			85						90					95	
Asp	Leu	Gly	His	Val	Val	Asn	Ala	Ile	Lys	Lys	Ile	Glu	Glu	Glu	Gly
			100					105						110	
Gln	Gly	Ile	Ser	Asp	Glu	Val	Lys	Ala	Glu	Ile	Leu	Lys	His	Glu	Arg
	115						120						125		
His	Ala	Ser	Thr	Ile	Leu	Glu	Glu	Thr	Gly	His	Ile	Glu	Ile	Leu	Asn
	130						135				140				
Glu	Leu	Gln	Ile	Glu	Glu	Ala	Met	Arg	Glu	Glu	Ala	Gly	Ala	Asp	Asp
145					150					155					160
Leu	Glu	Thr	Glu	Gln	Asp	Gln	Thr	Glu	Asn	Gln	Asp	Leu	Lys	Glu	Met
				165					170					175	
Gly	Leu	Lys	Val	Glu	Gln	Ser	Tyr	Asp	Ile	Ala	Gln	Val	Ala	Thr	Asp
			180					185						190	
Val	Thr	Ala	Tyr	Val	Gln	Ala	Ile	Val	Asp	Asp	Met	Asp	Val	Glu	Ala
	195						200						205		
Thr	Leu	Ser	Asn	Asp	Tyr	Asn	Arg	Arg	Ser	Ile	Asn	Leu	Gln	Ile	Asp
	210					215					220				
Thr	Asn	Glu	Pro	Gly	Arg	Ile	Ile	Gly	Tyr	His	Gly	Lys	Val	Leu	Lys
225					230					235					240
Ala	Leu	Gln	Leu	Leu	Ala	Gln	Asn	Tyr	Leu	Tyr	Asn	Arg	Tyr	Ser	Lys
				245					250					255	
Thr	Phe	Tyr	Val	Thr	Ile	Asn	Val	Asn	Asp	Tyr	Val	Glu	His	Arg	Ala
			260					265					270		
Glu	Val	Leu	Gln	Thr	Tyr	Ala	Gln	Lys	Leu	Ala	Asn	Arg	Val	Leu	Glu
	275						280					285			
Glu	Gly	Arg	Ser	His	Lys	Thr	Asp	Pro	Met	Ser	Asn	Ser	Glu	Arg	Lys
	290					295					300				
Ile	Ile	His	Arg	Ile	Ile	Ser	Arg	Met	Asp	Gly	Val	Thr	Ser	Tyr	Ser
305					310					315					320
Glu	Gly	Asp	Glu	Pro	Asn	Arg	Tyr	Val	Val	Val	Asp	Thr	Glu		
				325					330						

(2) INFORMATION FOR SEQ ID NO:3775:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 289 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...289

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3775:

Thr	Arg	Arg	Asn	Leu	Met	Leu	Gly	Ala	Ile	Ile	Gly	Asp	Ile	Val	Gly
1			5				10						15		
Ser	Val	Tyr	Glu	Trp	Asn	Asn	Ile	Lys	Thr	Lys	Asp	Phe	Pro	Leu	Phe
		20					25					30			
Arg	Lys	Asp	Cys	Phe	Phe	Thr	Asp	Asp	Thr	Val	Met	Thr	Cys	Ala	Val
		35				40					45				
Ala	Glu	Ala	Ile	Met	Asn	Gly	Gly	Gln	Lys	Asp	Asp	Phe	Ile	Asp	Ala
	50				55					60					
Met	Lys	Lys	Tyr	Gly	Arg	Met	Tyr	Pro	Asn	Ala	Asp	Tyr	Gly	Ala	Arg
65					70				75					80	
Phe	Asn	Ala	Trp	Leu	Asn	Ser	Asp	Asn	Arg	Glu	Pro	Tyr	Asn	Ser	Phe
			85					90					95		
Gly	Asn	Gly	Ser	Ala	Met	Arg	Ile	Ser	Pro	Cys	Ala	Trp	Ile	Met	Asp
			100				105						110		
Cys	Gly	Phe	Tyr	Ala	Lys	Thr	Gly	Met	Trp	Pro	Ser	Ser	Arg	Gly	Leu
		115					120					125			
Thr	Ser	Leu	Ser	Ala	Glu	Val	Thr	His	Asn	His	Pro	Glu	Gly	Val	Lys
	130					135					140				
Gly	Ala	Met	Ala	Thr	Ala	Asp	Ala	Ile	Phe	Leu	Cys	Arg	Phe	Tyr	Phe
145				150					155					160	
Gly	Gly	Tyr	Cys	Arg	Glu	Tyr	Glu	Gln	Ser	Ile	Asn	Asp	Asn	Pro	Thr
			165					170					175		
Glu	Cys	Lys	Arg	Arg	Ile	Lys	Asp	Tyr	Ile	Glu	Lys	Glu	Tyr	Asp	Tyr
			180				185						190		
Asn	Leu	Ser	Gln	Thr	Leu	Asp	Glu	Ile	Arg	Pro	Asn	Tyr	Arg	Phe	Asn
	195					200					205				
Glu	Thr	Cys	Gln	Glu	Thr	Val	Pro	Gln	Ala	Ile	Ile	Ala	Phe	Leu	Glu
	210				215						220				
Ser	Arg	Asp	Phe	Glu	Asp	Ala	Ile	Arg	Asn	Ala	Ile	Ser	Leu	Gly	Gly
225				230					235					240	
Asp	Ser	Asp	Thr	Leu	Ala	Ala	Ile	Thr	Cys	Ser	Ile	Ala	Glu	Ala	Ala
			245					250					255		
Tyr	Gly	Ile	Pro	Asp	Trp	Ile	Lys	Asp	Lys	Ala	Tyr	Ser	Tyr	Leu	Asp
		260					265						270		
Glu	Pro	Leu	Lys	Asp	Val	Val	Arg	Arg	Trp	Glu	Asn	Arg	Ile	Lys	Ala
		275					280					285			
Tyr															

(2) INFORMATION FOR SEQ ID NO:3776:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 425 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...425

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3776:

Glu	Arg	Arg	Lys	Thr	Lys	Met	Gln	Asn	Leu	Lys	Phe	Ala	Phe	Ser	Ser	1	5	10	15
Ile	Met	Ala	His	Lys	Met	Arg	Ser	Leu	Leu	Thr	Met	Ile	Gly	Ile	Ile	20	25	30	
Ile	Gly	Val	Ser	Ser	Val	Val	Val	Ile	Met	Ala	Leu	Gly	Asp	Ser	Leu	35	40	45	
Ser	Arg	Gln	Val	Asn	Lys	Asp	Met	Thr	Lys	Ser	Gln	Lys	Asn	Ile	Ser	50	55	60	
Val	Phe	Phe	Ser	Pro	Lys	Lys	Ser	Lys	Asp	Gly	Ser	Phe	Thr	Gln	Lys	65	70	75	80
Gln	Ser	Ala	Phe	Thr	Val	Ser	Gly	Lys	Glu	Glu	Glu	Val	Pro	Val	Glu	85	90	95	
Pro	Pro	Lys	Pro	Gln	Glu	Ser	Trp	Val	Gln	Glu	Ala	Ala	Lys	Leu	Lys	100	105	110	
Gly	Val	Asp	Ser	Tyr	Tyr	Val	Thr	Asn	Ser	Thr	Asn	Ala	Ile	Leu	Thr	115	120	125	
Tyr	Gln	Asp	Lys	Lys	Val	Glu	Asn	Ala	Asn	Leu	Thr	Gly	Gly	Asn	Arg	130	135	140	
Thr	Tyr	Met	Asp	Ala	Val	Lys	Asn	Glu	Ile	Ile	Ala	Gly	Arg	Ser	Leu	145	150	155	160
Arg	Glu	Gln	Asp	Phe	Lys	Glu	Phe	Ala	Ser	Val	Ile	Leu	Leu	Asp	Glu	165	170	175	
Glu	Leu	Ser	Ile	Ser	Leu	Phe	Glu	Ser	Pro	Gln	Glu	Ala	Ile	Asn	Lys	180	185	190	
Val	Val	Glu	Val	Asn	Gly	Phe	Ser	Tyr	Arg	Val	Ile	Gly	Val	Tyr	Thr	195	200	205	
Ser	Pro	Glu	Ala	Lys	Arg	Ser	Lys	Ile	Tyr	Gly	Phe	Gly	Gly	Leu	Pro	210	215	220	
Ile	Thr	Thr	Asn	Ile	Ser	Leu	Ala	Ala	Asn	Phe	Asn	Val	Asp	Glu	Ile	225	230	235	240
Ala	Asn	Ile	Val	Phe	Arg	Val	Asn	Asp	Thr	Ser	Leu	Thr	Pro	Thr	Leu	245	250	255	
Gly	Pro	Glu	Leu	Ala	Arg	Lys	Met	Thr	Glu	Leu	Ala	Gly	Leu	Gln	Gln	260	265	270	
Gly	Glu	Tyr	Gln	Val	Ala	Asp	Glu	Ser	Val	Val	Phe	Ala	Glu	Ile	Gln	275	280	285	
Gln	Ser	Phe	Ser	Phe	Met	Thr	Thr	Ile	Ile	Ser	Ser	Ile	Ala	Gly	Ile	290	295	300	
Ser	Leu	Phe	Val	Gly	Gly	Thr	Gly	Val	Met	Asn	Ile	Met	Leu	Val	Ser	305	310	315	320
Val	Thr	Glu	Arg	Thr	Ser	Glu	Ile	Gly	Leu	Arg	Lys	Ala	Leu	Gly	Ala	325	330	335	
Gln	Arg	Ala	Asn	Ile	Leu	Ile	Gln	Phe	Leu	Ile	Glu	Ser	Met	Ile	Leu	340	345	350	

Thr	Leu	Leu	Gly	Gly	Leu	Ile	Gly	Leu	Thr	Ile	Ala	Ser	Gly	Leu	Thr
		355					360					365			
Ala	Leu	Ala	Gly	Leu	Leu	Leu	Gln	Gly	Leu	Ile	Glu	Gly	Ile	Glu	Val
	370				375						380				
Gly	Val	Ser	Ile	Pro	Val	Ala	Leu	Phe	Ser	Leu	Ala	Val	Ser	Ala	Ser
385					390					395					400
Val	Gly	Met	Ile	Phe	Gly	Val	Leu	Pro	Ala	Asn	Lys	Ala	Ser	Lys	Leu
			405						410						415
Asp	Pro	Ile	Glu	Ala	Leu	Arg	Tyr	Glu							
			420					425							

(2) INFORMATION FOR SEQ ID NO:3777:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3777:

Phe	Leu	Gly	Asn	Gly	Asn	Gln	Cys	Leu	Cys	Ser	Arg	Phe	Gly	Cys	Gln
1			5				10						15		
Gly	Gly	Asp	His	Gln	Leu	Arg	Leu	Gly	Lys	Trp	Ser	Leu	Val	Arg	Lys
		20					25					30			
Pro	Asp	Leu	Asp	Arg	Pro	Val	His	Cys	Leu	Pro	Arg	Phe	Ser	Ser	His
	35				40						45				
Gln	Phe	Leu	Val	Tyr	Ser	Gly	Leu	Arg	Phe	Ile	Pro	Tyr	His	Ser	Gly
	50				55				60						
Pro	Ser	Ser	Gly	Val	Phe	Ile	Lys	Tyr	Leu	Tyr	Gly	Pro	Asn	Ser	Leu
65				70					75						80
Arg	Ser	Tyr	Gly	Ala	Asn	Leu	Ser	Thr	Gln	Tyr	Val	Cys	Arg	His	Gln
			85					90					95		
Gln	Ser	Arg	Val	Cys	Tyr	Gly	Glu	Thr	Ala	Phe	Asn	Leu	Trp	Arg	Ile
		100					105						110		
Trp	Leu	Gly	Tyr	Cys	Asp	Arg	Asn								
	115						120								

(2) INFORMATION FOR SEQ ID NO:3778:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...171

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3778:

Leu	Ser	Gly	Asn	Thr	Thr	Ala	Leu	Ser	Gln	Ser	Leu	Ser	Val	Thr	Pro
1				5					10					15	
Asn	Asn	Gly	Val	Ser	Ala	Ala	Asp	Asp	Gly	Tyr	Val	Phe	Asn	Pro	Asn
			20					25					30		
Asp	Ile	Val	Arg	Asp	Thr	Gly	Asp	Ala	Tyr	Ile	Val	Arg	His	Gly	Asp
			35				40					45			
His	Tyr	His	Tyr	Ile	Pro	Lys	Ser	Ser	Leu	Asn	Asn	Pro	Pro	Ser	His
			50			55					60				
Ser	Asn	Thr	Glu	Glu	Ala	Gly	Ser	Ser	Ser	Ser	Ser	Val	Leu	Ser	Asn
65					70				75					80	
Pro	Ser	Leu	His	Val	His	His	Glu	Glu	Glu	Asp	Gly	His	Gly	Phe	Asp
			85						90					95	
Ala	Asn	Arg	Ile	Ile	Ser	Glu	Asp	Ser	Glu	Gly	Phe	Val	Ile	Pro	His
			100					105					110		
Gly	Asp	His	Asn	His	Tyr	Ile	Lys	Val	Gln	Thr	Lys	Gly	Tyr	Glu	Ala
			115				120					125			
Ala	Leu	Lys	Asn	Lys	Ile	Pro	Ser	Leu	Gln	Ser	Asn	Tyr	Gln	Pro	Gly
			130			135					140				
Thr	Phe	Asp	Glu	Lys	Ala	Val	Leu	Ala	Lys	Val	Asp	Gln	Leu	Leu	Ala
145					150					155					160
Asp	Ser	Arg	Ser	Ile	Tyr	Lys	Asp	Arg	Leu	Ser					
				165					170						

(2) INFORMATION FOR SEQ ID NO:3779:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 214 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...214

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3779:

Arg	Lys	Gly	Lys	Ser	Val	Thr	Met	Ala	Asn	Val	Thr	Leu	Phe	Asp	Gln
1				5					10					15	
Thr	Gly	Lys	Glu	Ala	Gly	Gln	Val	Val	Leu	Ser	Asp	Ala	Val	Phe	Gly

		20					25			30					
Ile	Glu	Pro	Asn	Glu	Ser	Val	Val	Phe	Asp	Val	Ile	Ile	Ser	Gln	Arg
		35					40					45			
Ala	Ser	Leu	Arg	Gln	Gly	Thr	His	Ala	Val	Lys	Asn	Arg	Ser	Ala	Val
		50				55					60				
Ser	Gly	Gly	Gly	Arg	Lys	Pro	Trp	Arg	Gln	Lys	Gly	Thr	Gly	Arg	Ala
65					70					75					80
Arg	Gln	Gly	Ser	Ile	Arg	Ser	Pro	Gln	Trp	Arg	Gly	Gly	Gly	Val	Val
			85						90					95	
Phe	Gly	Pro	Thr	Pro	Arg	Ser	Tyr	Gly	Tyr	Lys	Leu	Pro	Gln	Lys	Val
		100						105					110		
Arg	Arg	Leu	Ala	Leu	Lys	Ser	Val	Tyr	Ser	Glu	Lys	Val	Ala	Glu	Asn
		115					120						125		
Lys	Phe	Val	Ala	Val	Asp	Ala	Leu	Ser	Phe	Thr	Ala	Pro	Lys	Thr	Ala
		130				135					140				
Glu	Phe	Ala	Lys	Val	Leu	Ala	Ala	Leu	Ser	Ile	Asp	Ser	Lys	Val	Leu
145					150					155					160
Val	Ile	Leu	Glu	Glu	Arg	Asn	Glu	Phe	Ala	Ala	Leu	Ser	Ala	Arg	Asn
			165					170						175	
Leu	Pro	Asn	Val	Lys	Ile	Ala	Thr	Ala	Thr	Thr	Ala	Ser	Phe	Pro	Asp
		180						185					190		
Ile	Ala	Asn	Ser	Asp	Lys	Leu	Leu	Val	Thr	Gln	Ala	Ala	Ile	Ser	Lys
		195					200					205			
Ile	Glu	Glu	Val	Leu	Ala										
		210													

(2) INFORMATION FOR SEQ ID NO:3780:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...64

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3780:

Met	Lys	Gly	Lys	Glu	Tyr	Glu	Asn	Arg	Thr	Val	Ser	Phe	Ala	Ile	Ser
1				5					10					15	
Ser	Lys	Gly	Glu	Lys	Met	Lys	Val	Glu	Asn	Ile	Ser	Tyr	Arg	Val	Asp
			20					25					30		
His	Arg	Ile	Leu	Phe	Asp	Asn	Ile	Ser	Phe	Asp	Thr	Ser	Ser	Ser	Gly
		35					40					45			
Val	Thr	Leu	Ile	Thr	Gly	Lys	Asn	Gly	Thr	Gly	Lys	Ser	Thr	Leu	Leu
		50				55					60				

(2) INFORMATION FOR SEQ ID NO:3781:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 82 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...82
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3781:

Ile	Thr	Asn	Leu	Leu	Ile	Phe	Ser	Pro	Glu	Gly	Gly	Ile	Asn	Phe	Asp
1			5						10					15	
His	Lys	Ile	Gly	Tyr	Ser	Leu	Tyr	Pro	Glu	Asn	Met	Leu	Arg	Met	Ile
		20					25						30		
Val	Ser	Lys	Gln	Tyr	Leu	Leu	Phe	Tyr	Leu	Ile	His	Glu	Lys	Glu	Val
		35					40					45			
His	Thr	Leu	Arg	Ile	Ile	Asn	Ser	Arg	Thr	Asp	Tyr	Leu	Asn	Gln	Leu
	50					55					60				
Asp	His	Leu	Phe	Arg	Thr	Cys	Arg	Lys	Leu	Phe	Ser	Ser	Gln	Ile	Ile
65					70					75					80
Ser	Leu														

(2) INFORMATION FOR SEQ ID NO:3782:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 95 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...95
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3782:

Glu	Pro	Asn	Leu	Lys	Thr	Ser	Leu	Ile	Leu	Phe	Glu	Asn	Leu	Phe	Lys
1			5						10					15	
Pro	Arg	Gln	Arg	Arg	Leu	Thr	Val	Tyr	Met	Leu	Leu	Thr	Ser	Ser	Val
		20					25						30		
Leu	Ser	Ala	Thr	Ser	Lys	Arg	Cys	Phe	Glu	Leu	Thr	Ser	Ser	Val	Ser

(2) INFORMATION FOR SEQ ID NO:3783:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3783:

(2) INFORMATION FOR SEQ ID NO:3784:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...63

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3784:

Phe	Val	Phe	Glu	Leu	Val	Ala	Phe	Val	Asp	Glu	Asp	Val	Ser	Asp	Glu
1				5					10					15	
Leu	Leu	Val	Leu	Glu	Phe	Asp	Val	Leu	Glu	Leu	Gly	Ala	Thr	Gly	Phe
			20					25					30		
Val	Val	Thr	Phe	Ile	Ile	Val	Ser	Asn	Gly	Val	Ile	Thr	Ala	Gly	Lys
			35				40					45			
Thr	Thr	Pro	Leu	Arg	Ser	Ile	Ala	Cys	Lys	Gly	Thr	Glu	Pro	Leu	
	50					55					60				

(2) INFORMATION FOR SEQ ID NO:3785:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 221 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...221

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3785:

Ile	Gly	Phe	Glu	Glu	Leu	Glu	Met	Lys	Val	Leu	Val	Thr	Gly	Phe	Glu
1				5					10					15	
Pro	Phe	Gly	Gly	Glu	Lys	Gly	Asn	Pro	Ala	Leu	Glu	Ala	Ile	Lys	Gly
			20					25					30		
Leu	Pro	Ala	Glu	Ile	His	Gly	Ala	Glu	Val	Arg	Trp	Leu	Glu	Val	Pro
		35					40					45			
Thr	Val	Phe	His	Lys	Ser	Ala	Gln	Val	Leu	Glu	Glu	Glu	Met	Asn	Arg
	50					55					60				
Tyr	Gln	Pro	Asp	Phe	Val	Leu	Cys	Ile	Gly	Gln	Ala	Gly	Gly	Arg	Thr
65					70				75					80	
Ser	Leu	Thr	Pro	Glu	Arg	Val	Thr	Ile	Asn	Gln	Asp	Asp	Ala	Cys	Ile
				85					90				95		
Ser	Asp	Asn	Glu	Asp	Asn	Gln	Pro	Ile	Asp	Arg	Pro	Ile	Arg	Pro	Asp
			100					105				110			
Gly	Ala	Ser	Ala	Tyr	Phe	Ser	Ser	Leu	Pro	Ile	Lys	Ala	Met	Val	Gln
		115					120					125			
Ala	Ile	Lys	Lys	Glu	Gly	Leu	Pro	Ala	Ser	Val	Ser	Asn	Thr	Ala	Gly
	130					135					140				
Thr	Phe	Val	Cys	Ser	His	Leu	Met	Tyr	Gln	Ala	Leu	Tyr	Leu	Val	Glu
145					150					155					160

Lys	Lys	Ser	Pro	Tyr	Val	Lys	Ala	Gly	Phe	Met	His	Ile	Pro	Tyr	Met
				165					170					175	
Met	Glu	Gln	Val	Val	Asn	Arg	Pro	Thr	Pro	Ala	Met	Ser	Leu	Val	
			180					185					190		
Asp	Ile	Arg	Arg	Gly	Ile	Glu	Ala	Ala	Ile	Gly	Ala	Ile	Ile	Glu	His
		195					200					205			
Gly	Asp	Gln	Glu	Leu	Lys	Leu	Val	Gly	Gly	Glu	Thr	His			
	210					215					220				

(2) INFORMATION FOR SEQ ID NO:3786:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...136

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3786:

Asn	Ser	Phe	Glu	Lys	Tyr	Val	Gln	Glu	His	Lys	Ile	Leu	Leu	Ser	Ile
1				5					10					15	
Phe	Asp	Leu	Asp	Glu	Thr	Val	Thr	Asp	Tyr	Tyr	Gly	Lys	Leu	Glu	Ser
		20						25					30		
Phe	Leu	Glu	Glu	Asn	Ser	Ser	Ile	Asp	Gly	Ile	Phe	Thr	Ile	Asn	Asp
		35					40					45			
Phe	Thr	Ala	Leu	Asp	Val	Ile	Glu	Ile	Leu	Glu	Lys	Asn	Gly	Lys	Arg
	50					55				60					
Ile	Pro	His	Asp	Val	Gln	Ile	Ile	Gly	Tyr	Asp	Gly	Ile	Lys	Met	Ala
65				70					75					80	
Gly	Asp	Arg	Asp	Tyr	Leu	Leu	Ser	Thr	Ile	Glu	Gln	Pro	Leu	Glu	Glu
			85					90					95		
Met	Ala	Lys	Glu	Ala	Val	Arg	Ile	Leu	Phe	Asp	Ile	Ile	Asp	Gly	Lys
		100						105					110		
Thr	Val	Asn	Leu	Gln	Thr	Ile	Leu	Pro	Val	Lys	Phe	Val	Glu	Gly	Lys
		115				120						125			
Thr	Thr	Lys	Asn	Glu	Asn	Lys	Ser								
	130					135									

(2) INFORMATION FOR SEQ ID NO:3787:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...100

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3787:

```
Ile Lys Phe Asp Lys Arg Thr Leu Ser Tyr Tyr Arg Gly Glu Glu Met
1          5          10          15
Asp Pro Lys Lys Ile Ala Arg Ile Asn Glu Leu Ala Lys Lys Lys Lys
20          25          30
Thr Glu Gly Leu Thr Pro Glu Glu Lys Val Glu Gln Ala Lys Leu Arg
35          40          45
Glu Glu Tyr Ile Glu Gly Tyr Arg Arg Ala Val Arg His His Ile Glu
50          55          60
Gly Ile Lys Ile Val Asp Glu Glu Arg Asn Asp Val Thr Pro Glu Lys
65          70          75          80
Leu Arg Gln Val Gln Arg Glu Lys Gly Leu His Gly Arg Ser Leu Asp
85          90          95
Asp Pro Asn Ser
100
```

(2) INFORMATION FOR SEQ ID NO:3788:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 511 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...511

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3788:

```
Arg Lys Phe Glu Ile Glu Ser Gly Val Leu Leu Ala Ile Asn Ala Gln
1          5          10          15
Glu Ile Ser Ala Leu Ile Lys Gln Gln Ile Glu Asn Phe Lys Pro Asn
20          25          30
Phe Asp Val Thr Glu Thr Gly Val Val Thr Tyr Ile Gly Asp Gly Ile
35          40          45
Ala Arg Ala His Gly Leu Glu Asn Ala Met Ser Gly Glu Leu Leu Asn
50          55          60
Phe Glu Asn Gly Ser Tyr Gly Met Ala Gln Asn Leu Glu Ser Thr Asp
65          70          75          80
Val Gly Ile Ile Ile Leu Gly Asp Phe Thr Asp Ile Arg Glu Gly Asp
```

				85				90					95				
Thr	Ile	Arg	Arg	Thr	Gly	Lys	Ile	Met	Glu	Val	Pro	Val	Gly	Glu	Ser		
			100					105					110				
Leu	Ile	Gly	Arg	Val	Val	Asp	Pro	Leu	Gly	Arg	Pro	Val	Asp	Gly	Leu		
		115					120					125					
Gly	Glu	Ile	His	Thr	Asp	Lys	Thr	Arg	Pro	Val	Glu	Ala	Pro	Ala	Pro		
	130					135					140						
Gly	Val	Met	Gln	Arg	Lys	Ser	Val	Ser	Glu	Pro	Leu	Gln	Thr	Gly	Leu		
145					150				155						160		
Lys	Ala	Ile	Asp	Ala	Leu	Val	Pro	Ile	Gly	Arg	Gly	Gln	Arg	Glu	Leu		
			165					170						175			
Ile	Ile	Gly	Asp	Arg	Gln	Thr	Gly	Lys	Thr	Thr	Ile	Ala	Ile	Asp	Thr		
	180						185						190				
Ile	Leu	Asn	Gln	Lys	Asp	Gln	Asp	Met	Ile	Cys	Ile	Tyr	Val	Ala	Ile		
	195						200					205					
Gly	Gln	Lys	Glu	Ser	Thr	Val	Arg	Thr	Gln	Val	Glu	Thr	Leu	Arg	Gln		
	210					215					220						
Tyr	Gly	Ala	Leu	Asp	Tyr	Thr	Ile	Val	Val	Thr	Ala	Ser	Ala	Ser	Gln		
225					230					235					240		
Pro	Ser	Pro	Leu	Leu	Phe	Leu	Ala	Pro	Tyr	Ala	Gly	Val	Ala	Met	Ala		
			245					250						255			
Glu	Glu	Phe	Met	Tyr	Gln	Gly	Lys	His	Val	Leu	Ile	Val	Tyr	Asp	Asp		
	260						265						270				
Leu	Ser	Lys	Gln	Ala	Val	Ala	Tyr	Arg	Glu	Leu	Ser	Leu	Leu	Leu	Arg		
	275						280					285					
Arg	Pro	Pro	Gly	Arg	Glu	Ala	Phe	Pro	Gly	Asp	Val	Phe	Tyr	Leu	His		
	290					295					300						
Ser	Arg	Leu	Leu	Glu	Arg	Ser	Ala	Lys	Val	Ser	Asp	Glu	Leu	Gly	Gly		
305					310					315					320		
Gly	Ser	Ile	Thr	Ala	Leu	Pro	Phe	Ile	Glu	Thr	Gln	Ala	Gly	Asp	Ile		
			325						330					335			
Ser	Ala	Tyr	Ile	Ala	Thr	Asn	Val	Ile	Ser	Ile	Thr	Asp	Gly	Gln	Ile		
	340						345					350					
Phe	Leu	Gly	Asp	Gly	Leu	Phe	Asn	Ala	Gly	Ile	Arg	Pro	Ala	Ile	Asp		
	355					360					365						
Ala	Gly	Ser	Ser	Val	Ser	Arg	Val	Gly	Gly	Ser	Ala	Gln	Ile	Lys	Ala		
	370					375					380						
Met	Lys	Lys	Val	Ala	Gly	Thr	Leu	Arg	Ile	Asp	Leu	Ala	Ser	Tyr	Arg		
385					390					395					400		
Glu	Leu	Glu	Ala	Phe	Thr	Lys	Phe	Gly	Ser	Asp	Leu	Asp	Ala	Ala	Thr		
			405						410					415			
Gln	Ala	Lys	Leu	Asn	Arg	Gly	Arg	Arg	Thr	Val	Glu	Val	Leu	Lys	Gln		
		420						425					430				
Pro	Val	His	Lys	Pro	Leu	Pro	Val	Glu	Lys	Gln	Val	Thr	Ile	Leu	Tyr		
		435					440					445					
Ala	Leu	Thr	His	Gly	Phe	Leu	Asp	Thr	Val	Pro	Val	Asp	Asp	Ile	Val		
	450					455					460						
Arg	Phe	Glu	Glu	Glu	Phe	His	Ala	Phe	Phe	Asp	Ala	Gln	His	Pro	Glu		
465					470					475					480		
Ile	Leu	Glu	Thr	Ile	Arg	Asp	Thr	Lys	Asp	Leu	Pro	Glu	Glu	Ala	Val		
			485						490					495			
Leu	Asp	Ala	Ala	Ile	Thr	Glu	Phe	Leu	Asn	Gln	Ser	Ser	Phe	Gln			
		500						505					510				

(2) INFORMATION FOR SEQ ID NO:3789:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 78 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...78

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3789:

Val	Arg	Phe	Glu	Asp	Ile	Leu	Ser	Ser	Phe	Ile	Leu	Phe	Pro	Thr	Ser
1			5						10					15	
His	Thr	Phe	Ile	Thr	Tyr	Ile	Tyr	His	Ile	His	Thr	Pro	Leu	Ile	Lys
			20					25					30		
Arg	Ile	Ala	His	Ser	Cys	His	Asn	Phe	Leu	Asn	Lys	Lys	Ile	Met	Thr
		35					40					45			
Lys	Gln	Gly	Ser	Asn	Leu	Leu	Met	Leu	Leu	Lys	Asn	Leu	Lys	Leu	Met
	50					55					60				
Ser	Ser	Tyr	Gln	Lys	Ser	Tyr	Leu	Gln	Pro	Gln	Asn	Ser	Thr		
65					70					75					

(2) INFORMATION FOR SEQ ID NO:3790:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 298 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...298

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3790:

Met	Arg	Phe	Glu	Phe	Ile	Ala	Asp	Glu	His	Val	Lys	Val	Lys	Thr	Phe
1			5						10					15	
Leu	Lys	Lys	His	Glu	Val	Ser	Lys	Gly	Leu	Leu	Ala	Lys	Ile	Lys	Phe
			20					25					30		
Arg	Gly	Gly	Ala	Ile	Leu	Val	Asn	Asn	Gln	Pro	Gln	Asn	Ala	Thr	Tyr
		35					40					45			
Leu	Leu	Asp	Val	Gly	Asp	Tyr	Val	Thr	Ile	Asp	Ile	Pro	Ala	Glu	Lys

50		55		60
Gly Phe Glu Thr Leu Glu Ala Ile Glu Leu Pro Leu Asp Ile Leu Tyr				
65	70	75	80	
Glu Asp Asp His Phe Leu Val Leu Asn Lys Pro Tyr Gly Val Ala Ser				
	85	90	95	
Ile Pro Ser Val Asn His Ser Asn Thr Ile Ala Asn Phe Ile Lys Gly				
	100	105	110	
Tyr Tyr Val Lys Gln Asn Tyr Glu Asn Gln Gln Val His Ile Val Thr				
	115	120	125	
Arg Leu Asp Arg Asp Thr Ser Gly Leu Met Leu Phe Ala Lys His Gly				
	130	135	140	
Tyr Ala His Ala Arg Leu Asp Lys Gln Leu Gln Lys Lys Ser Ile Glu				
145	150	155	160	
Lys Arg Tyr Phe Ala Leu Val Lys Gly Asp Gly His Leu Glu Pro Glu				
	165	170	175	
Gly Glu Ile Ile Ala Pro Ile Ala Arg Asp Glu Asp Ser Ile Ile Thr				
	180	185	190	
Arg Arg Val Ala Lys Gly Gly Lys Tyr Ala His Thr Ser Tyr Lys Ile				
	195	200	205	
Val Ala Ser Tyr Gly Asn Ile His Leu Val Tyr Ile His Leu His Thr				
	210	215	220	
Gly Arg Thr His Gln Ile Arg Val His Phe Ser His Ile Gly Phe Pro				
225	230	235	240	
Leu Leu Gly Asp Asp Leu Tyr Gly Gly Ser Leu Glu Asp Gly Ile Gln				
	245	250	255	
Arg Gln Ala Leu His Cys His Tyr Leu Ser Phe Tyr His Pro Phe Leu				
	260	265	270	
Glu Gln Asp Leu Gln Leu Glu Ser Pro Leu Pro Asp Asp Phe Ser Asn				
	275	280	285	
Leu Ile Thr Gln Leu Ser Thr Asn Thr Leu				
290	295			

(2) INFORMATION FOR SEQ ID NO:3791:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...106

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3791:

Leu Phe Leu Asp Lys Gly Arg Asn Ser Gly Glu Glu Val Arg Met Lys
1 5 10 15
Lys Phe Asp Asn Tyr Ile Ile Glu Lys Pro Cys Asp Ser Asn Ser Asp
20 25 30
Lys Leu Gln Lys Ile Leu Ile Ile Glu Asn Leu Val Asp Asp Ile Leu

		35					40				45				
Gln	Phe	Ser	Leu	Arg	Ile	Asn	Asn	Ser	Val	Gly	Glu	Ile	Phe	Leu	Leu
	50					55					60				
Gln	Pro	Phe	Gln	Lys	Lys	Thr	Ile	Phe	Ile	Pro	Cys	Tyr	Phe	Glu	Glu
65					70					75					80
Asp	Ile	Val	Lys	Val	Lys	Asp	Asp	Asp	Lys	Val	Glu	Trp	Asn	Leu	Leu
			85						90					95	
Glu	Phe	Gln	Lys	Phe	Arg	Ala	Phe	Leu	Ala						
			100					105							

(2) INFORMATION FOR SEQ ID NO:3792:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...257

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3792:

Arg	Arg	Leu	Asp	Arg	Gln	Arg	Leu	His	Gln	Arg	Ile	Cys	Glu	Ile	Met
1				5					10					15	
Thr	Glu	Ile	Arg	Leu	Glu	His	Val	Ser	Tyr	Ala	Tyr	Gly	Gln	Glu	Arg
			20					25					30		
Ile	Leu	Glu	Asp	Ile	Asn	Leu	Gln	Val	Thr	Ser	Gly	Glu	Val	Val	Ser
		35				40					45				
Ile	Leu	Gly	Pro	Ser	Gly	Val	Gly	Lys	Thr	Thr	Leu	Phe	Asn	Leu	Ile
	50				55						60				
Ala	Gly	Ile	Leu	Glu	Val	Gln	Ser	Gly	Arg	Ile	Val	Leu	Asp	Gly	Glu
65				70					75						80
Glu	Asn	Pro	Lys	Gly	Arg	Val	Ser	Tyr	Met	Leu	Gln	Lys	Asp	Leu	Leu
			85						90					95	
Leu	Glu	His	Lys	Thr	Val	Leu	Gly	Asn	Ile	Ile	Leu	Pro	Leu	Leu	Ile
		100					105						110		
Gln	Lys	Val	Asp	Lys	Ala	Glu	Ala	Ile	Ser	Arg	Ala	Asp	Lys	Ile	Leu
	115					120						125			
Ala	Thr	Phe	Gln	Leu	Thr	Ala	Val	Arg	Asp	Lys	Tyr	Pro	His	Glu	Leu
	130				135						140				
Ser	Gly	Gly	Met	Arg	Gln	Arg	Val	Ala	Leu	Leu	Arg	Thr	Tyr	Leu	Phe
145				150					155						160
Gly	His	Lys	Leu	Phe	Leu	Leu	Asp	Glu	Ala	Phe	Ser	Ala	Leu	Asp	Glu
			165					170						175	
Met	Thr	Lys	Met	Glu	Leu	His	Ala	Trp	Tyr	Leu	Glu	Ile	His	Lys	Gln
		180					185						190		
Leu	Gln	Leu	Thr	Thr	Leu	Ile	Ile	Thr	His	Ser	Ile	Glu	Glu	Ala	Leu
	195					200						205			
Asn	Leu	Ser	Asp	Arg	Ile	Tyr	Ile	Leu	Lys	Asn	Arg	Pro	Gly	Gln	Ile

210	215	220
Val Ser Glu Ile Lys Leu Asp Trp Ser Glu Asp Glu Asp Lys Glu Val		
225	230	235
Gln Lys Ile Ala Tyr Lys Arg Gln Ile Leu Ala Glu Leu Gly Leu Asp		240
	245	250
Lys		255

(2) INFORMATION FOR SEQ ID NO:3793:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...325

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3793:

Ser Met Leu Asp Trp Lys Gln Phe Phe Leu Ala Tyr Leu Arg Ser Arg		
1	5	10
Ser Arg Leu Phe Ile Tyr Leu Leu Ser Leu Ala Phe Leu Val Leu Leu		
	20	25
Phe Gln Phe Leu Phe Ala Ser Leu Gly Ile Tyr Phe Leu Tyr Phe Phe		
	35	40
Phe Leu Cys Cys Phe Val Thr Ile Leu Phe Phe Thr Trp Asp Ile Leu		
	50	55
Val Glu Thr Gln Val Tyr Arg Gln Glu Leu Leu Tyr Gly Glu Arg Glu		
65	70	75
Ala Lys Ser Pro Leu Glu Ile Ala Leu Ala Glu Lys Leu Glu Ala Arg		
	85	90
Glu Met Glu Leu Tyr Gln Gln Arg Ser Lys Ala Glu Arg Lys Leu Thr		
	100	105
Asp Leu Leu Asp Tyr Tyr Thr Leu Trp Val His Gln Ile Lys Thr Pro		
	115	120
Ile Ala Ala Ser Gln Leu Leu Val Ala Glu Val Val Asp Arg Gln Leu		
	130	135
Lys Gln Gln Leu Glu Gln Glu Ile Phe Lys Ile Asp Ser Tyr Thr Asn		
145	150	155
Leu Val Leu Gln Tyr Leu Arg Leu Glu Ser Phe His Asp Asp Leu Leu		
	165	170
Leu Lys Gln Val Gln Ile Glu Asp Leu Val Lys Glu Ile Ile Arg Lys		
	180	185
Tyr Ala Leu Phe Phe Ile Gln Lys Gly Leu Asn Val Asn Leu His Asp		
	195	200
Leu Asp Lys Glu Ile Val Thr Asp Lys Lys Trp Leu Leu Val Val Ile		
210	215	220

Glu	Gln	Ile	Ile	Ser	Asn	Ser	Leu	Lys	Tyr	Thr	Lys	Glu	Gly	Gly	Leu
225					230					235					240
Glu	Ile	Tyr	Met	Asp	Asp	Gln	Glu	Leu	Cys	Ile	Lys	Asp	Thr	Gly	Ile
				245					250					255	
Gly	Ile	Lys	Asn	Ser	Asp	Val	Leu	Arg	Val	Phe	Glu	Arg	Gly	Phe	Ser
			260					265					270		
Gly	Tyr	Asn	Gly	Arg	Leu	Thr	Gln	Gln	Ser	Ser	Gly	Leu	Gly	Leu	Tyr
		275					280					285			
Leu	Ser	Lys	Lys	Ile	Ser	Glu	Glu	Leu	Gly	His	Gln	Ile	Arg	Ile	Glu
	290					295					300				
Ser	Glu	Val	Gly	Lys	Gly	Thr	Thr	Val	Arg	Ile	Gln	Phe	Ala	Gln	Val
305					310					315					320
Asn	Leu	Val	Leu	Glu											
				325											

(2) INFORMATION FOR SEQ ID NO:3794:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...355

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3794:

Val	Leu	Ile	Asp	Gln	Thr	Glu	Arg	Ser	Asp	Glu	Met	Val	Thr	Glu	Arg
1				5					10					15	
Gln	Gln	Asp	Ile	Leu	Asn	Leu	Ile	Ile	Asp	Ile	Phe	Thr	Lys	Thr	His
			20					25					30		
Glu	Pro	Val	Gly	Ser	Lys	Ala	Leu	Gln	Glu	Ser	Ile	Asn	Ser	Ser	Ser
		35				40						45			
Ala	Thr	Ile	Arg	Asn	Asp	Met	Ala	Glu	Leu	Glu	Lys	Gln	Gly	Leu	Leu
	50				55						60				
Glu	Lys	Ala	His	Thr	Ser	Ser	Gly	Arg	Met	Pro	Ser	Val	Ala	Gly	Phe
65					70				75						80
Gln	Tyr	Tyr	Val	Lys	His	Ser	Leu	Asp	Phe	Asp	Arg	Leu	Ala	Glu	Asn
			85					90						95	
Glu	Val	Tyr	Glu	Ile	Val	Lys	Ala	Phe	Asp	Gln	Glu	Phe	Phe	Lys	Leu
		100					105						110		
Glu	Asp	Ile	Leu	Gln	Glu	Ala	Ala	Asn	Leu	Leu	Thr	Asp	Leu	Ser	Gly
		115				120						125			
Cys	Thr	Val	Val	Ala	Leu	Asp	Val	Glu	Pro	Ser	Arg	Gln	Arg	Leu	Thr
	130					135					140				
Ala	Phe	Asp	Ile	Val	Val	Leu	Gly	Gln	His	Thr	Ala	Leu	Ala	Val	Phe
145					150				155						160
Thr	Leu	Asp	Glu	Ser	Arg	Thr	Val	Thr	Ser	Gln	Phe	Leu	Ile	Pro	Arg
				165					170					175	

Asn	Phe	Leu	Gln	Glu	Asp	Leu	Leu	Lys	Leu	Lys	Ser	Ile	Ile	Gln	Glu
			180					185					190		
Arg	Phe	Leu	Gly	His	Thr	Val	Leu	Asp	Ile	His	Tyr	Lys	Ile	Arg	Thr
		195					200					205			
Glu	Ile	Pro	Gln	Ile	Ile	Gln	Arg	Tyr	Phe	Thr	Thr	Thr	Asp	Asn	Val
	210					215					220				
Ile	Asp	Leu	Phe	Glu	His	Ile	Phe	Lys	Glu	Met	Phe	Asn	Glu	Asn	Ile
225					230					235					240
Val	Met	Ala	Gly	Lys	Val	Asn	Leu	Leu	Asn	Phe	Ala	Asn	Leu	Ala	Ala
			245						250					255	
Tyr	Gln	Phe	Phe	Asp	Gln	Pro	Gln	Lys	Val	Ala	Leu	Glu	Ile	Arg	Glu
			260					265					270		
Gly	Leu	Arg	Glu	Asp	Gln	Met	Gln	Asn	Val	Arg	Val	Ala	Asp	Gly	Gln
	275						280					285			
Glu	Ser	Cys	Leu	Ala	Asp	Leu	Ala	Val	Ile	Ser	Ser	Lys	Phe	Leu	Ile
	290					295				300					
Pro	Tyr	Arg	Gly	Val	Gly	Ile	Leu	Ala	Ile	Thr	Gly	Pro	Val	Asn	Leu
305					310					315					320
Asp	Tyr	Gln	Gln	Leu	Ile	Asn	Gln	Val	Asn	Val	Val	Asn	Arg	Val	Leu
			325					330					335		
Thr	Met	Lys	Leu	Thr	Asp	Phe	Tyr	Arg	Tyr	Leu	Ser	Ser	Asn	His	Tyr
			340					345					350		
Glu	Val	His													
		355													

(2) INFORMATION FOR SEQ ID NO:3795:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 266 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...266
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3795:

Phe	Ser	Ile	Glu	Gln	Phe	Ser	Leu	Lys	Gly	Lys	Ile	Ala	Leu	Ile	Thr
1				5					10					15	
Gly	Ala	Ser	Tyr	Gly	Ile	Gly	Phe	Ala	Ile	Ala	Lys	Ser	Tyr	Ala	Glu
			20					25					30		
Ala	Gly	Ala	Thr	Ile	Val	Phe	Asn	Asp	Ile	Asn	Gln	Asp	Leu	Val	Asn
		35				40					45				
Lys	Gly	Ile	Glu	Ala	Tyr	Arg	Glu	Val	Gly	Ile	Glu	Ala	His	Gly	Tyr
	50					55				60					
Val	Cys	Asp	Val	Thr	Asp	Glu	Asp	Gly	Ile	Gln	Ala	Met	Val	Lys	Gln
65				70					75					80	
Ile	Glu	Gln	Glu	Val	Gly	Val	Ile	Asp	Ile	Leu	Val	Asn	Asn	Ala	Gly
			85					90						95	

Ile	Ile	Arg	Arg	Val	Pro	Met	Cys	Glu	Met	Ser	Ala	Ala	Asp	Phe	Arg
		100						105					110		
Lys	Val	Ile	Asp	Ile	Asp	Leu	Asn	Ala	Pro	Phe	Ile	Val	Ser	Lys	Ala
	115						120					125			
Val	Ile	Pro	Ser	Met	Ile	Lys	Lys	Gly	His	Gly	Lys	Ile	Ile	Asn	Ile
	130					135					140				
Cys	Ser	Met	Met	Ser	Glu	Leu	Gly	Arg	Glu	Thr	Val	Ser	Ala	Tyr	Ala
145					150					155					160
Ala	Ala	Lys	Gly	Gly	Leu	Lys	Met	Leu	Thr	Arg	Asn	Ile	Ala	Ser	Glu
			165						170						175
Tyr	Gly	Gly	Ala	Asn	Ile	Gln	Cys	Asn	Gly	Ile	Gly	Pro	Gly	Tyr	Ile
			180					185					190		
Ala	Thr	Pro	Gln	Thr	Ala	Pro	Leu	Arg	Glu	Leu	Gln	Glu	Asp	Gly	Ser
	195						200					205			
Arg	His	Pro	Phe	Asp	Gln	Phe	Ile	Ile	Ala	Lys	Thr	Pro	Ala	Ala	Arg
	210					215					220				
Trp	Gly	Asn	Pro	Glu	Asp	Leu	Met	Gly	Pro	Ala	Val	Phe	Leu	Ala	Ser
225					230					235					240
Asp	Ala	Ser	Asn	Phe	Val	Asn	Gly	His	Ile	Leu	Tyr	Val	Asp	Gly	Gly
			245					250						255	
Ile	Leu	Ala	Tyr	Ile	Gly	Lys	Gln	Pro	Glu						
		260						265							

(2) INFORMATION FOR SEQ ID NO:3796:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 202 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...202

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3796:

Lys	Glu	Ile	Glu	Lys	Asn	Val	Leu	Pro	Gly	Glu	Lys	Leu	Tyr	Glu	Ile
1				5					10					15	
Gly	Ser	Lys	Tyr	Asn	Gln	Ile	Phe	Pro	Arg	Pro	Val	Phe	Phe	Phe	Val
			20					25					30		
Phe	Lys	Lys	Glu	Phe	Gly	Gly	Asn	Glu	Asn	Phe	Arg	Lys	Thr	Gly	Leu
		35				40					45				
Ser	Lys	Val	Lys	Gly	Lys	Leu	Phe	Gln	Gln	Asp	Val	Val	Lys	Gly	Gly
	50					55				60					
Asn	Lys	Arg	Phe	Tyr	Arg	Pro	Thr	Phe	Arg	Met	His	Leu	Thr	Asn	Lys
65					70				75					80	
Glu	Ile	Leu	Asp	Lys	Ile	Leu	Ser	Tyr	Ser	Glu	Asp	Leu	Lys	His	His
			85					90					95		
Tyr	Gln	Ile	Tyr	Gln	Leu	Leu	Leu	Phe	His	Phe	Gln	Asn	Lys	Asp	Pro
		100						105					110		

Glu	Lys	Phe	Phe	Gly	Leu	Ile	Glu	Asp	Thr	Leu	Lys	Gln	Val	His	Pro
	115						120					125			
Ile	Phe	Gln	Thr	Val	Phe	Lys	Thr	Phe	Leu	Lys	Asn	Lys	Glu	Lys	Ile
	130					135					140				
Val	Asn	Ala	Leu	Gln	Leu	Pro	Tyr	Ser	Asn	Ala	Lys	Leu	Glu	Ala	Thr
145					150					155					160
Asn	Asn	Leu	Ile	Lys	Leu	Ile	Lys	Arg	Asn	Ala	Phe	Gly	Phe	Arg	Asn
				165					170					175	
Phe	Glu	Asn	Phe	Lys	Lys	Arg	Ile	Phe	Ile	Ala	Leu	Asn	Ile	Lys	Lys
		180						185					190		
Glu	Arg	Thr	Asn	Phe	Val	Leu	Ser	Arg	Ala						
	195						200								

(2) INFORMATION FOR SEQ ID NO:3797:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 107 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...107

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3797:

Lys	Arg	Ile	Asp	Met	Ser	Ile	Glu	Leu	Leu	Lys	Lys	Leu	Thr	Gly	Glu
1				5					10					15	
Glu	Asp	Thr	Gln	Leu	Leu	Met	Leu	Leu	Gln	Thr	Arg	Ala	Thr	Asn	Leu
		20						25					30		
Ile	Leu	Ser	Glu	Thr	Asn	Arg	Thr	Ser	Leu	Thr	Pro	Ala	Leu	Ser	Leu
	35					40					45				
Leu	Ile	Pro	Glu	Val	Ala	Ile	Glu	Leu	His	Asn	Arg	Ser	Gly	Ala	Glu
	50					55				60					
Gly	Glu	His	Ser	Arg	Thr	Glu	Gly	Gly	Ile	Ala	Val	Val	Tyr	Gly	Glu
65				70					75					80	
Asn	Gly	Leu	Ser	Thr	Asp	Leu	Leu	Gln	Arg	Ile	Arg	Met	His	Arg	Leu
				85				90						95	
Ala	Arg	Val	Ala	Gly	His	Val	Phe	Glu	Ala	Glu					
		100						105							

(2) INFORMATION FOR SEQ ID NO:3798:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 108 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...108

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3798:

Thr	Thr	Asp	Leu	Leu	Ile	Asn	Glu	Ser	Ile	Val	Thr	Thr	Glu	Ala	Arg
1				5					10					15	
Ala	Lys	Glu	Ile	Arg	Lys	Thr	Val	Glu	Lys	Met	Ile	Thr	Leu	Gly	Lys
			20					25					30		
Arg	Gly	Asp	Leu	His	Ala	Arg	Arg	Gln	Ala	Ala	Ala	Phe	Val	Arg	Asn
		35					40					45			
Glu	Ile	Ala	Ser	Glu	Asn	Tyr	Asp	Glu	Ala	Thr	Asp	Lys	Tyr	Thr	Ser
50						55					60				
Thr	Thr	Ala	Leu	Gln	Lys	Leu	Phe	Ser	Glu	Ile	Ala	Pro	Arg	Tyr	Ala
65					70					75					80
Glu	Arg	Asn	Gly	Gly	Tyr	Thr	Arg	Ile	Leu	Lys	Thr	Glu	Pro	Arg	Arg
			85						90					95	
Gly	Asp	Ala	Ala	Pro	Met	Ala	Ile	Ile	Glu	Leu	Val				
			100					105							

(2) INFORMATION FOR SEQ ID NO:3799:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...75

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3799:

Val	Val	Ser	Asp	Tyr	Leu	Cys	Cys	Leu	Tyr	Gly	Ser	Arg	Ile	Tyr	Phe
1				5					10					15	
Leu	Leu	Tyr	Gln	Ala	Asn	Gln	Glu	Lys	Val	Ile	Leu	Ile	Leu	Phe	Glu
			20					25					30		
Asn	Leu	Phe	Lys	Pro	Arg	Gln	Phe	Pro	Ser	Ala	Thr	Ser	Lys	His	Cys
		35					40					45			
Phe	Glu	Gln	Pro	Ala	Ala	Ser	Phe	Leu	Val	Cys	Ser	Leu	Ile	Phe	Ile
50						55					60				
Glu	Tyr	Lys	Ile	Gln	Gly	Ile	His	Phe	Arg	Ile					
65				70						75					

(2) INFORMATION FOR SEQ ID NO:3800:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 300 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3800:

Leu	Phe	Pro	Asp	Leu	Val	Phe	Gln	Tyr	Asp	Pro	Cys	Lys	Gly	Ala	Phe
1				5				10						15	
Pro	Met	Asp	Lys	Pro	Asp	Ile	Ala	Thr	Ile	Ile	Asp	Ser	His	Phe	Glu
			20					25					30		
Glu	Met	Thr	Asp	Leu	Glu	Gln	Glu	Ile	Ala	Arg	Tyr	Phe	Leu	Gln	Ala
			35				40					45			
Glu	Thr	Ile	Thr	Asp	Asp	Leu	Ser	Ser	Gln	Gln	Val	Thr	Gln	Lys	Leu
	50					55					60				
His	Ile	Ser	Gln	Ala	Ala	Leu	Thr	Arg	Phe	Ala	Lys	Lys	Cys	Gly	Phe
65					70				75						80
Thr	Gly	Tyr	Arg	Glu	Phe	Ile	Phe	Gln	Tyr	Gln	His	Gln	Ala	Glu	Asn
				85				90						95	
Gln	Ala	Asn	Gln	Val	Ser	Lys	His	Ser	Pro	Leu	Thr	Lys	Arg	Val	Leu
			100					105					110		
Arg	Ser	Tyr	Ser	Asn	Met	Arg	Glu	Gln	Thr	Gln	Asp	Leu	Ile	Asp	Glu
			115				120					125			
Ile	Gln	Leu	Glu	Arg	Ile	Ala	Gln	Leu	Ile	Glu	Asp	Ala	Glu	Arg	Ile
	130					135					140				
Tyr	Phe	Phe	Gly	Thr	Gly	Ser	Ser	Gly	Leu	Val	Ala	Arg	Glu	Met	Lys
145					150				155					160	
Leu	Arg	Phe	Met	Arg	Leu	Gly	Val	Val	Cys	Glu	Ala	Leu	Thr	Asp	Gln
			165					170						175	
Asp	Gly	Phe	Ala	Trp	Thr	Thr	Ser	Ile	Met	Asp	Glu	Asn	Cys	Leu	Val
			180					185					190		
Leu	Gly	Phe	Ser	Leu	Ser	Gly	Ser	Thr	Pro	Ser	Ile	Leu	Asp	Ser	Leu
	195					200						205			
Leu	Asp	Ala	Lys	Glu	Met	Gly	Ala	Lys	Thr	Val	Leu	Phe	Thr	Ser	Val
	210					215					220				
Pro	Asn	Lys	Asp	Ser	Gln	Thr	Tyr	Thr	Glu	Thr	Val	Leu	Val	Ala	Thr
225					230					235				240	
His	Ser	Gln	Pro	Ser	Tyr	Ile	Gln	Arg	Ile	Ser	Ala	Gln	Leu	Pro	Met
			245					250						255	
Leu	Phe	Phe	Ile	Asp	Leu	Ile	Tyr	Ala	Tyr	Phe	Leu	Glu	Ile	Asn	Arg
			260				265						270		
Glu	Ser	Lys	Glu	Lys	Ile	Phe	Asn	Ser	Tyr	Trp	Glu	Asn	Lys	Lys	Leu
		275					280					285			

Asn Gly Tyr Arg Arg Gln Lys Arg Val Arg Lys Ser
 290 295 300

(2) INFORMATION FOR SEQ ID NO:3801:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...113

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3801:

Arg	Leu	Thr	Glu	Ser	Ala	Ser	Cys	Cys	Ser	Leu	Val	Leu	Met	Ser	Thr
1				5					10					15	
Thr	Phe	Thr	Leu	Ile	Ser	Thr	Ile	Ser	Lys	Ser	Val	Ile	Leu	Ala	Thr
			20					25					30		
Ser	Glu	Asp	Thr	Ile	Ser	Leu	Ile	Ser	Glu	Tyr	Lys	Ala	Gly	Thr	Phe
		35					40					45			
Phe	Trp	Tyr	Ser	Thr	Ile	Thr	Phe	Lys	Ser	Thr	Ala	Thr	Cys	Val	Leu
	50					55				60					
Pro	Thr	Ser	Thr	Leu	Thr	Pro	Leu	Val	Thr	Ser	Ser	Leu	Leu	Thr	Ile
65					70					75				80	
Phe	Ser	Leu	Arg	Phe	Glu	Lys	Lys	Pro	Pro	Ser	Ile	Pro	Lys	Arg	Pro
			85					90					95		
Glu	Thr	Phe	Ser	Ser	Glu	Arg	Pro	Met	Ile	Phe	Trp	Ile	Thr	Leu	Ser
			100					105					110		
Ser															

(2) INFORMATION FOR SEQ ID NO:3802:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...309

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3802:

Glu	Arg	Thr	Glu	Asn	Ile	Met	Thr	Glu	Lys	Leu	Gln	Leu	Thr	Lys	Ser
1				5					10					15	
Asp	Arg	Lys	Lys	Val	Trp	Trp	Arg	Ser	Thr	Phe	Leu	Gln	Gly	Ser	Trp
			20					25					30		
Asn	Phe	Glu	Arg	Met	Gln	Asn	Leu	Gly	Trp	Ala	Tyr	Thr	Leu	Ile	Pro
		35					40					45			
Ala	Ile	Lys	Lys	Leu	Tyr	Thr	Lys	Lys	Glu	Asp	Gln	Ile	Ala	Ala	Leu
	50					55					60				
Glu	Arg	His	Leu	Glu	Phe	Phe	Asn	Thr	His	Pro	Tyr	Val	Ala	Ala	Pro
65					70					75					80
Val	Met	Gly	Val	Thr	Leu	Ala	Leu	Glu	Glu	Glu	Arg	Ala	Asn	Gly	Val
				85					90					95	
Glu	Ile	Asp	Asp	Ala	Ala	Ile	Gln	Gly	Val	Lys	Ile	Gly	Met	Met	Gly
			100					105					110		
Pro	Leu	Ala	Gly	Ile	Gly	Asp	Pro	Val	Phe	Trp	Phe	Thr	Val	Arg	Pro
		115					120						125		
Ile	Leu	Gly	Ser	Leu	Gly	Ala	Ser	Leu	Ala	Leu	Thr	Gly	Asn	Ile	Leu
	130					135						140			
Gly	Pro	Leu	Leu	Phe	Phe	Val	Ala	Trp	Asn	Leu	Ile	Arg	Met	Ser	Phe
145					150					155					160
Leu	Trp	Tyr	Val	Gln	Glu	Ile	Gly	Tyr	Lys	Ala	Gly	Ser	Glu	Ile	Thr
				165					170					175	
Lys	Asp	Met	Ser	Gly	Gly	Ile	Leu	Gln	Asp	Ile	Thr	Lys	Gly	Ala	Ser
			180					185					190		
Ile	Leu	Gly	Met	Phe	Ile	Leu	Ala	Val	Leu	Val	Gln	Arg	Trp	Val	Asn
	195						200					205			
Ile	Lys	Phe	Ala	Phe	Asp	Val	Ser	Lys	Val	Gln	Leu	Asp	Glu	Lys	Ala
	210					215					220				
Tyr	Ile	His	Trp	Asp	Lys	Leu	Pro	Glu	Gly	Ser	Lys	Gly	Ile	Gln	Glu
225					230					235					240
Ala	Phe	Ala	Gln	Val	Gly	Gln	Gly	Leu	Ser	Gln	Thr	Pro	Glu	Lys	Val
				245					250					255	
Thr	Thr	Phe	Gln	Gln	Asn	Leu	Asp	Met	Leu	Ile	Pro	Gly	Leu	Ser	Gly
			260					265					270		
Leu	Leu	Leu	Thr	Leu	Leu	Cys	Met	Tyr	Leu	Leu	Lys	Lys	Lys	Val	Ser
		275					280					285			
Pro	Ile	Thr	Ile	Ile	Leu	Ala	Leu	Phe	Ala	Val	Gly	Ile	Val	Ala	His
	290					295					300				
Val	Leu	His	Ile	Met											
305															

(2) INFORMATION FOR SEQ ID NO:3803:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3803:

```
Trp Arg Thr Glu Met Lys Asn Ile Asn Gly Lys Lys Val Thr Ile Tyr
1          5          10          15
Asp Ile Ala Arg Leu Ser Gly Phe Ser Pro Lys Thr Val Ser Arg Val
          20          25          30
Ile Asn Gly Gly Val Asn Val Lys Glu Glu Thr Tyr Gln Ala Ile Gln
          35          40          45
Lys Val Ile Glu Glu Leu Ser Tyr Ile Pro Asn Ala Tyr Ala Lys Asn
          50          55          60
Leu Thr Lys Lys Glu Ala Ile Asn Ile Leu Ile Ser Val Lys Lys Ile
65          70          75          80
Asp Ser Phe Pro Leu Ile Trp Phe His Thr Leu Leu Asp Lys Val Leu
          85          90          95
Arg Thr Cys Lys Glu Phe Gly Val Asn Ala Ile Val Glu Tyr Phe Gly
          100         105         110
Glu Glu Asp Thr Ile Ser Asn Ser Ile Ile Ser Ser Thr Gly Ser Leu
          115         120         125
Val Asp Gly Val Ile Val Phe Tyr Glu Ser Val Asp Asp Ile Arg Ile
          130         135         140
Gln Tyr Leu Lys Lys Asn His Met Pro Phe Leu Val Phe Gly Glu Ser
145         150         155         160
Gln Thr Ser Gly Val Val Tyr Val Ser Asn Asn Asn Phe Gln Ala Thr
          165         170         175
Tyr Asp Met Met Lys Ala Val Thr Glu Glu Lys Phe Lys Asn Met Trp
          180         185         190
Leu Leu Met Gly Gly Glu Ser His Val Asn Lys Asp Arg Glu Arg Gly
          195         200         205
Val Arg Ser Phe Leu Asn Asp Lys Asn Tyr Phe Met Asp Leu Lys Val
          210         215         220
Ile Leu Trp Leu Ile Tyr Asn
225         230
```

(2) INFORMATION FOR SEQ ID NO:3804:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 436 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...436

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3804:

Thr	Glu	Ala	Asp	Glu	Gly	Met	Gln	Ala	Ala	Arg	Ala	Ala	Leu	Pro	Ala	1	5	10	15
Trp	Arg	Ala	Leu	Ser	Ala	Ile	Glu	Arg	Ala	Ala	Tyr	Leu	His	Lys	Thr	20	25	30	
Ala	Ala	Ile	Leu	Glu	Arg	Asp	Lys	Glu	Lys	Ile	Gly	Thr	Ile	Leu	Ala	35	40	45	
Lys	Glu	Ile	Ala	Lys	Gly	Ile	Lys	Ala	Ala	Ile	Gly	Glu	Val	Val	Arg	50	55	60	
Thr	Ala	Asp	Leu	Ile	Arg	Tyr	Ala	Ala	Glu	Glu	Gly	Leu	Arg	Ile	Thr	65	70	75	80
Gly	Gln	Ala	Met	Glu	Gly	Gly	Gly	Phe	Glu	Ala	Ala	Ser	Lys	Asn	Lys	85	90	95	
Leu	Ala	Val	Val	Arg	Arg	Glu	Pro	Val	Gly	Ile	Val	Leu	Ala	Ile	Ala	100	105	110	
Pro	Phe	Asn	Tyr	Pro	Val	Asn	Leu	Ser	Ala	Ser	Lys	Ile	Ala	Pro	Ala	115	120	125	
Leu	Ile	Ala	Gly	Asn	Val	Val	Met	Phe	Lys	Pro	Pro	Thr	Gln	Gly	Ser	130	135	140	
Ile	Ser	Gly	Leu	Leu	Leu	Ala	Lys	Ala	Phe	Glu	Glu	Ala	Gly	Ile	Pro	145	150	155	160
Ala	Gly	Val	Phe	Asn	Thr	Ile	Thr	Gly	Arg	Gly	Ser	Glu	Ile	Gly	Asp	165	170	175	
Tyr	Ile	Ile	Glu	His	Lys	Glu	Val	Asn	Phe	Ile	Asn	Phe	Thr	Gly	Ser	180	185	190	
Thr	Pro	Ile	Gly	Glu	Arg	Ile	Gly	Arg	Leu	Ala	Gly	Met	Arg	Pro	Ile	195	200	205	
Met	Leu	Glu	Leu	Gly	Gly	Lys	Asp	Ala	Ala	Leu	Val	Leu	Glu	Asp	Ala	210	215	220	
Asp	Leu	Glu	His	Ala	Ala	Lys	Gln	Ile	Val	Ala	Gly	Ala	Phe	Ser	Tyr	225	230	235	240
Ser	Gly	Gln	Arg	Cys	Thr	Ala	Ile	Lys	Arg	Val	Ile	Val	Leu	Glu	Ser	245	250	255	
Val	Ala	Asp	Lys	Leu	Ala	Thr	Leu	Leu	Gln	Glu	Glu	Val	Ser	Lys	Leu	260	265	270	
Thr	Val	Gly	Asp	Pro	Phe	Asp	Asn	Ala	Asp	Ile	Thr	Pro	Val	Ile	Asp	275	280	285	
Asn	Ala	Ser	Ala	Asp	Phe	Ile	Trp	Gly	Leu	Ile	Glu	Asp	Ala	Gln	Glu	290	295	300	
Lys	Glu	Ala	Gln	Ala	Leu	Thr	Pro	Ile	Lys	Arg	Glu	Gly	Asn	Leu	Leu	305	310	315	320
Trp	Pro	Val	Leu	Phe	Asp	Gln	Val	Thr	Lys	Asp	Met	Lys	Val	Ala	Trp	325	330	335	
Glu	Glu	Pro	Phe	Gly	Pro	Val	Leu	Pro	Ile	Ile	Arg	Val	Ala	Ser	Val	340	345	350	
Glu	Glu	Ala	Ile	Ala	Phe	Ala	Asn	Glu	Ser	Glu	Phe	Gly	Leu	Gln	Ser	355	360	365	
Ser	Val	Phe	Thr	Asn	Asp	Phe	Lys	Lys	Ala	Phe	Glu	Ile	Ala	Glu	Lys	370	375	380	
Leu	Glu	Val	Gly	Thr	Val	His	Ile	Asn	Asn	Lys	Thr	Gln	Arg	Gly	Pro	385	390	395	400
Asp	Asn	Phe	Pro	Phe	Leu	Gly	Val	Lys	Gly	Ser	Gly	Ala	Gly	Val	Gln	405	410	415	
Gly	Ile	Lys	Tyr	Ser	Ile	Glu	Ala	Met	Thr	Asn	Val	Lys	Ser	Ile	Val	420	425	430	
Phe	Asp	Val	Lys													435			

(2) INFORMATION FOR SEQ ID NO:3805:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...206

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3805:

Ala	Gln	Ala	Glu	Thr	Val	Ser	Gln	Thr	Val	Ser	Leu	Pro	Asn	Ala	Lys
1			5					10						15	
Ile	Val	Leu	Asp	Arg	Phe	His	Ile	Val	Gln	His	Leu	Ser	Arg	Ala	Met
		20						25					30		
Ser	Arg	Val	Arg	Val	Gln	Ile	Met	Asn	Gln	Phe	His	Arg	Lys	Ser	His
		35					40					45			
Glu	Tyr	Lys	Ala	Ile	Lys	Arg	Tyr	Trp	Lys	Leu	Ile	Gln	Gln	Asp	Ser
	50					55					60				
Arg	Lys	Leu	Ser	Asp	Lys	Arg	Phe	Tyr	Arg	Pro	Thr	Phe	Arg	Met	His
65					70					75					80
Leu	Thr	Asn	Lys	Glu	Ile	Leu	Asp	Lys	Leu	Leu	Ser	Tyr	Ser	Gln	Asp
			85						90					95	
Leu	Lys	His	His	Tyr	Gln	Leu	Tyr	Gln	Leu	Leu	Leu	Phe	His	Phe	Gln
			100					105					110		
Asn	Lys	Glu	Pro	Glu	Lys	Phe	Phe	Gly	Leu	Ile	Glu	Asp	Asn	Leu	Lys
		115					120					125			
Gln	Val	His	Pro	Leu	Phe	Gln	Thr	Val	Phe	Lys	Thr	Phe	Leu	Lys	Asp
	130					135					140				
Lys	Glu	Lys	Ile	Val	Asn	Ala	Leu	Gln	Leu	His	Tyr	Ser	Asn	Ala	Lys
145					150					155					160
Leu	Glu	Ala	Thr	Asn	Asn	Leu	Ile	Lys	Leu	Ile	Lys	Arg	Asn	Ala	Phe
				165					170					175	
Gly	Phe	Arg	Asn	Phe	Glu	Asn	Phe	Lys	Lys	Arg	Ile	Phe	Ile	Ala	Leu
			180					185					190		
Asn	Ile	Lys	Lys	Glu	Arg	Thr	Lys	Phe	Val	Leu	Ser	Arg	Ala		
		195					200						205		

(2) INFORMATION FOR SEQ ID NO:3806:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...206

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3806:

Ala	Gln	Ala	Glu	Thr	Val	Ser	Gln	Thr	Val	Ser	Leu	Pro	Asn	Ala	Lys
1				5					10					15	
Ile	Val	Leu	Asp	Arg	Phe	His	Ile	Val	Gln	His	Leu	Ser	Arg	Ala	Met
			20					25					30		
Ser	Arg	Val	Arg	Val	Gln	Ile	Met	Asn	Gln	Phe	His	Arg	Lys	Ser	His
		35					40					45			
Glu	Tyr	Lys	Ala	Ile	Lys	Arg	Tyr	Trp	Lys	Leu	Ile	Gln	Gln	Asp	Ser
	50					55					60				
Arg	Lys	Leu	Ser	Asp	Lys	Arg	Phe	Tyr	Arg	Pro	Thr	Phe	Arg	Met	His
65					70				75					80	
Leu	Thr	Asn	Lys	Glu	Ile	Leu	Asp	Lys	Leu	Leu	Ser	Tyr	Ser	Gln	Asp
			85						90					95	
Leu	Lys	His	His	Tyr	Gln	Leu	Tyr	Gln	Leu	Leu	Leu	Phe	His	Phe	Gln
			100					105					110		
Asn	Lys	Glu	Pro	Glu	Lys	Phe	Phe	Gly	Leu	Ile	Glu	Asp	Asn	Leu	Lys
		115					120					125			
Gln	Val	His	Pro	Leu	Phe	Gln	Thr	Val	Phe	Lys	Thr	Phe	Leu	Lys	Asp
	130					135					140				
Lys	Glu	Lys	Ile	Val	Asn	Ala	Leu	Gln	Leu	His	Tyr	Ser	Asn	Ala	Lys
145					150					155				160	
Leu	Glu	Ala	Thr	Asn	Asn	Leu	Ile	Lys	Leu	Ile	Lys	Arg	Asn	Ala	Phe
				165					170				175		
Gly	Phe	Arg	Asn	Phe	Glu	Asn	Phe	Lys	Lys	Arg	Ile	Phe	Ile	Ala	Leu
			180					185				190			
Asn	Ile	Lys	Lys	Glu	Arg	Thr	Lys	Phe	Val	Leu	Ser	Gln	Ala		
		195					200					205			

(2) INFORMATION FOR SEQ ID NO:3807:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 198 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...198

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3807:

Ala	Gln	Ala	Glu	Thr	Val	Ser	Gln	Thr	Val	Ser	Leu	Pro	Asn	Ala	Lys
1			5						10					15	
Ile	Val	Leu	Asp	Arg	Phe	His	Ile	Val	Gln	His	Leu	Ser	Arg	Ala	Met
		20						25					30		
Ser	Arg	Val	His	Val	Gln	Ile	Met	Asn	Gln	Phe	His	Arg	Lys	Ser	His
		35					40					45			
Glu	Tyr	Lys	Ala	Ile	Lys	Arg	Tyr	Trp	Lys	Leu	Ile	Gln	Gln	Asp	Ser
	50					55					60				
Arg	Lys	Leu	Ser	Asp	Lys	Arg	Phe	Tyr	Arg	Pro	Thr	Phe	Arg	Met	His
65					70				75					80	
Leu	Thr	Asn	Lys	Glu	Ile	Leu	Asn	Lys	Leu	Leu	Ser	Tyr	Ser	Glu	Asp
			85					90						95	
Leu	Lys	His	His	Tyr	Gln	Leu	Tyr	Asn	Lys	Glu	Pro	Glu	Lys	Phe	Phe
		100						105					110		
Gly	Leu	Ile	Glu	Asp	Asn	Leu	Lys	Gln	Val	His	Pro	Ile	Phe	Gln	Thr
		115					120					125			
Val	Phe	Lys	Thr	Phe	Leu	Lys	Asp	Lys	Glu	Lys	Ile	Val	Asn	Ala	Leu
	130					135					140				
Gln	Leu	Pro	Tyr	Ser	Asn	Ala	Lys	Leu	Glu	Ala	Thr	Asn	Asn	Leu	Ile
145					150				155					160	
Lys	Leu	Ile	Lys	Arg	Asn	Ala	Phe	Gly	Phe	Arg	Asn	Phe	Glu	Asn	Phe
			165					170					175		
Lys	Lys	Arg	Ile	Phe	Ile	Ala	Leu	Asn	Ile	Lys	Lys	Glu	Arg	Thr	Lys
		180						185					190		
Phe	Val	Leu	Ser	Gln	Ala										
		195													

(2) INFORMATION FOR SEQ ID NO:3808:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...84

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3808:

Ala	Gln	Ala	Glu	Thr	Val	Ser	Gln	Thr	Val	Ser	Leu	Pro	Asn	Ala	Lys
1			5						10					15	
Ile	Val	Leu	Asp	Arg	Phe	His	Ile	Val	Gln	His	Leu	Ser	Arg	Ala	Met
		20						25					30		
Ser	Arg	Val	Arg	Val	Gln	Ile	Met	Asn	Gln	Phe	His	Arg	Lys	Ser	His
		35					40					45			
Glu	Tyr	Lys	Ala	Ile	Lys	Arg	Tyr	Trp	Lys	Leu	Ile	Gln	Gln	Asp	Ser
	50					55					60				
Arg	Lys	Leu	Ser	Asp	Lys	Arg	Phe	Tyr	Arg	Pro	Thr	Phe	Arg	Met	His

65
Leu Thr Asn Lys

70

75

80

(2) INFORMATION FOR SEQ ID NO:3809:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...206

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3809:

Ala	Gln	Ala	Glu	Thr	Val	Ser	Gln	Thr	Val	Ser	Leu	Pro	Asn	Ala	Lys
1				5				10						15	
Ile	Val	Leu	Asp	Arg	Phe	His	Ile	Val	Gln	His	Leu	Ser	Arg	Ala	Met
			20				25						30		
Ser	Arg	Val	Arg	Val	Gln	Ile	Met	Asn	Gln	Phe	His	Arg	Lys	Ser	His
			35				40						45		
Glu	Tyr	Lys	Ala	Ile	Lys	Arg	Tyr	Trp	Lys	Leu	Ile	Gln	Gln	Asp	Ser
			50				55					60			
Arg	Lys	Leu	Ser	Asp	Lys	Arg	Phe	Tyr	Arg	Pro	Thr	Phe	Arg	Met	His
65						70				75					80
Leu	Thr	Asn	Lys	Glu	Ile	Leu	Asn	Lys	Leu	Leu	Ser	Tyr	Ser	Gln	Asp
				85					90					95	
Leu	Lys	His	His	Tyr	Gln	Leu	Tyr	Gln	Leu	Leu	Leu	Phe	His	Phe	Gln
			100					105					110		
Asn	Lys	Glu	Pro	Glu	Lys	Phe	Phe	Glu	Leu	Ile	Glu	Asp	Asn	Leu	Lys
			115				120					125			
Gln	Val	His	Pro	Ile	Phe	Gln	Thr	Val	Phe	Lys	Thr	Phe	Leu	Lys	Asp
			130				135					140			
Lys	Glu	Lys	Ile	Ile	Asn	Ala	Leu	Gln	Leu	His	Tyr	Ser	Asn	Ala	Lys
145						150				155					160
Leu	Glu	Ala	Thr	Asn	Asn	Leu	Ile	Lys	Leu	Ile	Lys	Arg	Asn	Ala	Phe
				165					170					175	
Gly	Phe	Arg	Asn	Phe	Glu	Asn	Phe	Lys	Lys	Arg	Ile	Phe	Ile	Ala	Leu
			180					185					190		
Asn	Ile	Lys	Lys	Glu	Arg	Thr	Lys	Phe	Val	Leu	Ser	Arg	Ala		
			195				200						205		

(2) INFORMATION FOR SEQ ID NO:3810:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 409 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...409
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3810:

```

Val Gly Ala Glu Lys Phe Ser Gln Pro His Phe Leu Lys Trp Thr Tyr
1      5      10      15
Arg Lys Val Leu Gln Asp Cys Asn Met Lys Lys Glu Phe Asn Leu Ile
      20      25      30
Ala Thr Val Ala Ala Gly Leu Glu Ala Val Val Gly Arg Glu Val Arg
      35      40      45
Glu Met Gly Tyr Asp Cys Gln Val Glu Asn Gly Arg Val Arg Phe Gln
      50      55      60
Gly Asp Val Arg Ala Ile Ile Glu Thr Asn Leu Trp Leu Arg Ala Ala
      65      70      75      80
Asp Arg Ile Lys Ile Ile Val Gly Thr Phe Pro Ala Lys Thr Phe Glu
      85      90      95
Glu Leu Phe Gln Gly Val Phe Ala Leu Asp Trp Glu Asn Tyr Leu Pro
      100      105      110
Leu Gly Ala Arg Phe Pro Ile Ser Lys Ala Lys Cys Val Lys Ser Lys
      115      120      125
Leu His Asn Glu Pro Ser Val Gln Ala Ile Ser Lys Lys Ala Val Val
      130      135      140
Lys Lys Leu Gln Lys His Tyr Ala Arg Pro Glu Gly Val Pro Leu Met
      145      150      155      160
Glu Asn Gly Pro Glu Phe Lys Ile Glu Val Ser Ile Leu Lys Asp Val
      165      170      175
Ala Thr Val Met Ile Asp Thr Thr Gly Ser Ser Leu Phe Lys Arg Gly
      180      185      190
Tyr Arg Thr Glu Lys Gly Gly Ala Pro Ile Lys Glu Asn Met Ala Ala
      195      200      205
Ala Ile Leu Gln Leu Ser Asn Trp Tyr Pro Asp Lys Thr Leu Ile Asp
      210      215      220
Pro Thr Cys Gly Ser Gly Thr Phe Cys Ile Glu Ala Val Met Ile Ala
      225      230      235      240
Arg Lys Met Ala Pro Gly Leu Arg Arg Ser Phe Ala Phe Glu Glu Trp
      245      250      255
Asn Trp Ile Ser Asp Arg Leu Ile Gln Glu Val Arg Thr Glu Ala Ala
      260      265      270
Lys Lys Val Asp Arg Glu Leu Glu Leu Asp Ile Met Gly Cys Asp Ile
      275      280      285
Asp Ala Arg Met Val Glu Ile Ala Lys Ala Asn Ala Gln Ala Ala Gly
      290      295      300
Val Ala Gly Asp Ile Thr Phe Lys Gln Met Arg Val Gln Asp Leu Arg
      305      310      315      320
Ser Asp Lys Ile Asn Gly Val Ile Ile Ser Asn Pro Pro Tyr Gly Glu
      325      330      335
Arg Leu Ser Asp Asp Ala Gly Val Thr Lys Leu Tyr Ala Glu Met Gly

```

(2) INFORMATION FOR SEO ID NO:3811:

(A) LENGTH: 299 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: YES

(A) ORGANISM: *Streptococcus pneumoniae*

(A) NAME/KEY: misc_feature
(B) LOCATION 1...299

2760

Leu	Pro	Lys	Asp	Thr	Lys	Gln	Leu	Lys	Lys	Glu	Phe	Ile	Glu	Ile	Asn
210						215					220				
Ala	Pro	Val	Ile	Glu	Ala	Ile	Asp	Ile	Ser	Asn	Thr	Asn	Arg	Lys	Gln
225					230					235					240
Phe	Ile	Val	Lys	Gln	Ile	Leu	Glu	Arg	Lys	Pro	Lys	Ile	Val	Gly	Ile
			245						250					255	
Tyr	Lys	Leu	Gly	Met	Lys	Tyr	Asn	Ser	Asp	Asn	Tyr	Lys	Glu	Ser	Ala
		260						265					270		
Ile	Leu	Ser	Ile	Ile	Asn	Glu	Leu	Leu	Ile	Val	Gly	Ile	Lys	Ile	Leu
	275					280						285			
Val	Tyr	Glu	Pro	Asn	Leu	Asn	Val	Ser	Tyr	Arg					
290						295									

(2) INFORMATION FOR SEQ ID NO:3812:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...208

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3812:

Gln	Thr	Tyr	Glu	Thr	Arg	Thr	Val	Ile	Val	Ala	Thr	Gly	Ser	Lys	His
1			5					10						15	
Arg	Pro	Leu	Gly	Val	Pro	Gly	Glu	Glu	Glu	Leu	Asn	Ser	Arg	Gly	Val
	20					25						30			
Ser	Tyr	Cys	Ala	Val	Cys	Asp	Gly	Ala	Phe	Phe	Arg	Asp	Gln	Asp	Leu
	35					40					45				
Leu	Val	Val	Gly	Gly	Gly	Asp	Ser	Ala	Val	Glu	Glu	Ala	Leu	Phe	Leu
	50				55					60					
Thr	Arg	Phe	Ala	Lys	Thr	Val	Thr	Ile	Val	His	Arg	Arg	Asp	Gln	Leu
65				70						75				80	
Arg	Ala	Gln	Lys	Val	Leu	Gln	Asp	Arg	Ala	Phe	Ala	Asn	Glu	Lys	Ile
		85						90					95		
Ser	Phe	Ile	Trp	Asp	Ser	Val	Val	Arg	Glu	Ile	Lys	Gly	Glu	Asn	Arg
	100						105					110			
Val	Glu	Ser	Val	Val	Phe	Glu	Asn	Val	Lys	Thr	Gly	Gln	Val	Thr	Glu
	115					120					125				
Gln	Val	Phe	Gly	Gly	Val	Phe	Ile	Tyr	Val	Gly	Leu	Asp	Pro	Leu	Ser
	130				135					140					
Asp	Phe	Val	Lys	Glu	Leu	Asn	Ile	Gln	Asp	Gln	Ala	Gly	Trp	Ile	Val
145				150					155					160	
Thr	Asp	Asn	His	Met	Lys	Thr	Ala	Val	Asp	Gly	Ile	Phe	Ala	Val	Gly
		165				170						175			
Asp	Val	Arg	Leu	Lys	Asp	Leu	Arg	Gln	Val	Thr	Thr	Ala	Val	Gly	Asp

(2) INFORMATION FOR SEQ ID NO:3813:

(A) LENGTH: 218 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: YES

(A) ORGANISM: *Streptococcus pneumoniae*

```
(A) NAME/KEY: misc_feature
(B) LOCATION 1...218
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(2) INFORMATION FOR SEO ID NO:3814:

2762

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(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
      (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:
      (A) NAME/KEY: misc_feature
      (B) LOCATION 1...458
```

Leu	His	His	Glu	Lys	Val	Gly	Phe	Ile	Met	Lys	Ile	Ile	Leu	Val	Gly
1				5					10					15	
Gly	Gly	Lys	Val	Gly	Phe	Ala	Leu	Cys	Arg	Ser	Leu	Val	Ala	Glu	Lys
			20					25					30		
His	Asp	Val	Leu	Leu	Ile	Glu	Gln	Asp	Glu	Ala	Val	Leu	Asn	His	Ile
		35					40					45			
Val	Ser	Arg	Phe	Asp	Ile	Ile	Gly	Ile	Leu	Gly	Asn	Gly	Ala	Asp	Phe
	50					55					60				
Ala	Ile	Leu	Glu	Gln	Ala	Ser	Val	Gln	Asp	Cys	Asp	Ile	Phe	Ile	Ala
65					70					75					80
Leu	Thr	Glu	His	Asp	Glu	Val	Asn	Met	Ile	Ala	Ala	Val	Leu	Ala	Lys
				85					90					95	
Lys	Met	Gly	Ala	Lys	Glu	Thr	Ile	Val	Arg	Val	Arg	Asn	Pro	Glu	Tyr
			100					105					110		
Ser	Asn	Ser	Tyr	Phe	Lys	Glu	Lys	Asn	Ile	Leu	Gly	Phe	Ser	Leu	Ile
		115					120					125			
Val	Asn	Pro	Glu	Leu	Leu	Ala	Ala	Arg	Ala	Ile	Ala	Asn	Ile	Ile	Asp
	130					135					140				
Phe	Pro	Asn	Ala	Leu	Ser	Val	Glu	Arg	Phe	Ala	Gly	Gly	Arg	Val	Ser
145				150						155					160
Leu	Met	Glu	Phe	Val	Val	Lys	Ser	Thr	Ser	Gly	Leu	Cys	Gln	Met	Pro
				165					170					175	
Ile	Ser	Asp	Phe	Arg	Lys	Lys	Phe	Gly	Asn	Val	Ile	Val	Cys	Ala	Ile
			180					185					190		
Glu	Arg	Glu	His	Gln	Ile	Ile	Ile	Pro	Ser	Gly	Asp	Met	Thr	Val	Gln
		195					200					205			
Asp	Lys	Asp	Arg	Ile	Phe	Val	Thr	Gly	Asn	Arg	Val	Asp	Met	Ile	Leu
	210					215					220				
Phe	His	Asn	Tyr	Phe	Lys	Ser	Arg	Ala	Val	Lys	Ser	Leu	Leu	Ile	Val
225					230					235					240
Gly	Ala	Gly	Arg	Ile	Ala	Tyr	Tyr	Leu	Leu	Gly	Ile	Leu	Lys	Asp	Ser
				245					250					255	
Arg	Ile	Asp	Thr	Lys	Val	Ile	Glu	Ile	Asn	Pro	Glu	Ile	Ala	Ser	Phe
			260					265					270		
Phe	Ser	Glu	Lys	Phe	Pro	Asn	Leu	Tyr	Ile	Val	Gln	Gly	Asp	Gly	Thr
		275					280					285			
Ala	Lys	Asp	Ile	Leu	Leu	Glu	Glu	Ser	Ala	Gln	His	Tyr	Asp	Ala	Val
	290					295					300				
Ala	Thr	Leu	Thr	Gly	Val	Asp	Glu	Glu	Asn	Leu	Ile	Thr	Ser	Met	Phe
305					310					315					320

```

Leu Asp Arg Val Gly Val Gln Lys Asn Ile Thr Lys Val Asn Arg Thr
                325                330                335
Ser Leu Leu Glu Ile Ile Asn Ala Pro Asp Phe Ser Ser Ile Ile Thr
                340                345                350
Pro Lys Ser Ile Ala Val Asp Thr Ile Met His Phe Ile Arg Gly Arg
                355                360                365
Val Asn Ala Gln Tyr Ser Asp Leu Gln Ala Met His His Leu Ala Asn
                370                375                380
Gly Gln Ile Glu Thr Leu Gln Phe His Ile Lys Glu Ala Asn Lys Met
385                390                395                400
Thr Ala Lys Pro Leu Ser Gln Leu Lys Leu Lys Lys Gly Val Leu Ile
                405                410                415
Ala Ala Ile Ile Arg Lys Gly Lys Thr Ile Phe Pro Thr Gly Glu Asp
                420                425                430
Met Leu Glu Val Gly Asp Lys Leu Leu Val Thr Thr Leu Leu Pro Asn
                435                440                445
Ile Thr Lys Ile Tyr Asp Leu Ile Ala Arg
                450                455

```

(2) INFORMATION FOR SEQ ID NO:3815:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 429 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...429

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3815:

```

Lys Leu Asp Leu Leu Pro Leu Leu Asp Gln Arg Pro Gln Asp Leu Ser
1                5                10                15
Gly Gly Gln Lys Gln Arg Val Ser Leu Ala Gly Val Leu Ile Asp Glu
                20                25                30
Ser Pro Ile Leu Leu Phe Asp Glu Pro Leu Ala Asn Leu Asp Pro Lys
                35                40                45
Ser Gly Gln Asp Ile Ile Glu Leu Ile Asp Gln Ile His Lys Glu Glu
50                55                60
Gly Thr Thr Thr Leu Ile Ile Glu His Arg Leu Glu Asp Val Leu His
65                70                75                80
Arg Pro Val Asp Arg Ile Ile Leu Ile Asn Asp Gly Arg Ile Leu Phe
                85                90                95
Asn Gly Ser Pro Asp Gln Leu Leu Ala Thr Asp Leu Leu Thr Gln Asn
                100                105                110
Gly Ile Arg Glu Pro Leu Tyr Leu Thr Thr Leu Arg Gln Leu Gly Val
                115                120                125
Asp Leu Val Lys Glu Glu Gln Leu Ala Asn Leu Asp Asn Met Ser Ile
130                135                140

```

Ser	Lys	Gly	Gln	Val	Gln	Leu	Gln	Asn	Glu	Leu	Ala	Lys	Glu	Thr	Pro
145					150					155					160
Glu	Leu	Gln	Ser	Leu	Phe	Lys	Leu	Glu	Asp	Val	Ser	Phe	Ser	Tyr	Asp
			165						170						175
Asp	Arg	Pro	Ile	Leu	Lys	Ser	Leu	His	Leu	Asp	Ile	Lys	Lys	Gly	Glu
			180					185					190		
Lys	Ile	Ala	Ile	Val	Gly	Lys	Asn	Gly	Ala	Gly	Lys	Ser	Thr	Leu	Ala
			195					200							
Lys	Ala	Ile	Ser	Ser	Phe	Ile	Gln	Thr	Glu	Gly	Arg	Tyr	Leu	Trp	Glu
	210						215				220				
Lys	Gln	Asp	Ile	Lys	Gly	Asp	Ser	Val	Ala	Glu	Arg	Ala	Glu	Arg	Val
225					230					235					240
Gly	Tyr	Val	Leu	Gln	Asn	Pro	Asn	Gln	Met	Ile	Ser	Thr	Asn	Met	Ile
				245					250					255	
Phe	Asp	Glu	Val	Ala	Leu	Gly	Leu	Arg	Leu	Arg	Gly	Val	Asp	Glu	Lys
			260					265					270		
Glu	Ile	Glu	Thr	Arg	Val	Tyr	Glu	Thr	Leu	Lys	Ile	Cys	Gly	Leu	Tyr
	275						280					285			
Glu	Phe	Arg	Asn	Trp	Pro	Ile	Ser	Ala	Leu	Ser	Phe	Gly	Gln	Lys	Lys
	290					295					300				
Arg	Val	Thr	Ile	Ala	Ser	Ile	Leu	Val	Leu	Gly	Ala	Glu	Ile	Ile	Phe
305					310					315					320
Leu	Asp	Glu	Pro	Thr	Ala	Gly	Gln	Asp	Gln	Lys	Asn	Tyr	Thr	Glu	Ile
				325					330					335	
Met	Glu	Phe	Leu	Glu	Glu	Leu	His	Gln	Lys	Gly	His	Thr	Ile	Val	Met
			340					345					350		
Ile	Thr	His	Asp	Met	Gln	Leu	Met	Leu	Asp	Tyr	Ser	Asp	Arg	Val	Leu
	355						360					365			
Val	Met	Val	Asp	Gly	Glu	Leu	Ile	Ala	Asp	Thr	Val	Pro	Ala	Ser	Leu
	370					375				380					
Leu	Ser	Asp	Pro	Glu	Leu	Leu	Val	Lys	Ala	Asn	Leu	Lys	Glu	Thr	Ser
385					390				395						400
Ile	Phe	Asn	Leu	Ala	Lys	Lys	Leu	Asp	Val	Asp	Pro	Leu	Asp	Leu	Thr
				405					410					415	
Ala	Phe	Tyr	Lys	Glu	Arg	Arg	Glu	Gly	Cys	Lys	Leu	Asn			
			420					425							

(2) INFORMATION FOR SEQ ID NO:3816:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 262 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...262
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3816:

Gly	Val	His	Glu	Arg	Ser	Met	Ile	Gln	Ser	Ile	Thr	Ser	Gln	Gly	Leu
1				5					10					15	
Val	Leu	Tyr	Asn	Arg	Asn	Phe	Arg	Glu	Asp	Asp	Lys	Leu	Val	Lys	Ile
			20					25					30		
Phe	Thr	Glu	Gln	Val	Gly	Lys	Arg	Met	Phe	Phe	Val	Lys	His	Ala	Gly
		35				40						45			
Gln	Ser	Lys	Leu	Ala	Pro	Val	Ile	Gln	Pro	Leu	Val	Leu	Ala	Arg	Phe
	50					55					60				
Leu	Leu	Arg	Ile	Asn	Asp	Asp	Gly	Leu	Ser	Tyr	Ile	Glu	Asp	Tyr	His
65				70					75					80	
Glu	Val	Met	Thr	Phe	Pro	Lys	Ile	Asn	Ser	Asp	Leu	Phe	Val	Met	Ala
			85					90						95	
Tyr	Ala	Thr	Tyr	Val	Ala	Ala	Leu	Ala	Asp	Ala	Ser	Leu	Gln	Asp	Asn
			100					105						110	
Gln	Gln	Asp	Ala	Pro	Leu	Phe	Ala	Phe	Leu	Gln	Lys	Thr	Leu	Glu	Leu
		115					120						125		
Met	Glu	Ala	Gly	Leu	Asp	Tyr	Gln	Val	Leu	Thr	Asn	Ile	Phe	Glu	Ile
	130					135					140				
Gln	Ile	Leu	Thr	Arg	Phe	Gly	Ile	Ser	Leu	Asn	Phe	Asn	Glu	Cys	Val
145				150					155					160	
Phe	Cys	His	Arg	Val	Gly	Gln	Ala	Phe	Asp	Phe	Ser	Phe	Lys	Tyr	Gly
			165					170						175	
Ala	Cys	Leu	Cys	Pro	Glu	His	Tyr	His	Glu	Asp	Lys	Arg	Arg	Cys	His
			180					185					190		
Leu	Asn	Pro	Asn	Ile	Pro	Tyr	Leu	Leu	Asn	Gln	Phe	Gln	Ala	Ile	Asp
	195					200						205			
Phe	Glu	Thr	Leu	Glu	Thr	Ile	Ser	Leu	Lys	Pro	Gly	Ile	Lys	Gln	Glu
	210					215					220				
Leu	Arg	Gln	Phe	Met	Asp	Gln	Leu	Tyr	Glu	Glu	Tyr	Val	Gly	Ile	His
225				230					235					240	
Leu	Lys	Ser	Lys	Lys	Phe	Ile	Asp	Ser	Leu	Ala	Asp	Trp	Gly	Gln	Leu
			245					250						255	
Leu	Lys	Glu	Glu	Lys	Lys										
			260												

(2) INFORMATION FOR SEQ ID NO:3817:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 97 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...97
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3817:

Phe Leu Asn Glu Arg Asp Ile Thr Ser Arg His Ile Asn Ser Asp Asp

1				5					10					15		
Phe	Asn	Phe	Phe	Ser	Ser	Phe	Phe	Arg	Val	Leu	Glu	Glu	Met	Ile	Ser	
			20					25					30			
Asp	Gly	Cys	Leu	Thr	Ser	Val	Ile	Lys	Asn	Gly	His	Asp	Phe	Leu	Ser	
		35					40					45				
Val	Glu	Ile	Leu	Ser	Asn	Glu	Ser	Gln	Phe	Pro	Leu	Leu	Val	Gly	Glu	
	50					55					60					
Phe	Ile	Pro	Gly	Glu	Asp	Phe	Arg	Gln	Ser	Gly	Val	Ile	Leu	Leu	Glu	
65					70					75					80	
Met	Lys	Leu	Leu	Glu	Leu	Thr	Ile	Asp	Gly	Arg	Gly	Arg	Gly	Arg	Asp	
				85					90					95		

Gly

(2) INFORMATION FOR SEQ ID NO:3818:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...97

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3818:

Arg	Tyr	Asn	Glu	Glu	Lys	Ser	Ser	Lys	Glu	Lys	Glu	Leu	Thr	Asn	Ser	
1				5				10						15		
Lys	Tyr	Ile	Thr	Cys	Leu	Lys	Arg	Ser	Glu	Gly	Gln	Leu	Cys	Gly	Ile	
		20					25					30				
Gln	Lys	Met	Ile	Glu	Gly	Asp	Arg	Asp	Cys	Ala	Asp	Ile	Val	Thr	Gln	
		35					40					45				
Leu	Thr	Ala	Val	Lys	Ser	Ser	Val	Glu	Arg	Val	Ile	Glu	Met	Ile	Ile	
	50					55				60						
Thr	Glu	Asn	Leu	Thr	Glu	Cys	Ile	Asn	Gln	Pro	Leu	Asp	Asp	Ser	Glu	
65					70				75						80	
Ala	Gln	Lys	Glu	Arg	Leu	Glu	Lys	Ala	Ile	Arg	Tyr	Leu	Ile	Lys	Arg	
				85					90					95		

Lys

(2) INFORMATION FOR SEQ ID NO:3819:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 436 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...436

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3819:

```

Leu Glu Asn Glu Gly Gly Gly Phe Cys Xaa Xaa Phe Xaa Xaa Xaa Xaa
1      5      10      15
Xaa Xaa Xaa Phe Xaa Xaa Pro Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20      25      30
Xaa Xaa Xaa Xaa Phe Leu Gln Asn Arg Ala Thr Ile Leu Glu Phe Leu
35      40      45
Tyr Arg Asn Pro Ala Thr Ser Arg Thr Asp Ile Val Asn Glu Thr Gly
50      55      60
Leu Thr Pro Ala Thr Thr Asn Ile Ile Lys Glu Leu Ser Glu Gln
65      70      75      80
Ser Leu Ile Tyr Glu Thr Gly Asp Glu Phe Ser Glu Phe Ser Gly Ser
85      90      95
Gly Arg Arg Arg Lys Thr Ile Ser Ile Thr Asp Asn Ile Pro Tyr Val
100     105     110
Val Gly Gly Ile Glu Ile Asn Val Leu Gly Ile Phe Leu Ser Leu Cys
115     120     125
Asp Leu Gln Gly Lys Thr Leu Phe Glu Thr Glu Ile Leu Asn Glu Asp
130     135     140
Tyr Pro Ile Ser Glu Ile Asn Ser Thr Ile Thr Asn Met Ile Lys Thr
145     150     155     160
Ala Ile Glu Tyr Val Pro Leu Glu Thr Lys Leu Leu Gly Phe Gly Leu
165     170     175
Ser Ile Pro Gly His Tyr Tyr Lys Asp Ser Gly Ser Ile Ile Thr Asn
180     185     190
Asn Pro Ile Trp Glu Ser Phe Asn Leu Leu Asn Val Ile Lys Arg Phe
195     200     205
Asn Phe Pro Phe Ile Val Lys Asn Asn Ile Asp Cys Met Ala Ile Gly
210     215     220
Gln Tyr Leu Phe Asn Pro His Asn Thr Pro Asp Asn Phe Ile Phe Leu
225     230     235     240
His Ala Gly Leu Gly Ile Tyr Thr Ser Phe Phe Thr Lys Glu Lys Ile
245     250     255
Gly Ala Ser Lys Asn Pro Tyr Ile Gly Glu Ile Gly His Thr Ile Val
260     265     270
Glu Leu Asn Gly Gln Tyr Cys Glu Cys Gly Lys Lys Gly Cys Leu Gln
275     280     285
Thr Tyr Ile Ser Asp Ala Trp Leu Ile Lys His Ala Gln Leu Leu Phe
290     295     300
Lys Asn Ser Gln Leu Thr Val Leu Lys Ser Leu Val Lys Thr Glu Lys
305     310     315     320
Asp Ile His Leu Asp Thr Leu Leu Thr Ala Tyr Asn Leu Gly Asp Ser
325     330     335
Ala Leu Arg Gln Gln Ile Asp Lys Gly Val Asn Leu Leu Ala Thr Ser
340     345     350

```

```

Ile Ala Asn Leu Leu Leu Ile Asn Pro Ala Asp Lys Ile Tyr Ile Asn
    355                      360                      365
Ser Gln Leu Leu Asn Tyr Gln Pro Phe Thr His Glu Val Arg Asp Lys
    370                      375                      380
Ile Gln Asp Gln Leu His Phe Val Pro Phe Thr Arg Asn Ile Glu Ile
385                      390                      395                      400
Glu Ile Leu Pro Tyr Asn Lys His Arg Gly Ser Ile Gly Ala Cys Ala
    405                      410                      415
Leu Ala Ile Val Ala Phe Phe Ile Glu His Ser Asn Val Leu Gln Asp
    420                      425                      430
Ile Ile Ser Pro
    435

```

(2) INFORMATION FOR SEQ ID NO:3820:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...218

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3820:

```

Lys Arg Asn Glu Leu Asp Met Ser Lys Gly Phe Leu Val Ser Leu Glu
1      5      10      15
Gly Pro Glu Gly Ala Gly Lys Thr Ser Val Leu Glu Ala Leu Leu Pro
    20      25      30
Ile Leu Glu Glu Lys Gly Val Glu Val Leu Thr Thr Arg Glu Pro Gly
    35      40      45
Gly Val Leu Ile Gly Glu Lys Ile Arg Glu Val Ile Leu Asp Pro Ser
    50      55      60
His Thr Gln Met Asp Ala Lys Thr Glu Leu Leu Leu Tyr Ile Ala Ser
65      70      75      80
Arg Arg Gln His Leu Val Glu Lys Val Leu Pro Ala Leu Glu Ala Gly
    85      90      95
Lys Leu Val Ile Met Asp Arg Phe Ile Asp Ser Ser Val Ala Tyr Gln
    100     105     110
Gly Phe Gly Arg Gly Leu Asp Ile Glu Ala Ile Asp Trp Leu Asn Gln
    115     120     125
Phe Ala Thr Asp Gly Leu Lys Pro Asp Leu Thr Leu Tyr Phe Asp Ile
    130     135     140
Glu Val Glu Glu Gly Leu Ala Arg Ile Ala Ala Asn Ser Asp Arg Glu
145     150     155     160
Val Asn Arg Leu Asp Leu Glu Gly Leu Asp Leu His Lys Lys Val Arg
    165     170     175
Gln Gly Tyr Leu Ser Leu Leu Asp Lys Glu Gly Asn Arg Ile Val Lys

```


	180		185		190										
Ile	Asp	Ala	Ser	Leu	Pro	Leu	Glu	Gln	Val	Val	Glu	Thr	Thr	Lys	Ala
	195						200					205			
Val	Leu	Phe	Asp	Gly	Met	Gly	Leu	Ala	Lys						
	210					215									

(2) INFORMATION FOR SEQ ID NO:3821:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...172

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3821:

Gly	Gly	Asn	Asp	Met	Asp	Lys	Lys	Glu	Arg	Gln	Lys	Ile	Glu	Gln	Gln
1				5				10					15		
Arg	Arg	Glu	Met	Ala	Leu	Thr	Asn	Thr	Phe	Phe	Asn	Arg	Tyr	Leu	Leu
		20					25					30			
Leu	Arg	Tyr	Ser	Ile	Ala	Leu	Phe	Phe	Phe	Gly	Asn	Ile	Tyr	Trp	Leu
	35					40					45				
Leu	Asn	Gln	Phe	Ile	Asn	Pro	Ser	Pro	Ile	Ile	Ile	Phe	Pro	Ile	Met
	50				55					60					
Leu	Ile	Val	Phe	Ser	Ile	Leu	Ala	Thr	Val	Glu	Gln	Phe	Lys	Leu	Tyr
65				70				75					80		
Gly	Asn	Arg	Lys	Glu	Lys	Leu	Gly	Ile	Thr	Leu	Met	Phe	Val	Arg	Ile
		85					90						95		
Gln	Met	Leu	Ile	Ser	Ile	Gly	Leu	Leu	Val	Leu	Thr	Trp	Thr	Ser	Trp
	100					105						110			
Phe	Lys	Asn	Leu	Phe	Pro	Ile	Phe	Glu	Asn	Asn	Gln	Val	Ala	Arg	Leu
	115				120						125				
Phe	Val	Phe	Val	Val	Leu	Leu	Leu	Gly	Leu	Val	Leu	Ser	Leu	Leu	Asp
	130				135					140					
Ile	Arg	Arg	Ile	Lys	Lys	Ile	Tyr	Lys	Arg	Thr	Asp	Lys	Val	Tyr	Gln
145				150				155						160	
Gln	Phe	Val	Gln	Leu	Glu	Lys	Asn	Ser	Leu	Ser	Leu				
			165				170								

(2) INFORMATION FOR SEQ ID NO:3822:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...134
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3822:

```

Glu Ala Asn Glu Glu Ser Lys Met Lys Glu Ala Ile Ile Glu Trp Lys
1          5          10          15
Asp Phe Ser Phe Arg Tyr Glu Thr Gln Gln Glu Pro Thr Leu Gln Gly
20          25          30
Ile Asp Leu Thr Ile Tyr Lys Gly Glu Lys Val Leu Ile Val Gly Pro
35          40          45
Ser Gly Ser Gly Lys Ser Thr Leu Gly Gln Cys Leu Asn Gly Ile Ile
50          55          60
Pro Asn Ile Tyr Lys Gly Gln Thr Tyr Gly Glu Phe Leu Ile Lys Gly
65          70          75          80
Gln Thr Ala Phe Asp Met Ser Ile Tyr Asp Lys Ser His Leu Val Ser
85          90          95
Thr Val Leu Gln Asp Thr Asp Gly Gln Phe Ile Gly Leu Ser Val Ala
100         105         110
Glu Asp Leu Ala Phe Ala Leu Glu Asn Asp Val Thr Ala Leu Asp Glu
115         120         125
Met Lys Gly Ser Cys Leu
130

```

(2) INFORMATION FOR SEQ ID NO:3823:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 376 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...376
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3823:

```

Ser Phe Asp Glu Thr Ser Lys Ala Asp Thr Lys Thr Leu Pro Lys Val
1          5          10          15
Ser Gln Ser Thr Leu Thr Ser Ile Pro Lys Val Gln Ala Gln Thr Glu
20          25          30

```

His	Lys	Ser	Ile	Lys	Asn	Pro	Ser	Gln	Ala	Val	Thr	Glu	Glu	Thr	Tyr
	35						40					45			
Gln	Pro	Gln	Ala	Pro	Lys	Lys	His	Arg	Phe	Lys	Met	Arg	Tyr	Leu	Ile
	50					55					60				
Leu	Leu	Ala	Ser	Leu	Val	Leu	Val	Ala	Ala	Ser	Leu	Ile	Trp	Ile	Leu
65				70						75					80
Ser	Arg	Thr	Pro	Ala	Thr	Ile	Ala	Ile	Pro	Asp	Val	Ala	Gly	Gln	Thr
				85					90					95	
Val	Ala	Glu	Ala	Lys	Ala	Thr	Leu	Lys	Lys	Ala	Asn	Phe	Glu	Ile	Gly
			100					105					110		
Glu	Glu	Lys	Thr	Glu	Ala	Ser	Glu	Lys	Val	Glu	Glu	Gly	Arg	Ile	Ile
		115					120					125			
Arg	Thr	Asp	Pro	Gly	Ala	Gly	Thr	Gly	Arg	Lys	Glu	Gly	Thr	Lys	Ile
	130					135					140				
Asn	Leu	Val	Val	Ser	Ser	Gly	Lys	Gln	Ser	Phe	Gln	Ile	Ser	Asn	Tyr
145					150					155					160
Val	Gly	Arg	Lys	Ser	Ser	Asp	Val	Ile	Ala	Glu	Leu	Lys	Glu	Lys	Lys
			165						170					175	
Val	Pro	Asp	Asn	Leu	Ile	Lys	Ile	Glu	Glu	Glu	Glu	Ser	Asn	Glu	Ser
		180						185					190		
Glu	Ala	Gly	Thr	Val	Leu	Lys	Gln	Ser	Leu	Pro	Glu	Gly	Thr	Thr	Tyr
	195						200					205			
Asp	Leu	Ser	Lys	Ala	Thr	Gln	Ile	Val	Leu	Thr	Val	Ala	Lys	Lys	Ala
	210					215					220				
Thr	Thr	Ile	Gln	Leu	Gly	Asn	Tyr	Ile	Gly	Arg	Asn	Ser	Thr	Glu	Val
225				230						235					240
Ile	Ser	Glu	Leu	Lys	Gln	Lys	Lys	Val	Pro	Glu	Asn	Leu	Ile	Lys	Ile
			245						250					255	
Glu	Glu	Glu	Glu	Ser	Ser	Glu	Ser	Glu	Gln	Gly	Thr	Ile	Met	Lys	Gln
		260						265					270		
Ser	Pro	Gly	Ala	Gly	Thr	Thr	Tyr	Asp	Val	Ser	Lys	Pro	Thr	Gln	Ile
	275						280					285			
Val	Leu	Thr	Val	Ala	Lys	Lys	Val	Thr	Ser	Val	Ala	Met	Pro	Ser	Tyr
	290					295					300				
Ile	Gly	Ser	Ser	Leu	Glu	Phe	Thr	Lys	Asn	Asn	Leu	Ser	Gln	Ile	Val
305				310						315					320
Gly	Ile	Lys	Glu	Ala	Asn	Ile	Glu	Val	Val	Glu	Val	Thr	Thr	Ala	Pro
			325						330					335	
Ala	Gly	Ser	Val	Glu	Gly	Met	Val	Val	Glu	Gln	Ser	Pro	Arg	Ala	Gly
		340						345					350		
Glu	Lys	Val	Asp	Leu	Asn	Lys	Thr	Arg	Val	Lys	Ile	Ser	Ile	Tyr	Lys
	355					360						365			
Pro	Lys	Thr	Thr	Ser	Ala	Thr	Pro								
	370					375									

(2) INFORMATION FOR SEQ ID NO:3824:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...75

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3824:

Lys	Gly	Asp	Glu	Glu	Gln	Thr	Lys	Ile	Gln	Ala	Gly	Ile	Pro	Thr	Asp
1				5					10					15	
Asn	Glu	Val	Ser	Tyr	Ala	Leu	Ile	Tyr	Gln	Gln	Glu	Thr	Leu	Pro	Ala
			20					25					30		
Thr	Gly	Ser	Ser	Thr	Ser	Ala	Leu	Thr	Ala	Leu	Gly	Leu	Leu	Ala	Val
		35					40					45			
Gly	Ser	Leu	Val	Leu	Leu	Val	Arg	Asn	Ser	Phe	Leu	Leu	Pro	Leu	Lys
	50					55					60				
Ser	His	His	Leu	Met	Ala	Phe	Phe	Tyr	Ile	Gly					
65					70					75					

(2) INFORMATION FOR SEQ ID NO:3825:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...62

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3825:

Phe	Val	Asp	Asp	Ile	Phe	Asp	Gly	Ile	Pro	Val	Asn	Gly	Phe	Val	Val
1				5					10					15	
Ser	Phe	His	Leu	Lys	Ser	Leu	Ser	Val	Phe	Ser	Ile	Ala	Asn	Ser	Gln
			20					25					30		
Leu	Phe	Leu	Leu	Tyr	His	Asn	Ser	Ile	Gly	Val	Ser	His	Lys	Lys	Ser
		35					40					45			
Glu	Ala	Arg	Leu	Leu	Lys	Cys	Tyr	Ile	Asn	Tyr	Val	Met	Thr		
	50					55					60				

(2) INFORMATION FOR SEQ ID NO:3826:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 352 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...352

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3826:

Met	Lys	Asp	Asp	Gln	Lys	Tyr	Leu	Leu	Ala	Gly	Leu	Tyr	Ser	Leu	Leu
1				5					10					15	
Val	Ala	Ile	Phe	Tyr	Phe	Pro	Leu	Ile	Glu	Ser	Lys	Gly	Ile	Phe	Val
			20				25						30		
Ser	Ile	Leu	Met	Ala	Val	Leu	Leu	Leu	Tyr	Leu	Ile	Tyr	Phe	Ile	Ala
		35				40						45			
Thr	Val	Ile	His	Ile	Val	Ile	Ile	Lys	Phe	Ile	Arg	Lys	Lys	Ser	Phe
	50					55					60				
Lys	Tyr	Leu	Val	Leu	Tyr	Pro	Phe	Thr	Tyr	Asp	Gly	Ser	Trp	Arg	Phe
65					70					75				80	
Gln	Pro	Ile	Asn	Leu	Leu	Tyr	Phe	Pro	Glu	Met	Val	Arg	Asp	Val	Ile
			85						90					95	
Pro	Ile	Asn	Leu	Val	Gln	Glu	Tyr	Cys	Gln	Gly	Gln	Pro	Tyr	Gly	Leu
		100						105					110		
Leu	Lys	Lys	Met	Leu	Lys	Arg	Ile	Arg	Leu	Ser	Arg	Glu	Ile	Ser	Leu
		115					120					125			
Leu	Leu	Ala	Thr	Ile	Ile	Val	Tyr	Phe	Phe	Thr	His	Arg	Ile	Leu	Pro
	130					135					140				
Leu	Ser	Val	Phe	Thr	Phe	Ile	Phe	Ser	Tyr	Ile	Leu	Leu	Phe	Val	Gln
145					150					155				160	
Ser	Tyr	Leu	Gly	Ser	Asn	Thr	Ala	Trp	Ile	Gly	Asn	Arg	Arg	Leu	Ile
			165					170						175	
Ile	Asp	Asp	Glu	Phe	Glu	Lys	Ile	Leu	Leu	Ser	Lys	Ser	Tyr	Ile	Lys
		180						185					190		
Glu	Ile	Ser	Ser	Ala	Arg	Tyr	Ser	Glu	Tyr	Leu	Thr	Cys	Glu	Tyr	Lys
	195						200					205			
Asn	Leu	Thr	Pro	Ile	Ile	Leu	Ile	Ala	Ile	Phe	Glu	Asn	Leu	Leu	Asp
	210					215					220				
Ser	Tyr	Leu	Leu	Gln	Asn	Gln	Ser	Glu	Val	Asp	Leu	Asp	Ile	Phe	Tyr
225				230						235				240	
Lys	Val	Leu	Pro	Leu	Leu	Tyr	Lys	Glu	Lys	Tyr	Thr	Met	Gly	Phe	Asn
			245						250					255	
Tyr	Phe	Val	Ser	Leu	Asn	Tyr	Leu	Leu	Tyr	Lys	Val	Gly	Phe	Leu	Gly
		260					265						270		
Ile	Ile	Tyr	Asp	Asn	Glu	Ala	Leu	Arg	Asp	Leu	Ser	Lys	Gln	Tyr	Leu
	275						280					285			
Asn	Lys	Asn	Ile	Ser	Glu	Leu	Gln	Asp	Gly	Ser	Phe	Glu	Gly	Gly	Ile
	290					295					300				
Gln	Asp	Ala	Val	Ala	Ser	Lys	Gln	Ile	Val	Val	Ile	Asn	Glu	Phe	Ile
305					310					315				320	
Ala	Cys	Leu	Asn	Ser	Arg	Cys	Val	Pro	Ser	Gln	Tyr	Asp	Arg	Phe	Phe
			325					330					335		
Tyr	Lys	Asp	Arg	Pro	Tyr	Ile	Phe	Ser	Arg	Lys	Ser	Pro	Ile	Lys	Gly
		340						345					350		

(2) INFORMATION FOR SEQ ID NO:3827:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...265

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3827:

Lys	Gly	Asp	Glu	Leu	Met	Val	Tyr	Thr	Ser	Leu	Ser	Ser	Lys	Asp	Gly
1				5					10					15	
Asn	Tyr	Pro	Tyr	Gln	Leu	Asn	Ile	Ala	His	Leu	Tyr	Gly	Asn	Leu	Met
			20					25					30		
Asn	Thr	Tyr	Gly	Asp	Asn	Gly	Asn	Ile	Leu	Met	Leu	Lys	Tyr	Val	Ala
			35				40					45			
Glu	Lys	Leu	Gly	Ala	His	Val	Thr	Val	Asp	Ile	Val	Ser	Leu	His	Asp
	50					55					60				
Asp	Phe	Asp	Glu	Asn	His	Tyr	Asp	Ile	Ala	Phe	Phe	Gly	Gly	Gly	Gln
65					70					75					80
Asp	Phe	Glu	Gln	Ser	Ile	Ile	Ala	Asp	Asp	Leu	Pro	Ala	Lys	Lys	Glu
				85					90					95	
Ser	Ile	Asp	Asn	Tyr	Ile	Gln	Asn	Asp	Gly	Val	Val	Leu	Ala	Ile	Cys
			100					105					110		
Gly	Gly	Phe	Gln	Leu	Leu	Gly	Gln	Tyr	Tyr	Val	Glu	Ala	Ser	Gly	Lys
		115					120					125			
Arg	Ile	Glu	Gly	Leu	Gly	Val	Met	Gly	His	Tyr	Thr	Leu	Asn	Gln	Thr
	130					135					140				
Asn	Asn	Arg	Phe	Ile	Gly	Asp	Ile	Lys	Ile	His	Asn	Glu	Asp	Phe	Asp
145					150					155					160
Glu	Thr	Tyr	Tyr	Gly	Phe	Glu	Asn	His	Gln	Gly	Arg	Thr	Phe	Leu	Ser
				165					170					175	
Asp	Asp	Gln	Lys	Pro	Leu	Gly	Gln	Val	Tyr	Gly	Asn	Gly	Asn	Asn	
			180					185				190			
Glu	Glu	Lys	Val	Gly	Glu	Gly	Val	His	Tyr	Lys	Asn	Val	Phe	Gly	Ser
		195					200					205			
Tyr	Phe	His	Gly	Pro	Ile	Leu	Ser	Arg	Asn	Ala	Asn	Leu	Ala	Tyr	Arg
	210					215					220				
Leu	Val	Thr	Thr	Ala	Leu	Lys	Lys	Lys	Tyr	Gly	Gln	Asp	Ile	Gln	Leu
225				230						235					240
Pro	Ala	Tyr	Glu	Asp	Ile	Leu	Ser	Gln	Glu	Ile	Ala	Glu	Glu	Tyr	Ser
				245					250					255	
Asp	Val	Lys	Ser	Lys	Ala	Asp	Phe	Ser							
			260					265							

(2) INFORMATION FOR SEQ ID NO:3828:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 133 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...133

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3828:

Lys	Asn	Cys	Glu	Glu	Lys	Lys	Met	Ala	Lys	Thr	Ile	His	Thr	Asp	Lys
1			5						10					15	
Ala	Pro	Lys	Ala	Ile	Gly	Pro	Tyr	Val	Gln	Gly	Lys	Ile	Val	Gly	Asn
		20						25					30		
Leu	Leu	Phe	Ala	Ser	Gly	Gln	Val	Pro	Leu	Ser	Pro	Glu	Thr	Gly	Glu
	35					40						45			
Ile	Val	Gly	Glu	Asn	Ile	Gln	Glu	Gln	Thr	Glu	Gln	Val	Leu	Lys	Asn
	50				55					60					
Ile	Gly	Ala	Ile	Leu	Ala	Glu	Ala	Gly	Thr	Asp	Phe	Asp	His	Val	Val
65				70					75					80	
Lys	Thr	Thr	Cys	Phe	Leu	Ser	Asp	Met	Asn	Asp	Phe	Val	Pro	Phe	Asn
			85					90					95		
Glu	Val	Tyr	Gln	Thr	Ala	Phe	Lys	Glu	Glu	Phe	Pro	Ala	Arg	Ser	Ala
		100						105				110			
Val	Glu	Val	Ala	Arg	Leu	Pro	Arg	Asp	Val	Lys	Val	Glu	Ile	Glu	Val
	115					120						125			
Ile	Ala	Glu	Ile	Gly											
130															

(2) INFORMATION FOR SEQ ID NO:3829:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 218 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...218
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3829:

Lys	Gly	Cys	Asp	Phe	Val	Lys	Asp	Lys	Gln	Phe	Ala	Ile	Pro	Lys	Ala
1			5						10					15	
Thr	Ala	Lys	Arg	Leu	Ser	Leu	Tyr	Tyr	Arg	Ile	Phe	Lys	Arg	Phe	His
			20					25					30		
Ala	Glu	Lys	Ile	Glu	Arg	Ala	Asn	Ser	Lys	Gln	Ile	Ala	Glu	Ala	Ile
		35					40					45			
Gly	Ile	Asp	Ser	Ala	Thr	Val	Arg	Arg	Asp	Phe	Ser	Tyr	Phe	Gly	Glu
	50					55					60				
Leu	Gly	Arg	Arg	Gly	Phe	Gly	Tyr	Asp	Val	Lys	Lys	Leu	Met	Thr	Phe
65				70						75					80
Phe	Ala	Asp	Leu	Leu	Asn	Asp	Asn	Ser	Ile	Thr	Asn	Val	Met	Leu	Val
			85						90				95		
Gly	Ile	Gly	Asn	Met	Gly	His	Ala	Leu	Leu	His	Tyr	Arg	Phe	His	Glu
			100					105					110		
Arg	Asn	Lys	Met	Lys	Ile	Ile	Met	Ala	Phe	Asp	Leu	Asp	Asp	His	Pro
		115					120					125			
Glu	Val	Gly	Thr	Gln	Thr	Pro	Asp	Gly	Ile	Pro	Ile	Tyr	Gly	Ile	Ser
	130					135					140				
Gln	Ile	Lys	Asp	Lys	Ile	Lys	Asp	Ala	Asp	Val	Lys	Thr	Ala	Ile	Leu
145				150						155					160
Thr	Val	Pro	Ser	Val	Lys	Ser	Gln	Glu	Val	Ala	Asn	Leu	Leu	Val	Asp
			165					170					175		
Ala	Gly	Val	Lys	Gly	Ile	Leu	Ser	Phe	Ser	Pro	Val	His	Leu	His	Leu
		180					185					190			
Pro	Lys	Asp	Val	Val	Val	Gln	Tyr	Val	Asp	Leu	Thr	Ser	Glu	Leu	Gln
	195					200						205			
Thr	Leu	Leu	Tyr	Phe	Met	Arg	Lys	Glu	Asp						
	210					215									

(2) INFORMATION FOR SEQ ID NO:3830:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 71 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...71
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3830:

Asp	Cys	Cys	Glu	Thr	Met	Arg	Val	Ala	Ala	Leu	Asn	Ser	Ser	Ile	Ile
1			5						10					15	
Gly	Ser	Phe	Arg	Ser	Arg	Ala	Pro	Gln	Val	Ala	Asp	Gly	Gly	Thr	Gly
		20					25					30			
Ala	Leu	Asn	Val	Val	Asn	Arg	Ile	Gly	Arg	Leu	Ala	Arg	Leu	Thr	Ser
		35				40					45				
Asn	Gly	Val	Leu	His	Thr	Arg	His	Ala	Leu	Thr	Val	Asn	Gly	His	Asn
	50					55				60					

Ala Gln Leu Arg Thr Phe Val
65 70

(2) INFORMATION FOR SEQ ID NO:3831:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3831:

Cys	Arg	Cys	Asp	Arg	Ile	Ser	Gly	Glu	Phe	Ile	Met	Arg	Gln	Leu	Lys
1				5					10					15	
Arg	Val	Gly	Val	Phe	Leu	Leu	Leu	Pro	Phe	Phe	Val	Leu	Ile	Asp	Ala
			20					25					30		
His	Ile	Ser	Gln	Leu	Leu	Gly	Ser	Phe	Phe	Pro	His	Val	His	Leu	Ala
		35				40					45				
Ser	His	Phe	Leu	Phe	Leu	Phe	Leu	Leu	Phe	Glu	Thr	Ile	Glu	Val	Ser
	50				55					60					
Glu	Tyr	Leu	Tyr	Leu	Val	Tyr	Cys	Phe	Val	Ile	Gly	Leu	Val	Tyr	Asp
65				70					75					80	
Val	Tyr	Phe	Phe	His	Leu	Ile	Gly	Ile	Thr	Thr	Leu	Leu	Phe	Ile	Leu
				85				90						95	
Leu	Gly	Ala	Phe	Leu	His	Lys	Leu	Asn	Ser	Val	Ile	Leu	Leu	Asn	Arg
		100					105					110			
Trp	Thr	Arg	Met	Leu	Ala	Met	Ile	Val	Leu	Thr	Phe	Leu	Phe	Glu	Met
		115				120						125			
Gly	Ser	Tyr	Leu	Leu	Ala	Phe	Met	Val	Gly	Leu	Thr	Val	Asp	Ser	Met
	130				135					140					
Ser	Ile	Phe	Ile	Val	Tyr	Ser	Leu	Val	Pro	Thr	Met	Ile	Leu	Asn	Phe
145				150					155					160	
Leu	Trp	Ile	Thr	Val	Phe	Gln	Phe	Ile	Phe	Glu	Lys	Tyr	Tyr	Leu	
			165					170						175	

(2) INFORMATION FOR SEQ ID NO:3832:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 853 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...853

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3832:

Ile	Leu	Cys	Glu	Lys	Asp	Lys	Phe	Ser	Cys	Glu	Phe	Ala	Tyr	Phe	Lys
1				5					10					15	
Asn	Phe	Leu	Phe	Ser	Leu	Gly	Ile	Leu	Trp	Ala	Leu	Tyr	Leu	Met	Ser
			20					25					30		
Asn	Ile	Gln	Asn	Met	Ser	Leu	Glu	Asp	Ile	Met	Gly	Glu	Arg	Phe	Gly
		35					40					45			
Arg	Tyr	Ser	Lys	Tyr	Ile	Ile	Gln	Asp	Arg	Ala	Leu	Pro	Asp	Ile	Arg
	50					55					60				
Asp	Gly	Leu	Lys	Pro	Val	Gln	Arg	Arg	Ile	Leu	Tyr	Ser	Met	Asn	Lys
65					70					75				80	
Asp	Ser	Asn	Thr	Phe	Asp	Lys	Ser	Tyr	Arg	Lys	Ser	Ala	Lys	Ser	Val
			85						90					95	
Gly	Asn	Ile	Met	Gly	Asn	Phe	His	Pro	His	Gly	Asp	Ser	Ser	Ile	Tyr
		100						105						110	
Asp	Ala	Met	Val	Arg	Met	Ser	Gln	Asn	Trp	Lys	Asn	Arg	Glu	Ile	Leu
		115					120					125			
Val	Glu	Met	His	Gly	Asn	Asn	Gly	Ser	Met	Asp	Gly	Asp	Pro	Pro	Ala
	130					135					140				
Ala	Met	Arg	Tyr	Thr	Glu	Ala	Arg	Leu	Ser	Glu	Ile	Ala	Gly	Tyr	Leu
145					150					155					160
Leu	Gln	Asp	Ile	Glu	Lys	Lys	Thr	Val	Pro	Phe	Ala	Trp	Asn	Phe	Asp
				165					170					175	
Asp	Thr	Glu	Lys	Glu	Pro	Thr	Val	Leu	Pro	Ala	Ala	Phe	Pro	Asn	Leu
		180					185						190		
Leu	Val	Asn	Gly	Ser	Thr	Gly	Ile	Ser	Ala	Gly	Tyr	Ala	Thr	Asp	Ile
		195					200					205			
Pro	Pro	His	Asn	Leu	Ala	Glu	Val	Ile	Asp	Ala	Ala	Val	Tyr	Met	Ile
	210					215					220				
Asp	His	Pro	Thr	Ala	Lys	Ile	Asp	Lys	Leu	Met	Glu	Phe	Leu	Pro	Gly
225				230					235					240	
Pro	Asp	Phe	Pro	Thr	Gly	Ala	Ile	Ile	Gln	Gly	Arg	Asp	Glu	Ile	Lys
			245						250					255	
Lys	Ala	Tyr	Glu	Thr	Gly	Lys	Gly	Arg	Val	Val	Val	Arg	Ser	Lys	Thr
		260					265						270		
Glu	Ile	Glu	Lys	Leu	Lys	Gly	Gly	Lys	Glu	Gln	Ile	Val	Ile	Thr	Glu
	275					280						285			
Ile	Pro	Tyr	Glu	Ile	Asn	Lys	Ala	Asn	Leu	Val	Lys	Lys	Ile	Asp	Asp
	290					295					300				
Val	Arg	Val	Asn	Asn	Lys	Val	Ala	Gly	Ile	Ala	Glu	Val	Arg	Asp	Glu
305				310						315					320
Ser	Asp	Arg	Asp	Gly	Leu	Arg	Ile	Ala	Ile	Glu	Leu	Lys	Lys	Asp	Ala
			325						330					335	
Asn	Thr	Glu	Leu	Val	Leu	Asn	Tyr	Leu	Phe	Lys	Tyr	Thr	Asp	Leu	Gln
		340					345						350		
Ile	Asn	Tyr	Asn	Phe	Asn	Met	Val	Ala	Ile	Asp	Asn	Phe	Thr	Pro	Arg
	355					360						365			
Gln	Val	Gly	Ile	Val	Pro	Ile	Leu	Ser	Ser	Tyr	Ile	Ala	His	Arg	Arg
	370					375					380				

Glu	Val	Ile	Leu	Ala	Arg	Ser	Arg	Phe	Asp	Lys	Glu	Lys	Ala	Glu	Lys
385					390				395						400
Arg	Leu	His	Ile	Val	Glu	Gly	Leu	Ile	Arg	Val	Ile	Ser	Ile	Leu	Asp
			405						410						415
Glu	Val	Ile	Ala	Leu	Ile	Arg	Ala	Ser	Glu	Asn	Lys	Ala	Asp	Ala	Lys
			420					425					430		
Glu	Asn	Leu	Lys	Val	Ser	Tyr	Asp	Phe	Thr	Glu	Glu	Gln	Ala	Glu	Ala
	435						440					445			
Ile	Val	Thr	Leu	Gln	Leu	Tyr	Arg	Leu	Thr	Asn	Thr	Asp	Val	Val	Val
	450					455					460				
Leu	Gln	Glu	Glu	Glu	Ala	Glu	Leu	Arg	Glu	Lys	Ile	Ala	Met	Leu	Ala
465					470					475					480
Ala	Ile	Ile	Gly	Asp	Glu	Arg	Thr	Met	Tyr	Asn	Leu	Met	Lys	Lys	Glu
			485						490						495
Leu	Arg	Glu	Val	Lys	Lys	Lys	Phe	Ala	Thr	Pro	Arg	Leu	Ser	Ser	Leu
			500					505					510		
Glu	Asp	Thr	Ala	Lys	Ala	Ile	Glu	Ile	Asp	Thr	Ala	Ser	Leu	Ile	Ala
	515							520				525			
Glu	Glu	Asp	Thr	Tyr	Val	Ser	Val	Thr	Lys	Ala	Gly	Tyr	Ile	Lys	Arg
	530					535					540				
Thr	Ser	Pro	Arg	Ser	Phe	Ala	Ala	Ser	Thr	Leu	Glu	Glu	Ile	Gly	Lys
545					550					555					560
Arg	Asp	Asp	Asp	Arg	Leu	Ile	Phe	Val	Gln	Ser	Ala	Lys	Thr	Thr	Gln
				565					570						575
His	Leu	Leu	Met	Phe	Thr	Ser	Leu	Gly	Asn	Val	Ile	Tyr	Arg	Pro	Ile
			580					585					590		
His	Glu	Leu	Ala	Asp	Ile	Arg	Trp	Lys	Asp	Ile	Gly	Glu	His	Leu	Ser
	595						600					605			
Gln	Thr	Ile	Thr	Asn	Phe	Glu	Thr	Asn	Glu	Glu	Ile	Leu	Tyr	Val	Glu
	610					615					620				
Val	Leu	Asp	Gln	Phe	Asp	Asp	Ala	Thr	Thr	Tyr	Phe	Ala	Val	Thr	Arg
625					630					635					640
Leu	Gly	Gln	Ile	Lys	Arg	Val	Glu	Arg	Lys	Glu	Phe	Thr	Pro	Trp	Arg
				645					650					655	
Thr	Tyr	Arg	Ser	Lys	Ser	Val	Lys	Tyr	Ala	Lys	Leu	Lys	Asp	Asp	Thr
			660					665					670		
Asp	Gln	Ile	Val	Ala	Val	Ala	Pro	Ile	Lys	Leu	Asp	Asp	Val	Val	Leu
	675					680						685			
Val	Ser	Gln	Asn	Gly	Tyr	Ala	Leu	Arg	Phe	Asn	Ile	Glu	Glu	Val	Pro
	690					695				700					
Val	Val	Gly	Ala	Lys	Ala	Ala	Gly	Val	Lys	Ala	Met	Asn	Leu	Lys	Glu
705					710					715					720
Asp	Asp	Val	Leu	Gln	Ser	Gly	Phe	Ile	Cys	Asn	Thr	Ser	Ser	Phe	Tyr
				725					730					735	
Leu	Leu	Thr	Gln	Arg	Gly	Ser	Leu	Lys	Arg	Val	Ser	Ile	Glu	Glu	Ile
			740					745					750		
Leu	Ala	Thr	Ser	Arg	Ala	Lys	Arg	Gly	Leu	Gln	Val	Leu	Arg	Glu	Leu
	755						760					765			
Lys	Asn	Lys	Pro	His	Arg	Val	Phe	Leu	Ala	Gly	Ala	Val	Ala	Glu	Gln
	770					775					780				
Gly	Phe	Val	Gly	Asp	Phe	Phe	Ser	Thr	Glu	Val	Asp	Val	Asn	Asp	Gln
785					790					795					800
Thr	Leu	Leu	Val	Gln	Ser	Asn	Lys	Gly	Thr	Ile	Tyr	Glu	Ser	Arg	Leu
				805					810					815	
Gln	Asp	Leu	Asn	Leu	Ser	Glu	Arg	Thr	Ser	Asn	Gly	Ser	Phe	Ile	Ser
			820					825					830		
Asp	Thr	Ile	Ser	Asp	Glu	Glu	Val	Phe	Asp	Ala	Tyr	Leu	Gln	Glu	Val

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...242
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3834:

```

Ser Met Arg Asp Ala Asn Arg Gly Gly Cys Ser Gln Ser Cys Arg Trp
1      5      10      15
Lys Tyr Asp Leu Tyr Asp Met Pro Phe Gly Lys Glu Arg Lys Ser Leu
      20      25      30
Gln Gly Glu Ile Pro Glu Glu Phe Ser Met Ser Ala Val Asp Met Ser
      35      40      45
Met Ile Asp His Ile Pro Asp Met Ile Glu Asn Gly Val Asp Ser Leu
      50      55      60
Lys Ile Glu Gly Arg Met Glu Ser Ile His Tyr Val Leu Thr Val Thr
      65      70      75      80
Asn Cys Tyr Lys Ala Ala Val Asp Ala Tyr Leu Glu Ser Pro Glu Lys
      85      90      95
Phe Glu Ala Ile Lys Gln Asp Leu Val Asp Glu Met Trp Lys Val Ala
      100     105     110
Gln Arg Glu Leu Ala Thr Gly Phe Tyr Tyr Gly Thr Pro Ser Glu Asn
      115     120     125
Glu Gln Leu Phe Gly Ala Arg Arg Lys Ile Pro Glu Tyr Lys Phe Val
      130     135     140
Ala Glu Val Val Ser Tyr Asp Asp Ala Ala Gln Thr Ala Thr Ile Arg
      145     150     155     160
Gln Arg Asn Val Ile Asn Glu Gly Asp Gln Val Glu Phe Tyr Gly Pro
      165     170     175
Gly Phe Arg His Phe Glu Thr Tyr Ile Glu Asp Leu His Asp Ala Lys
      180     185     190
Gly Asn Lys Ile Asp Arg Ala Pro Asn Pro Met Glu Leu Leu Thr Ile
      195     200     205
Lys Val Pro Gln Pro Val Gln Ser Gly Asp Met Val Arg Ala Leu Lys
      210     215     220
Glu Gly Leu Ile Asn Leu Tyr Lys Glu Asp Gly Thr Ser Val Thr Val
      225     230     235     240
Arg Ala

```

(2) INFORMATION FOR SEQ ID NO:3835:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 65 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...65

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3835:

```
Lys Met Arg Glu His Glu His Leu Gln Asn Arg Asn Ser Ile Lys Ser
1           5           10           15
His Leu Leu Val Pro Leu Thr Phe Leu Phe Leu Glu Ser Ile Tyr Val
20           25           30
Gly Ser Asn Leu Phe Asn Leu Thr Glu Met Ile Gln Ala Ser Thr Asp
35           40           45
Ala Gly Phe Ser Ala Ser Ile Ser Cys Phe Thr Asn Phe Asn Cys Ser
50           55           60
Ile
65
```

(2) INFORMATION FOR SEQ ID NO:3836:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 126 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3836:

```
Thr Lys Ser Asp Ser Ala Val Phe Asp Cys Phe Ser Arg Arg Asn Gln
1           5           10           15
Ile Met Arg Tyr Ile Thr Val Glu Asp Leu Ser Phe Tyr Tyr Asp Lys
20           25           30
Glu Pro Val Leu Glu His Ile Asn Tyr Cys Val Asp Ser Gly Glu Phe
35           40           45
Val Thr Leu Thr Gly Glu Asn Gly Ala Ala Lys Thr Thr Leu Ile Lys
50           55           60
Ala Ser Leu Gly Ile Leu His Pro Arg Ile Gly Lys Val Ala Ile Ser
65           70           75           80
Lys Thr Asn Thr Gln Gly Lys Lys Leu Arg Ile Ala Tyr Leu Pro Gln
85           90           95
His Ile Ala Ser Phe Asn Ala Gly Phe Gln Val Arg Ser Met Asn Leu
100          105          110
Ser Ser Arg Val Ala Ile Arg Glu Met Ala Gly Ser Val Val
115          120          125
```

(2) INFORMATION FOR SEQ ID NO:3837:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...382

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3837:

Gln	Lys	Ser	Glu	Val	Asn	Ala	Met	Trp	Met	Glu	Glu	Leu	Pro	Asn	Gly	
1				5					10					15		
Lys	Phe	Lys	Tyr	Phe	Glu	Arg	Tyr	Lys	Asp	Pro	Tyr	Thr	Glu	Lys	Leu	
			20					25					30			
Lys	Lys	Val	Ser	Val	Thr	Met	Glu	Lys	Lys	Thr	Pro	Gln	Ala	Arg	Asn	
		35					40					45				
Gln	Ala	Ala	Ile	Leu	Leu	Gln	Glu	Lys	Ile	Asn	Lys	Lys	Leu	Ser	Thr	
	50					55				60						
Lys	Gln	Val	Glu	Ser	Ile	Thr	Phe	Glu	Glu	Ile	Tyr	Asn	Leu	Phe	Tyr	
65					70				75						80	
Lys	Ser	Trp	Ala	Gln	Thr	Val	Lys	Glu	Ser	Thr	Lys	His	Asn	Cys	Lys	
			85					90					95			
Ser	Val	Asp	Lys	Lys	Met	Lys	Glu	Val	Ile	Pro	Ser	Asp	Thr	Ile	Leu	
		100					105					110				
Ala	Asn	Leu	Asp	Arg	Arg	Phe	Leu	Gln	Glu	Ala	Ile	Glu	Lys	Ile	Ile	
	115					120					125					
Glu	Ser	Asn	Gly	Tyr	Ile	Thr	Ala	Lys	Lys	Val	Arg	His	Arg	Leu	Arg	
	130				135					140						
Gly	Ile	Phe	Asn	Tyr	Ala	Val	Gln	Tyr	Ser	Tyr	Ile	Glu	Asn	Asn	Glu	
145				150					155						160	
Val	Asp	Tyr	Thr	Thr	Ile	Pro	Gln	Lys	Pro	Lys	Thr	Leu	Glu	Glu	Leu	
			165				170					175				
Glu	Lys	Lys	Arg	Asn	Asn	Phe	Leu	Thr	Met	Gln	Glu	Ile	Lys	Ala	Leu	
		180					185					190				
Val	Asp	Val	Leu	Asn	Arg	Arg	Glu	Tyr	His	Gln	Lys	Tyr	Ala	Asp	Met	
	195					200					205					
Val	Leu	Val	Leu	Thr	Leu	Thr	Gly	Met	Arg	Tyr	Gly	Glu	Leu	Thr	Ala	
	210				215					220						
Leu	Gln	Leu	Lys	Asn	Ile	Asp	Phe	Glu	Asn	Asn	Lys	Ile	Glu	Ile	Thr	
225				230					235						240	
Gly	Asn	Phe	Asp	Ser	Val	Asn	Lys	Ile	Lys	Thr	Leu	Pro	Lys	Thr	Thr	
		245					250					255				
Asn	Ser	Ile	Arg	Thr	Ile	Lys	Val	Ser	Glu	Ser	Val	Ile	Glu	Ala	Ile	
		260				265					270					
Gln	Arg	Gln	Ile	Val	Arg	Leu	Ser	Glu	Arg	Phe	Gln	Pro	Leu	Ser	Ser	
	275					280					285					

Asp	Asp	Tyr	Ile	Phe	Cys	Phe	Glu	Lys	Trp	Asn	Gln	Pro	Thr	Thr	Ile
290						295					300				
Ala	Cys	Phe	Ile	Gln	Ile	Leu	Lys	Lys	Tyr	Gly	Lys	Gln	Ala	Lys	Ile
305					310					315					320
Glu	Lys	Asn	Leu	Ser	Ser	His	Ile	Phe	Arg	His	Ser	His	Ile	Ser	Phe
				325					330					335	
Leu	Ala	Glu	Ser	Gly	Leu	Pro	Ile	Lys	Ser	Ile	Met	Asp	Arg	Val	Gly
			340					345					350		
His	Ser	Asn	Ala	Lys	Met	Thr	Leu	Glu	Ile	Tyr	Ser	Ser	Phe	Thr	Glu
		355					360					365			
Asp	Met	Glu	Asp	Lys	Leu	Val	Asn	Lys	Leu	Asp	Thr	Ile	Phe		
	370					375					380				

(2) INFORMATION FOR SEQ ID NO:3838:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...257

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3838:

Tyr	Arg	Ser	Asp	Glu	Met	Val	Val	Tyr	Ile	Arg	Gln	Ser	Lys	Leu	Pro
1				5				10						15	
Ser	Glu	Val	Ser	Ile	Asn	Lys	Tyr	Asn	Ala	Gln	Val	Gly	Ala	Tyr	Leu
		20					25					30			
Gln	Gly	Glu	Glu	Ala	Val	Leu	Tyr	Gln	Ser	Phe	Ser	Glu	Ile	Lys	Glu
	35					40						45			
Leu	Thr	Ser	Glu	Asp	Ile	Val	Val	Asp	Tyr	Ile	Met	Glu	Thr	Arg	Ala
	50					55					60				
Leu	Leu	Lys	Met	Met	Gly	Leu	Asn	Val	Pro	Val	His	Asp	Tyr	Pro	Ile
65				70					75					80	
Glu	Leu	Lys	Glu	Phe	Tyr	Gly	Arg	Lys	Ile	Tyr	Ala	Gly	Ile	Leu	Gly
				85				90						95	
Glu	Ile	Val	Asn	Ile	Pro	Asp	Asn	Trp	Gly	Lys	Phe	Ile	Lys	Pro	Lys
		100					105					110			
Ala	Gly	Ser	Lys	Val	Phe	Thr	Gly	Arg	Val	Val	Asn	Gly	Thr	His	Asp
	115						120					125			
Leu	Ile	Gly	Ile	Gly	Leu	Pro	Phe	Asp	Tyr	Pro	Ile	Trp	Ile	Ser	Glu
	130					135					140				
Val	Val	Glu	Phe	Ile	Ala	Glu	Trp	Arg	Cys	Phe	Val	Leu	Asp	Gly	Arg
145					150				155					160	
Val	Leu	Asp	Val	Arg	Pro	Tyr	Thr	Gly	Asp	Tyr	His	Ala	Gln	Phe	Asp
			165					170					175		
Ala	Ser	Val	Ile	Asp	Glu	Ala	Ile	Ser	Cys	Trp	Lys	Asp	Ala	Pro	Ile
			180					185					190		

Ala	Tyr	Gly	Leu	Asp	Ile	Gly	Val	Thr	Arg	Asp	Gly	Arg	Thr	Leu	Val
		195					200					205			
Val	Glu	Val	Asn	Asp	Gly	Tyr	Ala	Leu	Gly	Asn	Tyr	Gly	Leu	Ser	Pro
	210					215					220				
Leu	Lys	Ser	Ile	Asn	Phe	His	Arg	Ala	Arg	Trp	Lys	Glu	Met	Val	Lys
225					230					235					240
Pro	Tyr	Phe	Glu	Lys	Asn	Glu	Ile	Phe	Lys	Ile	Gln	Gln	Asp	Val	Ile
				245					250					255	
Phe															

(2) INFORMATION FOR SEQ ID NO:3839:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...247

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3839:

Asp	Thr	Gly	Asp	Ala	Tyr	Ile	Val	Pro	His	Gly	Asp	His	Tyr	His	Tyr
1				5					10					15	
Ile	Pro	Lys	Asn	Glu	Leu	Ser	Ala	Ser	Glu	Leu	Ala	Ala	Ala	Glu	Ala
			20					25					30		
Phe	Leu	Ser	Gly	Arg	Gly	Asn	Leu	Ser	Asn	Ser	Arg	Thr	Tyr	Arg	Arg
		35				40					45				
Gln	Asn	Ser	Asp	Asn	Thr	Ser	Arg	Thr	Asn	Trp	Val	Pro	Ser	Val	Ser
	50				55					60					
Asn	Pro	Gly	Thr	Thr	Asn	Thr	Asn	Thr	Ser	Asn	Asn	Ser	Asn	Thr	Asn
65					70					75					80
Ser	Gln	Ala	Ser	Gln	Ser	Asn	Glu	Asp	Val	Asp	Ser	Leu	Leu	Lys	Gln
				85					90					95	
Leu	Tyr	Ala	Leu	Pro	Leu	Ser	Lys	Arg	His	Val	Glu	Ser	Asp	Gly	Leu
			100					105					110		
Val	Phe	Asp	Pro	Ala	Gln	Ile	Thr	Ser	Arg	Thr	Ala	Arg	Gly	Val	Ala
	115					120					125				
Val	Pro	His	Gly	Asp	His	Tyr	His	Phe	Ile	Pro	Tyr	Ser	Gln	Met	Ser
	130					135					140				
Glu	Leu	Glu	Glu	Arg	Ile	Ala	Arg	Ile	Ile	Pro	Leu	Arg	Tyr	Arg	Ser
145					150					155					160
Asn	His	Trp	Val	Pro	Asp	Ser	Arg	Leu	Glu	Gln	Pro	Ser	Leu	Gln	Pro
				165					170					175	
Thr	Pro	Glu	Pro	Ser	Pro	Gly	Pro	Gln	Pro	Ala	Pro	Asn	Leu	Lys	Ile
			180					185					190		
Asp	Ser	Asn	Ser	Ser	Leu	Val	Ser	Gln	Leu	Val	Arg	Lys	Val	Gly	Glu

	195		200		205
Gly	Tyr	Val	Phe	Glu	Glu
	210			215	
Asp	Leu	Pro	Ser	Glu	Thr
225				230	
Gln	Glu	Ser	Val	His	Thr
				245	

(2) INFORMATION FOR SEQ ID NO:3840:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3840:

Gly	Lys	Gly	Glu	Asn	Met	Ala	Lys	Leu	Ile	Pro	Gly	Lys	Ile	Arg	Ile
1				5					10					15	
Glu	Gly	Val	Ala	Leu	Tyr	Glu	Thr	Gly	Lys	Val	Asp	Ile	Ile	Lys	Glu
			20					25					30		
Lys	Asn	Asn	Arg	Leu	Tyr	Ala	Arg	Val	Ala	Glu	Glu	Glu	Leu	Arg	His
		35				40					45				
Ser	Leu	Glu	Asp	Asp	Leu	Val	Phe	Cys	Ala	Cys	Asp	Phe	Phe	Gln	Lys
50					55				60						
Arg	Gly	Tyr	Cys	Val	His	Leu	Ala	Ala	Leu	Glu	His	Phe	Leu	Lys	Asn
65				70				75						80	
Asp	Glu	Arg	Gly	Gln	Glu	Ile	Leu	Trp	Ser	Leu	Glu	Glu	Gly	His	Glu
			85					90						95	
Glu	Lys	Glu	Ala	Val	Glu	Thr	Lys	Val	His	Leu	Gly	Trp	Gln	Val	Phe
			100					105					110		
Gly	Ser	Asn	Phe	Ile	Ser	Lys	Ile	Arg	Met	Arg	Leu				
		115					120								

(2) INFORMATION FOR SEQ ID NO:3841:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3841:

```

Asn Gly Gly Asp Gln Val Ile Asp Gly Lys Arg Leu Leu Phe Ser Leu
1          5          10          15
Thr Ile Val Ser Tyr Ala Leu Thr Leu Val Ser Gly Val Val Tyr Leu
20        25        30
Phe Asn Asn Asn Asn Val Ser Leu Leu Ser Thr Leu Leu Phe Leu Leu
35        40        45
Val Ser Ser Leu Ile Ala Cys Trp Asn Asp Ile Lys Tyr Tyr Leu Ile
50        55        60
His Phe Ile Phe Tyr Leu Thr Ile Phe Val Phe Leu Val Ser Arg Pro
65        70        75        80
Thr Ile Asp Tyr Phe Arg Asp Gly Ala Leu Asp Thr Tyr His Pro Ile
85        90        95
Ala Tyr Arg Phe Ala Phe Ile Val Val Met Val Ser Ile Leu Gly Leu
100       105       110
Thr Thr Gly Gly Ile Leu Ala Arg Tyr Phe Ile Ala Arg Lys Lys Ile
115       120       125
Lys Val Ala Asn Ile Gly Asn Ser Leu Lys Glu Val Tyr Ile Lys Arg
130       135       140
Leu Arg Phe Val Ser Leu
145       150
  
```

(2) INFORMATION FOR SEQ ID NO:3842:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 618 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...618

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3842:

```

Leu Phe Cys Leu Leu Pro Leu Ser Val Phe Ala Ile Asp Phe Lys Ile
1          5          10          15
Asn Ser Tyr Gln Gly Asp Leu Tyr Ile His Ala Asp Asn Thr Ala Glu
20        25        30
Phe Arg Gln Lys Ile Val Tyr Gln Phe Glu Glu Asp Phe Lys Gly Gln
35        40        45
Ile Val Gly Leu Gly Arg Ala Gly Lys Met Pro Ser Gly Phe Asp Ile
  
```

50	55	60
Asp Pro His Pro Lys Val Gln Ala Ala Lys Asn Gly Ala Glu Leu Ala		
65	70	75
Asp Val Thr Ser Glu Val Thr Glu Glu Ala Asp Gly Tyr Thr Val Arg		
	85	90
Val Tyr Asn Pro Gly Gln Glu Gly Asp Ile Val Glu Val Asp Leu Val		
	100	105
Trp Asn Leu Lys Asn Leu Leu Phe Leu Tyr Asp Asp Ile Ala Glu Leu		
115	120	125
Asn Trp Gln Pro Leu Thr Asp Ser Ser Glu Ser Ile Glu Lys Phe Glu		
130	135	140
Phe His Val Arg Gly Asp Lys Gly Ala Glu Lys Leu Phe Phe His Thr		
145	150	155
Gly Lys Leu Phe Arg Glu Gly Thr Ile Glu Lys Ser Asn Leu Asp Tyr		
	165	170
Thr Ile Arg Leu Asp Asn Leu Pro Ala Lys Arg Gly Val Glu Leu His		
	180	185
Ala Tyr Trp Ser Arg Thr Asp Phe Ala Ser Ala Arg Asp Gln Gly Leu		
	195	200
Lys Gly Asn Arg Leu Glu Glu Phe Asn Lys Ile Glu Asp Ser Ile Val		
	210	215
Arg Glu Lys Asp Gln Ser Lys Gln Leu Val Thr Trp Val Leu Pro Ser		
225	230	235
Ile Leu Ser Ile Ser Leu Leu Leu Ser Val Cys Phe Tyr Phe Ile Tyr		
	245	250
Arg Arg Lys Thr Thr Pro Ser Val Lys Tyr Ala Lys Asn His Arg Leu		
	260	265
Tyr Glu Pro Pro Met Glu Leu Glu Pro Met Val Leu Ser Glu Ala Val		
	275	280
Tyr Ser Thr Ser Leu Glu Glu Val Ser Pro Leu Val Lys Gly Ala Gly		
	290	295
Lys Phe Thr Phe Asp Gln Leu Ile Gln Ala Thr Leu Leu Asp Val Ile		
305	310	315
Asp Arg Gly Asn Val Ser Ile Ile Ser Glu Gly Asp Ala Val Gly Leu		
	325	330
Arg Leu Val Lys Glu Asp Gly Leu Ser Arg Phe Glu Arg Asp Cys Leu		
	340	345
Asn Leu Ala Phe Ser Gly Lys Lys Glu Ala Thr Leu Ser Asn Leu Phe		
	355	360
Ala Asp Tyr Lys Val Ser Asp Ser Leu Tyr Arg Arg Ala Lys Val Ser		
	370	375
Asp Glu Lys Arg Ile Gln Ala Arg Gly Leu Gln Leu Lys Ser Ser Phe		
385	390	395
Glu Glu Val Leu Asn Gln Met Gln Glu Gly Val Arg Lys Arg Val Ser		
	405	410
Phe Trp Gly Leu Pro Asp Tyr Tyr Arg Pro Leu Thr Gly Leu Glu Lys		
	420	425
Thr Leu Gln Val Gly Met Gly Val Leu Thr Ile Leu Pro Leu Phe Ile		
	435	440
Gly Phe Gly Leu Phe Leu Tyr Ser Leu Asp Val His Gly Tyr Leu Tyr		
	450	455
Leu Pro Leu Pro Ile Leu Gly Phe Leu Gly Leu Val Leu Ser Val Phe		
465	470	475
Tyr Tyr Trp Lys Leu Arg Leu Asp Asn Arg Asp Gly Val Leu Asn Glu		
	485	490
Ala Gly Ala Glu Val Tyr Tyr Leu Trp Thr Ser Phe Glu Asn Met Leu		
		495

	500		505		510										
Arg	Glu	Ile	Ala	Arg	Leu	Asp	Lys	Ala	Glu	Leu	Glu	Ser	Ile	Val	Val
	515					520						525			
Trp	Asn	Arg	Leu	Leu	Val	Tyr	Ala	Thr	Leu	Phe	Gly	Tyr	Ala	Asp	Lys
	530					535						540			
Val	Ser	His	Leu	Met	Lys	Val	His	Gln	Ile	Gln	Val	Glu	Asn	Pro	Asp
545					550					555					560
Ile	Asn	Leu	Tyr	Val	Ala	Tyr	Gly	Trp	His	Ser	Met	Phe	Tyr	His	Ser
			565						570					575	
Ser	Ala	Gln	Met	Ser	His	Tyr	Ala	Ser	Val	Ala	Asn	Thr	Ala	Ser	Thr
			580						585					590	
Tyr	Ser	Val	Ser	Ser	Gly	Ser	Gly	Ser	Ser	Gly	Gly	Gly	Phe	Ser	Gly
		595				600						605			
Gly	Gly	Gly	Gly	Gly	Ser	Ile	Gly	Ala	Phe						
	610					615									

(2) INFORMATION FOR SEQ ID NO:3843:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 71 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...71
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3843:

Thr	Lys	Ile	Glu	Leu	Tyr	Ile	Gly	Glu	Ile	Met	Asn	Lys	Thr	Thr	Phe
1				5					10					15	
Met	Ala	Lys	Pro	Gly	Gln	Val	Glu	Arg	Lys	Trp	Tyr	Val	Val	Asp	Ala
			20					25					30		
Thr	Asp	Val	Pro	Leu	Gly	Arg	Leu	Ser	Ala	Val	Val	Ala	Ser	Val	Leu
		35				40						45			
Arg	Gly	Lys	Asn	Asp	Pro	Thr	Phe	Thr	Pro	His	Thr	Ala	Ala	Ser	Phe
	50					55					60				
Ser	Thr	Ser	Ser	Pro	His	Pro									
65					70										

(2) INFORMATION FOR SEQ ID NO:3844:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 158 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...158

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3844:

```

Ser Phe Val Glu Met Phe Val Gly Val Gly Ala Ser Arg Val Arg Asp
1          5          10          15
Met Phe Glu Gln Ala Lys Lys His Ala Pro Cys Ile Ile Phe Ile Asp
          20          25          30
Glu Ile Asp Ala Val Gly Arg His Arg Gly Ala Gly Leu Gly Gly Gly
          35          40          45
His Asp Glu Arg Glu Gln Thr Leu Asn Gln Leu Leu Val Glu Met Asp
          50          55          60
Gly Phe Glu Met Asn Asp Gly Ile Ile Val Ile Ala Ala Thr Asn Arg
65          70          75          80
Pro Asp Val Met Asp Pro Ala Leu Leu Arg Pro Gly Arg Phe Asp Arg
          85          90          95
Gln Val Val Val Gly Leu Pro Asp Ile Arg Gly Arg Glu Gln Ile Leu
          100          105          110
Lys Val His Met Arg Lys Val Pro Leu Gly Asp His Val Asp Pro Ala
          115          120          125
Val Ile Ala Arg Gly Thr Pro Gly Phe Ser Gly Ala Asp Gly Pro Arg
          130          135          140
Ser Ile Phe Lys Asn Ala Lys Lys Leu Lys Lys Lys Gly Pro
145          150          155

```

(2) INFORMATION FOR SEQ ID NO:3845:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 99 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...99

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3845:

```

Gln Tyr Val Glu Asp Thr Val Thr Gln Phe Lys Asp Arg Asp Val Glu
1          5          10          15
Cys Thr Thr Thr Lys Val Lys Tyr Gln Asp Phe Phe Phe Phe Val Ser
          20          25          30
Leu Val Gln Thr Ile Ser Lys Ser Cys Cys Ser Trp Phe Val Asn Asn
          35          40          45

```

Thr	Phe	Tyr	Phe	Lys	Thr	Ser	Asn	Phe	Thr	Ser	Val	Phe	Cys	Cys	Leu
50						55					60				
Thr	Leu	Ser	Val	Val	Glu	Val	Ser	Arg	Asn	Cys	Asp	Asn	Ser	Phe	Gly
65					70					75					80
Tyr	Phe	Leu	Thr	Lys	Val	Val	Phe	Ser	Val	Ala	Phe	Gln	Val	Leu	Lys
				85					90					95	
Asp	His	Ser													

(2) INFORMATION FOR SEQ ID NO:3846:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...143

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3846:

Lys	Ile	Cys	Leu	Leu	Thr	Phe	Arg	Gly	Ser	Lys	Val	Asp	Met	Ile	Leu
1			5					10						15	
Cys	Asn	Pro	Pro	Tyr	Phe	Lys	Val	Asn	Pro	Tyr	Ser	Asn	Leu	Asn	Glu
		20						25					30		
Ser	Glu	His	Tyr	Leu	Leu	Ala	Arg	His	Glu	Ile	Thr	Thr	Asn	Leu	Glu
		35					40					45			
Glu	Ile	Cys	Arg	Ser	Ala	Gln	Ser	Ile	Leu	Lys	Ser	Asn	Gly	Arg	Leu
	50				55					60					
Ala	Met	Val	His	Arg	Pro	Asp	Arg	Leu	Leu	Asp	Ile	Leu	Asp	Thr	Leu
65				70					75						80
Lys	Arg	His	Asn	Leu	Ala	Pro	Lys	Arg	Leu	Gln	Phe	Val	Tyr	Pro	Lys
			85						90					95	
Arg	Glu	Lys	Glu	Ala	Asn	Met	Leu	Leu	Ile	Glu	Ala	Ile	Lys	Asp	Gly
		100						105					110		
Ser	Thr	Ser	Gly	Phe	Lys	Val	Leu	Pro	Pro	Leu	Ile	Val	His	Asn	Asp
		115				120						125			
Asp	Gly	Ser	Tyr	Thr	Pro	Glu	Ile	Glu	Glu	Ile	Tyr	Tyr	Gly	Ser	
	130					135					140				

(2) INFORMATION FOR SEQ ID NO:3847:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3847:

```
Val Phe Ala Asp Val Glu Lys Thr Asn Glu Ser Thr Gln Ser Glu Asn
1      5      10      15
Gln Ser Phe Asp Lys Thr Thr Phe Ser Glu Glu Ser Ile Thr Ser Glu
      20      25      30
Thr Thr Glu Ser Gln Ser Glu Ala Ser Thr Asn Lys Arg Gln Glu Glu
      35      40      45
Asn Lys Thr Ser Glu Thr Ser Glu Val Ala Glu Gln Thr Ser Asp Ser
      50      55      60
Ser Glu Ala Ala Leu Ala Arg Ala Val Ser Ala Asp Gly Tyr Ser Glu
      65      70      75      80
Ala Ala Thr Thr Glu Glu Leu Ala Gln Leu Leu Ala Asp Glu Ser Val
      85      90      95
Thr Lys Ile Arg Leu Ile Gln Pro Leu Thr Leu Asp Arg Glu Leu Glu
      100      105      110
Ile Lys Arg Asp Ile Val Ile Asp Phe Gly Gly Phe Ala His Asn Phe
      115      120      125
Gly Thr His His Ile Tyr
      130
```

(2) INFORMATION FOR SEQ ID NO:3848:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 378 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3848:

```
Glu Gly Ala Asp Leu Phe Ala Leu Arg Lys Pro Gly Asn Ile Tyr Thr
1      5      10      15
Arg Ile Thr Asn Pro Thr Thr Ala Ala Leu Glu Gly Gly Val Glu Ala
      20      25      30
Leu Ala Thr Ala Ser Gly Met Thr Ala Val Thr Tyr Thr Ile Leu Ala
      35      40      45
Leu Ala His Ala Gly Glu His Val Val Ala Ala Ser Thr Ile Tyr Gly
```


50		55		60
Gly Thr Phe Asn Leu	Leu Lys Glu Pro Leu	Pro Arg Tyr Gly Ile Thr		
65	70	75	80	
Thr Thr Phe Val Asp	Val Asp Asn Leu Glu	Val Glu Ala Ala Ile		
	85	90	95	
Lys Asp Asn Thr Lys	Leu Val Leu Ile Glu	Thr Leu Gly Asn Pro Leu		
	100	105	110	
Ile Asn Ile Pro Asp	Leu Glu Lys Leu Ala Glu	Ile Ala His Lys His		
	115	120	125	
Gln Ile Pro Leu Val	Ser Asp Asn Thr Phe Ala	Thr Pro Tyr Leu Ile		
	130	135	140	
Asn Val Phe Ser His	Gly Val Asp Ile Ala Ile	His Ser Ala Thr Lys		
145	150	155	160	
Phe Ile Gly Gly His	Gly Thr Thr Ile Gly Gly	Ile Ile Val Asp Ser		
	165	170	175	
Gly Arg Phe Asp Trp	Thr Ala Ser Gly Lys Phe	Pro Gln Phe Val Asp		
	180	185	190	
Glu Ser Pro Ser Cys	His Asn Leu Ser Tyr Thr	His Asp Val Gly Ala		
	195	200	205	
Ala Ala Phe Ile Ile	Ala Val Arg Val Gln Leu	Arg Arg Asp Thr Gly		
	210	215	220	
Ala Ala Leu Ser Pro	Phe Asn Ala Phe Leu Leu	Gln Arg Leu Glu		
225	230	235	240	
Thr Leu Ser Leu Arg	Val Glu Arg His Val Gln	Asn Ala Glu Thr Ile		
	245	250	255	
Val Asp Phe Leu Val	Asn His Pro Lys Val Glu	Lys Val Asn Tyr Pro		
	260	265	270	
Lys Leu Ala Asp Ser	Pro Tyr Tyr Ala Leu Ala	Glu Lys Tyr Leu Pro		
	275	280	285	
Lys Gly Val Gly Ser	Ile Phe Thr Phe His Val	Lys Gly Asp Glu Glu		
	290	295	300	
Glu Ala Arg Lys Val	Ile Asp Asn Leu Glu Ile	Phe Ser Asp Leu Ala		
305	310	315	320	
Asn Ala Ala Asp Ala	Lys Ser Leu Val Val His	Pro Ala Thr Ile Thr		
	325	330	335	
His Gly Gln Leu Ser	Glu Lys Asp Leu Glu Ala	Ala Gly Val Thr Pro		
	340	345	350	
Asn Gln Ile His Leu	Ser Ile Gly Leu Glu Asn	Val Glu Asp Leu Ile		
	355	360	365	
Glu Asp Leu Arg Leu	Ala Leu Glu Lys Ile			
370	375			

(2) INFORMATION FOR SEQ ID NO:3849:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 650 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...650

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3849:

Lys	Thr	Tyr	Asp	Tyr	Leu	Glu	Cys	Leu	Arg	Glu	Thr	Cys	Tyr	Thr	Thr
1				5					10					15	
Cys	Met	Ile	Ile	Leu	Gln	Ala	Asn	Lys	Ile	Glu	Arg	Ser	Phe	Ala	Gly
			20					25					30		
Glu	Val	Leu	Phe	Asp	Asn	Ile	Asn	Leu	Gln	Val	Asp	Glu	Arg	Asp	Arg
		35					40					45			
Ile	Ala	Leu	Val	Gly	Lys	Asn	Gly	Ala	Gly	Lys	Ser	Thr	Leu	Leu	Lys
	50					55					60				
Ile	Leu	Val	Gly	Glu	Glu	Glu	Pro	Thr	Ser	Gly	Glu	Ile	Asn	Lys	Lys
65					70					75				80	
Lys	Asp	Ile	Ser	Leu	Ser	Tyr	Leu	Ala	Gln	Asp	Ser	Arg	Phe	Glu	Ser
			85						90					95	
Glu	Asn	Thr	Ile	Tyr	Asp	Glu	Met	Leu	His	Val	Phe	Asp	Asp	Leu	Arg
		100					105					110			
Arg	Thr	Asp	Lys	Gln	Leu	Arg	Gln	Met	Glu	Leu	Glu	Met	Gly	Glu	Lys
	115						120					125			
Ser	Gly	Glu	Asp	Leu	Asp	Lys	Leu	Met	Ser	Asp	Tyr	Asp	Arg	Leu	Ser
	130					135					140				
Glu	Asn	Phe	Arg	Gln	Ala	Gly	Gly	Phe	Thr	Tyr	Glu	Ala	Asp	Ile	Arg
145				150						155				160	
Ala	Ile	Leu	Asn	Gly	Phe	Lys	Phe	Asp	Glu	Ser	Met	Trp	Gln	Met	Lys
			165						170					175	
Ile	Ala	Glu	Leu	Ser	Gly	Gly	Gln	Asn	Thr	Arg	Leu	Ala	Leu	Ala	Lys
		180						185					190		
Met	Leu	Leu	Glu	Lys	Pro	Asn	Leu	Leu	Val	Leu	Asp	Glu	Pro	Thr	Asn
	195					200					205				
His	Leu	Asp	Ile	Glu	Thr	Ile	Ser	Trp	Leu	Glu	Asn	Tyr	Leu	Val	Asn
	210					215					220				
Tyr	Ser	Gly	Ala	Leu	Ile	Ile	Val	Ser	His	Asp	Arg	Tyr	Phe	Leu	Asp
225				230						235				240	
Lys	Val	Ala	Thr	Ile	Thr	Leu	Asp	Leu	Thr	Lys	His	Ser	Leu	Asp	Arg
			245						250					255	
Tyr	Val	Gly	Asn	Tyr	Ser	Arg	Phe	Val	Glu	Leu	Lys	Glu	Gln	Lys	Leu
		260						265					270		
Ala	Thr	Glu	Ala	Lys	Asn	Tyr	Glu	Lys	Gln	Gln	Lys	Glu	Ile	Ala	Ala
	275						280					285			
Leu	Glu	Asp	Phe	Val	Asn	Arg	Asn	Leu	Val	Arg	Ala	Ser	Thr	Thr	Lys
	290					295					300				
Arg	Ala	Gln	Ser	Arg	Arg	Lys	Gln	Leu	Glu	Lys	Met	Glu	Arg	Leu	Asp
305				310						315				320	
Lys	Pro	Glu	Ala	Gly	Lys	Lys	Ala	Ala	Asn	Met	Thr	Phe	Gln	Ser	Glu
			325						330					335	
Lys	Thr	Ser	Gly	Asn	Val	Val	Leu	Thr	Val	Glu	Asn	Ala	Ala	Val	Gly
		340						345					350		
Tyr	Asp	Gly	Glu	Val	Leu	Ser	Gln	Pro	Ile	Asn	Leu	Asp	Leu	Arg	Lys
	355						360					365			
Met	Asn	Ala	Val	Ala	Ile	Val	Gly	Pro	Asn	Gly	Ile	Gly	Lys	Ser	Thr
	370					375					380				
Phe	Ile	Lys	Ser	Ile	Val	Asp	Gln	Ile	Pro	Phe	Ile	Lys	Gly	Glu	Lys
385				390						395				400	
Arg	Phe	Gly	Ala	Asn	Val	Glu	Val	Gly	Tyr	Tyr	Asp	Gln	Thr	Gln	Ser
			405						410					415	

Lys	Leu	Thr	Pro	Ser	Asn	Thr	Val	Leu	Asp	Glu	Leu	Trp	Asn	Asp	Phe
			420					425					430		
Lys	Leu	Thr	Pro	Glu	Val	Glu	Ile	Arg	Asn	Arg	Leu	Gly	Ala	Phe	Leu
		435					440					445			
Phe	Ser	Gly	Asp	Asp	Val	Lys	Lys	Ser	Val	Gly	Met	Leu	Ser	Gly	Gly
	450					455					460				
Glu	Lys	Ala	Arg	Leu	Leu	Leu	Ala	Lys	Leu	Ser	Met	Glu	Asn	Asn	Asn
465					470					475					480
Phe	Leu	Ile	Leu	Asp	Glu	Pro	Thr	Asn	His	Leu	Asp	Ile	Asp	Ser	Lys
			485						490					495	
Glu	Val	Leu	Glu	Asn	Ala	Leu	Ile	Asp	Phe	Asp	Gly	Thr	Leu	Leu	Phe
		500						505					510		
Val	Ser	His	Asp	Arg	Tyr	Phe	Ile	Asn	Arg	Val	Ala	Thr	His	Val	Leu
	515						520					525			
Glu	Leu	Ser	Glu	Asn	Gly	Ser	Thr	Leu	Tyr	Leu	Gly	Asp	Tyr	Asp	Tyr
	530					535					540				
Tyr	Val	Glu	Lys	Lys	Ala	Thr	Ala	Glu	Met	Ser	Gln	Thr	Glu	Glu	Ala
545					550					555					560
Ser	Thr	Ser	Asn	Gln	Ala	Lys	Glu	Ala	Ser	Pro	Val	Asn	Asp	Tyr	Gln
			565						570					575	
Ala	Gln	Lys	Glu	Ser	Gln	Lys	Glu	Val	Arg	Lys	Leu	Met	Arg	Gln	Ile
		580						585					590		
Glu	Ser	Leu	Glu	Ala	Glu	Ile	Glu	Glu	Leu	Glu	Ser	Gln	Ser	Gln	Ala
	595						600					605			
Ile	Ser	Glu	Gln	Met	Leu	Glu	Thr	Asn	Asp	Ala	Asp	Lys	Leu	Met	Glu
	610					615					620				
Leu	Gln	Ala	Glu	Leu	Asp	Lys	Ile	Ser	His	Arg	Gln	Glu	Glu	Ala	Met
625					630					635					640
Leu	Glu	Trp	Glu	Glu	Leu	Ser	Asp	Gln	Val						
			645					650							

(2) INFORMATION FOR SEQ ID NO:3850:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3850:

Ser	Asn	Asn	Asp	Leu	Ala	Lys	Cys	Lys	Lys	Tyr	Glu	Glu	Phe	Gly	Leu
1				5				10						15	
Asp	Ser	Leu	Leu	Gln	Glu	Thr	Arg	Gly	Gly	Arg	Asn	His	Ala	Tyr	Met
		20						25					30		
Thr	Val	Glu	Glu	Lys	Ala	Phe	Leu	Ala	Arg	His	Leu	Lys	Ala	Thr	
	35					40					45				

```

Glu Ala Gly Glu Phe Val Thr Ile Asp Ala Leu Phe Gln Ala Tyr Lys
 50          55          60
Lys Glu Leu Gly Arg Ser Tyr Thr Arg Asp Ala Phe Tyr Gln Leu Leu
65          70          75          80
Lys His His Gly Trp Arg Asn Ile Met Pro Arg Pro Glu His Pro Arg
          85          90          95
Lys Ala Asp Ala Gln Thr Ile Val Ala Ser Lys Asn Lys Ile Ser Ile
          100          105          110
Gln Glu Gly Lys Lys Ala Leu
          115

```

(2) INFORMATION FOR SEQ ID NO:3851:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...221

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3851:

```

Ala Cys Asn Glu Gln Leu Pro Asp Glu Met Thr Leu Ala Lys Gln Phe
 1          5          10          15
Ala Cys Ser Arg Met Thr Ile Lys Lys Ala Leu Asp Leu Leu Val Ser
          20          25          30
Glu Gly Leu Ile Phe Arg Lys Arg Gly Gln Gly Ser Phe Val Leu Ser
          35          40          45
Arg Gly Ser Ser Lys Arg Lys Leu Ile Val Pro Glu Arg Asp Ile Arg
          50          55          60
Gly Leu Thr Lys Ile Ser Glu Asp Ala His Ser Thr Ile Asp Ser Arg
          65          70          75          80
Ile Ile His Phe Lys Leu Glu Phe Ala Asn Glu Phe Leu Ala Glu Lys
          85          90          95
Leu Gln Val Ala Leu Gln Ser Pro Val Tyr Asn Ile Tyr Arg Leu Arg
          100          105          110
Ile Ile Asp Gly Lys Pro Tyr Val Leu Glu Gln Thr Tyr Met Ser Thr
          115          120          125
Asp Val Ile Pro Gly Ile Thr Glu Asp Ile Leu Gln Lys Ser Ile Tyr
          130          135          140
Asn Tyr Ile Glu Gly Lys Leu Gly Leu His Ile Ala Ser Ala Thr Lys
          145          150          155          160
Ile Leu Arg Ala Ser Ser Ser Ser Glu Asn Glu Gln His Tyr Leu Gln
          165          170          175
Leu Leu Pro Thr Glu Pro Val Phe Glu Val Glu Gln Val Ala Tyr Leu
          180          185          190
Asp Asn Gly Thr Pro Phe Glu Tyr Ser Ile Ser Arg His Arg Tyr Asp
          195          200          205

```

Leu Phe Glu Phe Asn Ser Phe Ala Leu Arg His Ser Ser
 210 215 220

(2) INFORMATION FOR SEQ ID NO:3852:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...463

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3852:

Phe	Lys	Asn	Glu	Leu	Lys	Ile	Glu	Lys	Asp	Phe	Ile	Thr	Met	Gly	Lys
1				5					10					15	
Tyr	Phe	Gly	Thr	Asp	Gly	Val	Arg	Gly	Glu	Ala	Asn	Leu	Glu	Leu	Thr
			20					25					30		
Pro	Glu	Leu	Ala	Phe	Lys	Leu	Gly	Arg	Phe	Gly	Gly	Tyr	Val	Leu	Ser
		35					40					45			
Gln	His	Glu	Thr	Glu	Ala	Pro	Lys	Val	Phe	Val	Gly	Arg	Asp	Thr	Arg
	50					55					60				
Ile	Ser	Gly	Glu	Met	Leu	Glu	Ser	Ala	Leu	Val	Ala	Gly	Leu	Leu	Ser
65					70					75				80	
Val	Gly	Ile	His	Val	Tyr	Lys	Leu	Gly	Val	Leu	Ala	Thr	Pro	Ala	Val
			85						90					95	
Ala	Tyr	Leu	Val	Glu	Thr	Glu	Gly	Ala	Ser	Ala	Gly	Val	Met	Ile	Ser
		100						105					110		
Ala	Ser	His	Asn	Pro	Ala	Leu	Asp	Asn	Gly	Ile	Lys	Phe	Phe	Gly	Gly
		115					120					125			
Asp	Gly	Phe	Lys	Leu	Asp	Asp	Glu	Lys	Glu	Ala	Glu	Ile	Glu	Ala	Leu
	130					135					140				
Leu	Asp	Ala	Glu	Glu	Asp	Thr	Leu	Pro	Arg	Pro	Ser	Ala	Glu	Gly	Leu
145					150					155				160	
Gly	Ile	Leu	Val	Asp	Tyr	Pro	Glu	Gly	Leu	Arg	Lys	Tyr	Glu	Gly	Tyr
			165						170					175	
Arg	Val	Ser	Thr	Gly	Thr	Pro	Leu	Asp	Gly	Met	Lys	Val	Ala	Leu	Asp
		180						185					190		
Thr	Ala	Asn	Gly	Ala	Ala	Ser	Thr	Ser	Ala	Arg	Gln	Ile	Phe	Ala	Asp
		195					200					205			
Leu	Gly	Ala	Gln	Leu	Thr	Val	Ile	Gly	Glu	Thr	Pro	Asp	Gly	Leu	Asn
	210					215					220				
Ile	Asn	Leu	Asn	Val	Gly	Ser	Thr	His	Pro	Glu	Ala	Leu	Gln	Glu	Val
225				230						235				240	
Val	Lys	Glu	Ser	Gly	Ser	Ala	Ile	Gly	Leu	Ala	Phe	Asp	Gly	Asp	Ser
			245						250					255	
Asp	Arg	Leu	Ile	Ala	Val	Asp	Glu	Asn	Gly	Asp	Ile	Val	Asp	Gly	Asp
		260						265					270		

Lys	Ile	Met	Tyr	Ile	Ile	Gly	Lys	Tyr	Leu	Ser	Glu	Lys	Gly	Gln	Leu
	275						280					285			
Ala	Gln	Asn	Thr	Ile	Val	Thr	Thr	Val	Met	Ser	Asn	Leu	Gly	Phe	His
	290					295					300				
Lys	Ala	Leu	Asn	Arg	Glu	Gly	Ile	Asn	Lys	Ala	Val	Thr	Ala	Val	Gly
305					310					315					320
Asp	Arg	Tyr	Val	Val	Glu	Glu	Met	Arg	Lys	Ser	Gly	Tyr	Asn	Leu	Gly
			325						330					335	
Gly	Glu	Gln	Ser	Gly	His	Val	Ile	Leu	Met	Asp	Tyr	Asn	Thr	Thr	Gly
			340					345					350		
Asp	Gly	Gln	Leu	Ser	Ala	Val	Gln	Leu	Thr	Lys	Ile	Met	Lys	Glu	Thr
		355					360					365			
Gly	Lys	Ser	Leu	Ser	Glu	Leu	Ala	Ala	Glu	Val	Thr	Ile	Tyr	Pro	Gln
	370					375					380				
Lys	Leu	Val	Asn	Ile	Arg	Val	Glu	Asn	Val	Met	Lys	Glu	Lys	Ala	Met
385					390					395					400
Glu	Val	Pro	Ala	Ile	Lys	Ala	Ile	Ile	Glu	Lys	Met	Glu	Glu	Glu	Met
				405					410					415	
Ala	Gly	Asn	Gly	Arg	Ile	Leu	Val	Arg	Pro	Ser	Gly	Thr	Glu	Pro	Leu
		420						425					430		
Leu	Arg	Val	Met	Ala	Glu	Ala	Pro	Thr	Thr	Glu	Glu	Val	Asp	Tyr	Tyr
	435						440					445			
Val	Asp	Thr	Ile	Thr	Asp	Val	Val	Arg	Ala	Glu	Ile	Gly	Ile	Asp	
	450					455					460				

(2) INFORMATION FOR SEQ ID NO:3853:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...335

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3853:

Ser	Glu	Asp	Asp	Leu	Ile	Lys	Thr	Asp	Asn	Arg	Thr	Ser	Tyr	Thr	Val
1				5					10					15	
Gln	Tyr	Gly	Asp	Thr	Leu	Ser	Thr	Ile	Ala	Glu	Ala	Leu	Gly	Val	Asp
			20					25					30		
Val	Thr	Val	Leu	Ala	Asn	Leu	Asn	Lys	Ile	Thr	Asn	Met	Asp	Leu	Ile
		35					40					45			
Phe	Pro	Glu	Thr	Val	Leu	Thr	Thr	Thr	Val	Asn	Glu	Ala	Glu	Glu	Val
	50					55					60				
Thr	Glu	Val	Glu	Ile	Gln	Thr	Pro	Gln	Ala	Asp	Ser	Ser	Glu	Glu	Val
65					70					75					80
Thr	Thr	Ala	Thr	Ala	Asp	Leu	Thr	Thr	Asn	Gln	Val	Thr	Val	Asp	Asp
				85					90					95	

Gln	Thr	Val	Gln	Val	Ala	Asp	Leu	Ser	Gln	Pro	Ile	Ala	Glu	Val	Thr	100	105	110
Lys	Thr	Val	Ile	Ala	Ser	Glu	Glu	Val	Ala	Pro	Ser	Thr	Gly	Thr	Ser	115	120	125
Val	Pro	Glu	Glu	Gln	Thr	Thr	Glu	Thr	Thr	Arg	Pro	Val	Glu	Glu	Ala	130	135	140
Thr	Pro	Gln	Glu	Thr	Thr	Pro	Ala	Glu	Lys	Gln	Glu	Thr	Gln	Ala	Ser	145	150	155
Pro	Gln	Ala	Ala	Ser	Ala	Val	Glu	Val	Thr	Thr	Thr	Ser	Ser	Glu	Ala	165	170	175
Lys	Glu	Val	Ala	Ser	Ser	Asn	Gly	Ala	Thr	Ala	Ala	Val	Ser	Thr	Tyr	180	185	190
Gln	Pro	Glu	Glu	Thr	Lys	Ile	Ile	Ser	Thr	Thr	Tyr	Glu	Ala	Pro	Ala	195	200	205
Ala	Pro	Asp	Tyr	Ala	Gly	Leu	Ala	Val	Ala	Lys	Ser	Glu	Asn	Ala	Gly	210	215	220
Leu	Gln	Pro	Gln	Thr	Ala	Ala	Phe	Lys	Glu	Glu	Ile	Ala	Asn	Leu	Phe	225	230	235
Gly	Ile	Thr	Ser	Phe	Ser	Gly	Tyr	Arg	Pro	Gly	Asp	Ser	Gly	Asp	His	245	250	255
Gly	Lys	Gly	Leu	Ala	Ile	Asp	Phe	Met	Val	Pro	Glu	Arg	Ser	Glu	Leu	260	265	270
Gly	Asp	Lys	Ile	Ala	Glu	Tyr	Ala	Ile	Gln	Asn	Met	Ala	Ser	Arg	Gly	275	280	285
Ile	Ser	Tyr	Ile	Ile	Trp	Lys	Gln	Arg	Phe	Tyr	Ala	Pro	Phe	Asp	Ser	290	295	300
Lys	Tyr	Gly	Pro	Ala	Asn	Thr	Trp	Asn	Pro	Met	Pro	Asp	Arg	Gly	Ser	305	310	315
Val	Thr	Glu	Asn	His	Tyr	Asp	His	Val	His	Val	Ser	Met	Asn	Gly		325	330	335

(2) INFORMATION FOR SEQ ID NO:3854:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...65

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3854:

Ala	Gln	Asp	Asp	Gln	Glu	Asp	Leu	Thr	Ala	Ile	Val	Arg	Asp	His	Phe	1	5	10	15
Ser	Asp	Met	Gly	Glu	Ile	Ala	Thr	Leu	Tyr	Val	Gln	Val	Tyr	Glu	Ser	20	25	30	
Ser	Leu	Glu	Ser	Leu	Leu	Gly	Gly	Val	Ile	Phe	Glu	Asp	Gly	Arg	His				

	35		40		45
Tyr	Thr	Phe	Val	Tyr	Glu
		Asn	Glu	Asp	Leu
			Val	Tyr	Glu
				Glu	Glu
				Val	
Leu					
65					

(2) INFORMATION FOR SEQ ID NO:3855:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 72 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...72
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3855:

Arg	Ile	Cys	Glu	Ile	Cys	Leu	Lys	Gln	Glu	Lys	Gln	Leu	Leu	Leu	Lys
1			5				10					15			
Leu	Leu	Pro	Cys	Trp	Ile	Asn	Gln	Glu	Gly	Arg	Val	Val	Glu	Ile	Glu
			20				25					30			
Ala	Asp	Tyr	Thr	Cys	Phe	Thr	Ile	Pro	Asn	Glu	Phe	Val	Val	Gly	Tyr
			35				40					45			
Gly	Leu	Asp	Tyr	Lys	Glu	Asn	Tyr	Arg	Asn	Leu	Pro	Tyr	Ile	Gly	Val
			50			55					60				
Leu	Lys	Glu	Glu	Val	Tyr	Ser	Asn								
65						70									

(2) INFORMATION FOR SEQ ID NO:3856:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 76 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...76
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3856:

Thr	Phe	Cys	Glu	Thr	Lys	Ile	Gln	His	Asn	Lys	Thr	Met	Asn	Asp	Glu
1				5					10					15	
Ala	Ser	Lys	Gln	Leu	Arg	Asp	Ser	Arg	Phe	Lys	Ser	Leu	Ala	Gly	Val
			20					25					30		
Gln	Arg	Thr	Thr	Phe	Glu	Glu	Met	Leu	Ala	Val	Leu	Lys	Thr	Thr	Tyr
		35					40					45			
Gln	Arg	Lys	His	Ala	Lys	Gly	Gly	Arg	Lys	Thr	Lys	Leu	Ser	Leu	Asp
		50				55					60				
Asp	Leu	Leu	Met	Val	Thr	Ile	Gln	Tyr	Met	Arg	Glu				
65					70					75					

(2) INFORMATION FOR SEQ ID NO:3857:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 312 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...312

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3857:

Ser	Leu	Arg	Glu	Thr	Thr	Asp	Tyr	Val	Glu	Val	Ser	Lys	Asn	Ile	Gln
1				5				10						15	
Glu	Arg	Val	Ala	Phe	Ser	Cys	Gly	Lys	Pro	Ala	Trp	Asn	Tyr	Cys	Ser
			20					25					30		
Asp	Cys	Lys	Cys	Leu	His	Ser	Lys	Tyr	Gln	Ser	Cys	Arg	Arg	Ile	Thr
		35					40					45			
Val	Ser	Lys	Ile	Thr	Thr	Ser	Leu	Phe	Gln	Glu	Met	Val	Gln	Ala	Ala
		50				55					60				
Ser	Thr	Arg	Leu	Asn	Lys	Gln	Ala	Glu	Tyr	Val	Asn	Ser	Leu	Asn	Val
65				70						75				80	
Phe	Pro	Val	Pro	Asp	Gly	Asp	Thr	Gly	Thr	Asn	Met	Gly	Met	Thr	Ile
			85					90						95	
Glu	Asn	Gly	Ala	Lys	Glu	Val	Ala	Asp	Lys	Pro	Ala	Ser	Thr	Val	Gly
		100						105					110		
Glu	Val	Ala	Ser	Ile	Leu	Ala	Lys	Gly	Leu	Leu	Met	Gly	Ala	Arg	Gly
		115					120					125			
Asn	Ser	Gly	Val	Ile	Thr	Ser	Gln	Leu	Phe	Arg	Gly	Phe	Ser	Gln	Ala
		130				135					140				
Ile	Lys	Asp	Lys	Asp	Glu	Leu	Thr	Gly	Gln	Asp	Leu	Ala	Leu	Ala	Phe
145				150					155					160	
Gln	Ser	Gly	Val	Glu	Val	Ala	Tyr	Lys	Ala	Val	Met	Lys	Pro	Val	Glu
			165					170					175		
Gly	Thr	Ile	Leu	Thr	Val	Ser	Arg	Gly	Ala	Ala	Ile	Gly	Ala	Lys	Lys
		180					185					190			
Lys	Ala	Glu	Gln	Thr	Asp	Asp	Ala	Val	Glu	Val	Met	Arg	Ala	Ala	Leu

		195					200				205								
Glu	Gly	Ala	Lys	Thr	Ala	Leu	Ala	Lys	Thr	Pro	Asp	Met	Leu	Pro	Val				
	210					215					220								
Leu	Lys	Glu	Val	Gly	Val	Val	Asp	Ser	Gly	Gly	Gln	Gly	Leu	Val	Phe				
225					230					235					240				
Ile	Tyr	Glu	Gly	Phe	Leu	Ser	Ala	Leu	Thr	Gly	Glu	Tyr	Ile	Ala	Ser				
			245						250				255						
Glu	Asp	Phe	Val	Ala	Thr	Pro	Ala	Asn	Met	Ser	Glu	Met	Ile	Thr	Val				
		260						265					270						
Glu	His	His	Lys	Ser	Val	Ala	Gly	His	Val	Ala	Thr	Glu	Asp	Ile	Thr				
	275						280					285							
Phe	Cys	Tyr	Cys	Thr	Glu	Ile	Met	Val	Ala	Leu	Lys	Gln	Gly	Pro	Thr				
	290					295					300								
Tyr	Ala	Lys	Asp	Phe	Asp	Tyr	Glu												
305					310														

(2) INFORMATION FOR SEQ ID NO:3858:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 550 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...550

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3858:

Gly	Glu	Ser	Glu	Arg	Ser	Lys	Lys	Ser	Phe	Gly	Arg	Glu	Gln	Ala	Ala				
1			5					10						15					
Asn	Leu	Lys	Tyr	Gln	Gln	Glu	Leu	Val	Lys	Tyr	Ile	Lys	Tyr	Thr	Arg				
	20						25					30							
Glu	Asn	Asn	Ser	Thr	Lys	Arg	Thr	Glu	Ala	Glu	Lys	Val	Met	Thr	Ala				
	35					40					45								
Ala	Lys	Lys	Glu	His	Glu	Lys	Lys	Gln	Thr	Glu	Leu	Ala	Lys	Val	Leu				
	50				55			60											
Ala	Lys	Val	Ile	Pro	Ser	Ala	Glu	Glu	Leu	Glu	Asn	Thr	Arg	Gln	Lys				
65				70				75						80					
Ala	Glu	Lys	Ala	Lys	Glu	Lys	Glu	Pro	Glu	Leu	Thr	Lys	Lys	Leu	Glu				
	85						90						95						
Glu	Ala	Lys	Ala	Lys	Ser	Glu	Glu	Ala	Glu	Lys	Lys	Ala	Thr	Glu	Ala				
	100						105					110							
Lys	Gln	Lys	Val	Asp	Ala	Glu	His	Ala	Glu	Glu	Val	Val	Pro	Gln	Ala				
	115					120					125								
Lys	Ile	Ala	Glu	Leu	Glu	Asn	Glu	Val	Gln	Lys	Leu	Glu	Lys	Asp	Leu				
	130				135			140											
Lys	Glu	Ile	Asp	Glu	Ser	Asp	Ser	Glu	Asp	Tyr	Val	Lys	Glu	Gly	Leu				
145				150				155						160					
Arg	Ala	Pro	Leu	Gln	Ser	Glu	Leu	Asp	Ala	Lys	Gln	Ala	Lys	Leu	Ser				

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3859:

```

Arg Gly Ser Asp Val Met Ala Arg Glu Gly Phe Phe Thr Gly Leu Asp
1      5      10      15
Ile Gly Thr Ser Ser Val Lys Val Leu Val Ala Glu Gln Arg Asn Gly
      20      25      30
Glu Leu Asn Val Ile Gly Val Ser Asn Ala Lys Ser Lys Gly Val Lys
      35      40      45
Asp Gly Ile Ile Val Asp Ile Asp Thr Ala Ala Thr Ala Ile Lys Ser
      50      55      60
Ala Ile Ser Gln Ala Glu Glu Lys Ala Gly Ile Ser Ile Lys Ser Val
      65      70      75      80
Asn Val Gly Leu Pro Gly Asn Leu Leu Gln Val Glu Pro Thr Gln Gly
      85      90      95
Met Ile Pro Val Thr Ser Asp Thr Lys Glu Ile Thr Asp Gln Asp Val
      100     105     110
Glu Asn Val Val Lys Ser Ala Leu Thr Lys Ser Met Thr Pro Asp Arg
      115     120     125
Glu Val Ile Thr Phe Ile Pro Glu Glu Phe Ile Val Asp Gly Phe Gln
      130     135     140
Gly Ile Arg Asp Pro Arg Gly Met Met Gly Val Arg Leu Glu Met Arg
      145     150     155     160
Gly Leu Leu Tyr Thr Gly Pro Arg Thr Ile Leu His Asn Leu Arg Lys
      165     170     175
Thr Val Glu Arg Ala Gly Val Gln Val Glu Asn Val Ile Ile Ser Pro
      180     185     190
Leu Ala Met Val Gln Ser Val Leu Asn Glu Gly Glu Arg Glu Phe Gly
      195     200     205
Ala Thr Val Ile Asp Met Gly Ala Gly Gln Thr Thr Val Ala Thr Ile
      210     215     220
Arg Asn Gln Glu Leu Gln Phe Thr His Ile Leu Gln Glu Gly Gly Asp
      225     230     235     240
Tyr Val Thr Lys Asp Ile Ser Lys Val Leu Lys Thr Ser Arg Lys Leu
      245     250     255
Ala Glu Gly Leu Lys Leu Asn Tyr Gly Glu Ala Tyr Pro Pro Leu Ala
      260     265     270
Ser Lys Glu Thr Phe Gln Val Glu Val Ile Gly Glu Val Glu Ala Val
      275     280     285
Glu Val Thr Glu Ala Tyr Leu Ser Glu Ile Ile Ser Ala Arg Ile Lys
      290     295     300
His Ile Leu Glu Gln Ile Lys Gln Glu Leu Asp Arg Arg Arg Leu Leu
      305     310     315     320
Asp Leu Pro Gly Gly Ile Val Leu Ile Gly Gly Asn Ala Ile Leu Pro
      325     330     335
Gly Met Val Glu Leu Ala Gln Glu Val Phe Gly Val Arg Val Lys Leu

```

		340				345				350					
Tyr	Val	Pro	Asn	Gln	Val	Gly	Ile	Arg	Asn	Pro	Ala	Phe	Ala	His	Val
		355				360					365				
Ile	Ser	Leu	Ser	Glu	Phe	Ala	Gly	Gln	Leu	Thr	Glu	Val	Asn	Leu	Leu
		370				375					380				
Ala	Gln	Gly	Ala	Ile	Lys	Gly	Glu	Asn	Asp	Leu	Ser	His	Gln	Pro	Ile
385					390					395					400
Ser	Phe	Gly	Gly	Met	Leu	Gln	Lys	Thr	Ala	Gln	Phe	Val	Gln	Ser	Thr
				405					410					415	
Pro	Val	Gln	Pro	Ala	Pro	Ala	Pro	Glu	Val	Glu	Pro	Val	Ala	Pro	Thr
			420					425					430		
Glu	Pro	Met	Ala	Asp	Phe	Gln	Gln	Ala	Ser	Gln	Asn	Lys	Pro	Lys	Leu
		435						440				445			
Ala	Asp	Arg	Phe	Arg	Gly	Leu	Ile	Gly	Ser	Met	Phe	Asp	Glu		
		450				455					460				

(2) INFORMATION FOR SEQ ID NO:3860:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...70

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3860:

Trp	Val	Gly	Glu	Lys	Leu	Gln	Ser	Gly	Glu	Tyr	Glu	Ile	Arg	Thr	Leu
1				5					10					15	
Phe	Phe	Asp	Val	Gln	Ser	His	Gln	Asn	Pro	Phe	Phe	Lys	Ile	Val	Lys
			20					25					30		
Val	Pro	Glu	Thr	Lys	Gly	Phe	Ala	Leu	Asp	Asn	Leu	Asn	Gln	Ile	Ile
		35					40					45			
Gly	Arg	Phe	Lys	Phe	Ser	Val	Gly	Ile	Arg	Gln	Leu	Lys	Cys	Val	Asp
		50				55					60				
Asn	Leu	Ile	Ser	Ile	Pro										
65					70										

(2) INFORMATION FOR SEQ ID NO:3861:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...73

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3861:

```
Phe Leu Gly Asp Gln Arg Ser Leu Ser Arg Pro Ser Val Ser Leu Val
1          5          10          15
Pro Val Asn Asp Pro Thr Leu Leu Trp Ile Asn Ser Gly Val Ala Thr
          20          25          30
Leu Lys Lys Tyr Phe Asp Gly Thr Ile Ile Pro Glu Asn Pro Arg Ile
          35          40          45
Thr Asn Ala Gln Lys Ala Ile Arg Thr Asn Asp Ile Glu Asn Val Gly
          50          55          60
Gln Asp Cys Ala Ser Pro Tyr His Val
65          70
```

(2) INFORMATION FOR SEQ ID NO:3862:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 88 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...88

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3862:

```
Arg Asn Ser Leu Cys Leu Glu Leu Phe Trp Cys Gly Ser Thr Arg Val
1          5          10          15
Ile Thr Ser Ala Lys Ala Glu Gly Ala Glu Gln Val Ile Leu Thr Asp
          20          25          30
His Asn Glu Phe Gln Gln Ser Val Ser Asp Ile Ala Glu Val Glu Val
          35          40          45
Tyr Gly Val Val Asp His His Arg Val Leu Thr Leu Lys Leu Gln Ala
          50          55          60
His Phe Thr Cys Val Trp Ser Gln Leu Asp Gln Arg Leu Gln Ser Phe
65          70          75          80
Thr Val Cys Ser Lys Asn Met Val
          85
```

(2) INFORMATION FOR SEQ ID NO:3863:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 173 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3863:

Phe	Ser	Leu	Glu	Asn	Ile	Ile	Arg	Arg	Lys	Leu	Arg	Lys	Met	Ala	Glu	
1				5					10					15		
Lys	Thr	Tyr	Pro	Met	Thr	Leu	Glu	Glu	Lys	Glu	Lys	Leu	Glu	Lys	Glu	
			20					25					30			
Leu	Glu	Glu	Leu	Lys	Leu	Val	Arg	Arg	Pro	Glu	Val	Val	Glu	Arg	Ile	
		35					40					45				
Lys	Ile	Ala	Arg	Ser	Tyr	Gly	Asp	Leu	Ser	Glu	Asn	Ser	Glu	Tyr	Glu	
	50					55					60					
Ala	Ala	Lys	Asp	Glu	Gln	Ala	Phe	Val	Glu	Gly	Gln	Ile	Ser	Ser	Leu	
65					70				75						80	
Glu	Thr	Lys	Ile	Arg	Tyr	Ala	Glu	Ile	Val	Asn	Ser	Asp	Ala	Val	Ala	
			85						90					95		
Gln	Asp	Glu	Val	Ala	Ile	Gly	Lys	Thr	Val	Thr	Ile	Gln	Glu	Ile	Gly	
		100						105					110			
Glu	Asp	Glu	Glu	Glu	Val	Tyr	Ile	Ile	Val	Gly	Ser	Ala	Gly	Ala	Asp	
	115					120						125				
Ala	Phe	Ala	Gly	Lys	Val	Ser	Asn	Glu	Ser	Pro	Ile	Gly	Gln	Ala	Leu	
	130					135						140				
Ile	Gly	Lys	Lys	Thr	Gly	Asp	Thr	Ala	Thr	Ile	Glu	Thr	Pro	Val	Gly	
145					150					155					160	
Ser	Tyr	Asp	Val	Lys	Ile	Leu	Lys	Val	Glu	Lys	Thr	Ala				
			165						170							

(2) INFORMATION FOR SEQ ID NO:3864:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 171 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...171

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3864:

Ser	Met	Leu	Glu	Asn	Gly	Asp	Leu	Ile	Phe	Val	Arg	Asp	Gly	Ser	Asp
1				5					10					15	
Met	Gly	Gln	Ala	Ile	Gln	Thr	Ser	Thr	Gly	Asn	Tyr	Ser	His	Val	Ala
		20						25					30		
Ile	Tyr	Leu	Asp	Gly	Met	Ile	Tyr	His	Ala	Ser	Gly	Gln	Ala	Gly	Val
		35					40					45			
Val	Cys	Gln	Glu	Pro	Ala	Asp	Phe	Phe	Glu	Ser	Asn	His	Leu	Tyr	Asp
	50					55					60				
Leu	Tyr	Val	Tyr	Pro	Glu	Met	Asp	Ile	Gln	Ser	Val	Lys	Glu	Arg	Ala
65					70				75					80	
Cys	Arg	His	Leu	Gly	Ala	Pro	Tyr	Asn	Ala	Ser	Phe	Tyr	Pro	Asp	Ala
			85						90					95	
Ala	Gly	Phe	Tyr	Cys	Ser	Gln	Tyr	Ile	Ala	Glu	Ile	Leu	Pro	Ile	Phe
			100					105					110		
Glu	Thr	Ile	Pro	Met	Lys	Phe	Gly	Asp	Gly	Glu	Gln	Glu	Ile	Ser	Asp
	115						120					125			
Phe	Trp	Arg	Glu	Tyr	Tyr	Ile	Glu	Leu	Gly	Leu	Pro	Val	Pro	Leu	Asn
	130					135					140				
Gln	Ala	Gly	Thr	Asn	Pro	Ser	Gln	Leu	Ala	Ala	Ser	Pro	Leu	Leu	Gln
145					150					155					160
Cys	Lys	Glu	Arg	Asn	Leu	His	Asp	Ser	Asp	Phe					
				165					170						

(2) INFORMATION FOR SEQ ID NO:3865:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...140

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3865:

Lys	Met	Leu	Glu	Asn	Asp	Ile	Lys	Lys	Val	Leu	Val	Ser	His	Asp	Glu
1				5					10					15	
Ile	Thr	Glu	Ala	Ala	Lys	Lys	Leu	Gly	Ala	Gln	Leu	Thr	Lys	Asp	Tyr
		20						25					30		
Ala	Gly	Lys	Asn	Pro	Ile	Leu	Val	Gly	Ile	Leu	Lys	Gly	Ser	Ile	Pro
		35					40					45			
Phe	Met	Ala	Glu	Leu	Val	Lys	His	Ile	Asp	Thr	His	Ile	Glu	Met	Asp
	50					55					60				
Phe	Met	Met	Val	Ser	Ser	Tyr	His	Gly	Gly	Thr	Ala	Ser	Ser	Gly	Val
65					70				75					80	
Ile	Asn	Ile	Lys	Gln	Asp	Val	Thr	Gln	Asp	Ile	Lys	Gly	Arg	His	Val

				85					90					95					
Leu	Phe	Val	Glu	Asp	Ile	Ile	Asp	Thr	Gly	Gln	Thr	Leu	Lys	Asn	Leu				
			100					105					110						
Arg	Asp	Met	Phe	Lys	Ala	Arg	Glu	Ala	Ala	Ser	Val	Lys	Ile	Ala	Thr				
		115					120					125							
Leu	Leu	Asp	Lys	Pro	Arg	Arg	Thr	Cys	Cys	Arg	Asn								
	130					135					140								

(2) INFORMATION FOR SEQ ID NO:3866:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...287

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3866:

Lys	Gly	Leu	Glu	Met	Ile	Leu	Ile	Thr	Gly	Ala	Asn	Gly	Gln	Leu	Gly				
1				5				10						15					
Thr	Glu	Leu	Arg	Tyr	Leu	Leu	Asp	Glu	Arg	Asn	Glu	Glu	Tyr	Val	Ala				
			20					25					30						
Val	Asp	Val	Ala	Lys	Met	Asp	Ile	Thr	Asn	Glu	Glu	Met	Val	Glu	Lys				
		35				40						45							
Val	Phe	Glu	Glu	Val	Lys	Pro	Thr	Leu	Val	Tyr	His	Cys	Ala	Ala	Tyr				
	50				55						60								
Thr	Ala	Val	Asp	Ala	Ala	Glu	Asp	Glu	Gly	Lys	Glu	Leu	Asp	Phe	Ala				
65					70					75				80					
Ile	Asn	Val	Thr	Gly	Thr	Lys	Asn	Val	Ala	Lys	Ala	Ser	Glu	Lys	His				
			85					90					95						
Gly	Ala	Thr	Leu	Val	Tyr	Ile	Ser	Thr	Asp	Tyr	Val	Phe	Asp	Gly	Lys				
		100						105					110						
Lys	Pro	Val	Gly	Gln	Glu	Trp	Glu	Val	Asp	Asp	Arg	Pro	Asp	Pro	Gln				
		115				120					125								
Thr	Glu	Tyr	Gly	Arg	Thr	Lys	Arg	Met	Gly	Glu	Glu	Leu	Val	Glu	Lys				
	130					135					140								
His	Val	Ser	Asn	Phe	Tyr	Ile	Ile	Arg	Thr	Ala	Trp	Val	Phe	Gly	Asn				
145					150					155				160					
Tyr	Gly	Lys	Asn	Phe	Val	Phe	Thr	Met	Gln	Asn	Leu	Ala	Lys	Thr	His				
		165						170					175						
Lys	Thr	Leu	Thr	Val	Val	Asn	Asp	Gln	Tyr	Gly	Arg	Pro	Thr	Trp	Thr				
		180						185					190						
Arg	Thr	Leu	Ala	Glu	Phe	Met	Thr	Tyr	Leu	Ala	Glu	Asn	Arg	Lys	Glu				
		195				200						205							
Phe	Gly	Tyr	Tyr	His	Leu	Ser	Asn	Asp	Ala	Thr	Glu	Asp	Thr	Thr	Trp				
	210					215					220								
Tyr	Asp	Phe	Ala	Val	Glu	Ile	Leu	Lys	Asp	Thr	Asp	Val	Glu	Val	Lys				

225		230		235		240									
Pro	Val	Asp	Ser	Ser	Gln	Phe	Pro	Ala	Lys	Ala	Lys	Arg	Pro	Leu	Asn
		245		250		255									
Ser	Thr	Met	Ser	Leu	Ala	Lys	Ala	Lys	Ala	Thr	Gly	Phe	Val	Ile	Pro
		260		265		270									
Thr	Trp	Gln	Asp	Ala	Leu	Gln	Glu	Phe	Tyr	Lys	Gln	Glu	Val	Arg	
	275				280						285				

(2) INFORMATION FOR SEQ ID NO:3867:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3867:

Lys	Leu	Leu	Glu	Glu	Gly	Lys	Met	Lys	Thr	Arg	Lys	Ile	Pro	Leu	Arg
1			5						10					15	
Lys	Ser	Val	Val	Ser	Asn	Glu	Val	Ile	Asp	Lys	Arg	Asp	Leu	Leu	Arg
		20						25					30		
Ile	Val	Lys	Asn	Lys	Glu	Gly	Gln	Val	Phe	Ile	Asp	Pro	Thr	Gly	Lys
		35				40						45			
Ala	Asn	Gly	Arg	Gly	Ala	Tyr	Ile	Lys	Leu	Asp	Asn	Ala	Glu	Ala	Leu
	50					55				60					
Glu	Ala	Lys	Lys	Lys	Lys	Val	Phe	Asn	Arg	Ser	Phe	Ser	Met	Glu	Val
65					70					75				80	
Glu	Glu	Ser	Phe	Tyr	Asp	Glu	Leu	Ile	Ala	Tyr	Val	Asp	His	Lys	Val
			85					90						95	
Lys	Arg	Arg	Glu	Leu	Gly	Leu	Glu								
			100												

(2) INFORMATION FOR SEQ ID NO:3868:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...163

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3868:

```

Asn Gln Leu Asp Cys Asn His Val Val Ser Arg Asp Asp Leu Asn Leu
1      5      10      15
Val Tyr Asp Tyr Leu Phe Gln Lys Glu Arg Trp Glu Ser Tyr Glu Ile
      20      25      30
Thr Leu Ile Gly Asn Leu Tyr His Leu Phe Glu Thr Asp Tyr Ile Tyr
      35      40      45
Met Val Gly Lys Glu Ile Leu Glu Arg Thr His Tyr Tyr Glu Lys Ile
      50      55      60
Gly Lys Asn Arg Asn Leu Val Val Ser Ala Cys Leu Asn Phe Trp Phe
65      70      75      80
Cys Cys Leu Glu Asn Ser His Leu Ile Tyr Ala Asp Tyr Phe Glu Met
      85      90      95
Lys Leu Gln Lys Leu Leu Lys Asp Asp Thr Lys Val Phe Glu Lys Ser
      100     105     110
Thr Phe Lys Phe Val Glu Gly Tyr Lys Ile Tyr Leu Thr Glu Ser Lys
      115     120     125
Glu Ser Gly Ile Lys Gln Met Asp Asn Val Ile Lys Tyr Phe Glu Phe
      130     135     140
Ile Glu Ser Lys Ser Ile Ala Leu Tyr Phe Gln Lys Arg Leu Asn Glu
145     150     155     160
Leu Ile Asp
  
```

(2) INFORMATION FOR SEQ ID NO:3869:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 363 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...363

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3869:

```

Arg Lys Leu Glu Val Lys Arg Met Lys Leu Asn Arg Val Val Val Thr
1      5      10      15
Gly Tyr Gly Val Thr Ser Pro Ile Gly Asn Thr Pro Glu Glu Phe Trp
      20      25      30
Asn Ser Leu Ala Thr Gly Lys Ile Gly Ile Gly Gly Ile Thr Lys Phe
      35      40      45
Asp His Ser Asp Phe Asp Val His Asn Ala Ala Glu Ile Gln Asp Phe
      50      55      60
  
```

Pro	Phe	Asp	Lys	Tyr	Phe	Val	Lys	Lys	Asp	Thr	Asn	Arg	Phe	Asp	Asn
65					70				75						80
Tyr	Ser	Leu	Tyr	Ala	Leu	Tyr	Ala	Ala	Gln	Glu	Ala	Val	Asn	His	Ala
				85					90					95	
Asn	Leu	Asp	Val	Glu	Ala	Leu	Asn	Arg	Asp	Arg	Phe	Gly	Val	Ile	Val
			100					105					110		
Ala	Ser	Gly	Ile	Gly	Gly	Ile	Lys	Glu	Ile	Glu	Asp	Gln	Val	Leu	Arg
		115					120					125			
Leu	His	Glu	Lys	Gly	Pro	Lys	Arg	Val	Lys	Pro	Met	Thr	Leu	Pro	Lys
	130					135					140				
Ala	Leu	Pro	Asn	Met	Ala	Ser	Gly	Asn	Val	Ala	Met	Arg	Phe	Gly	Ala
145					150					155					160
Asn	Gly	Val	Cys	Lys	Ser	Ile	Asn	Thr	Ala	Cys	Ser	Ser	Ser	Asn	Asp
			165						170					175	
Ala	Ile	Gly	Asp	Ala	Phe	Arg	Ser	Ile	Lys	Phe	Gly	Phe	Gln	Asp	Val
			180					185					190		
Met	Leu	Val	Gly	Gly	Thr	Glu	Ala	Ser	Ile	Thr	Pro	Phe	Ala	Ile	Ala
		195					200					205			
Gly	Phe	Gln	Ala	Leu	Thr	Ala	Leu	Ser	Thr	Thr	Glu	Asp	Pro	Thr	Arg
	210					215					220				
Ala	Ser	Ile	Pro	Phe	Asp	Lys	Asp	Arg	Asn	Gly	Phe	Val	Met	Gly	Glu
225				230						235					240
Gly	Ser	Gly	Met	Leu	Val	Leu	Glu	Ser	Leu	Glu	His	Ala	Glu	Lys	Arg
			245						250					255	
Gly	Ala	Thr	Ile	Leu	Ala	Glu	Val	Val	Gly	Tyr	Gly	Asn	Thr	Cys	Asp
			260				265						270		
Ala	Tyr	His	Met	Thr	Ser	Pro	His	Pro	Glu	Gly	Gln	Gly	Ala	Ile	Lys
	275						280					285			
Ala	Ile	Lys	Leu	Ala	Leu	Glu	Glu	Ala	Glu	Ile	Ser	Pro	Glu	Gln	Val
	290					295					300				
Ala	Tyr	Val	Asn	Ala	His	Gly	Thr	Ser	Thr	Pro	Ala	Asn	Glu	Lys	Gly
305				310						315					320
Glu	Ser	Gly	Ala	Ile	Val	Ala	Val	Leu	Gly	Lys	Glu	Val	Pro	Val	Ser
			325						330					335	
Ser	Thr	Lys	Ser	Phe	Thr	Gly	His	Leu	Leu	Gly	Ala	Ala	Ala	Cys	Ser
		340					345						350		
Arg	Ser	Tyr	Arg	His	His	Arg	Ser	Tyr	Ala	Ser					
		355					360								

(2) INFORMATION FOR SEQ ID NO:3870:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...84

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3870:

Glu	Gly	Leu	Glu	Ile	Ile	Pro	Tyr	Ser	Ile	Phe	Phe	Phe	Phe	Val	Phe
1				5					10					15	
His	Lys	His	Phe	Ile	Phe	Gly	Phe	Tyr	Asn	Ser	Leu	Thr	Asn	Met	Glu
			20					25					30		
Val	Thr	Asn	Glu	Ser	Asn	Pro	Lys	Ile	Leu	Gly	Leu	Cys	Gln	Gln	Lys
		35					40					45			
Ala	Thr	Glu	Lys	Phe	Tyr	Phe	Ile	Ser	Asp	Phe	Ile	Gly	Leu	Ile	Gly
	50					55					60				
Arg	Asn	Phe	Ser	Leu	Phe	Asp	Ser	Asp	Glu	Val	Gln	Gln	Asn	Ser	Arg
65					70				75						80
Lys	Gln	Ser	Leu												

(2) INFORMATION FOR SEQ ID NO:3871:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 284 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...284

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3871:

Leu	Phe	Ile	Asp	Asn	Met	Ala	Phe	Gly	Leu	Lys	Leu	Arg	Lys	Tyr	Ser
1				5					10					15	
Lys	Glu	Asp	Ile	Asn	Lys	Arg	Val	Gln	Glu	Ala	Ala	Glu	Ile	Leu	Gly
			20					25					30		
Leu	Lys	Glu	Phe	Leu	Glu	Arg	Lys	Pro	Ala	Asp	Leu	Ser	Gly	Gly	Gln
		35					40					45			
Arg	Gln	Arg	Val	Ala	Met	Gly	Arg	Ala	Ile	Val	Arg	Asp	Ala	Lys	Val
	50					55					60				
Phe	Leu	Met	Asp	Glu	Pro	Leu	Ser	Asn	Leu	Asp	Ala	Lys	Leu	Arg	Val
65					70				75						80
Ser	Met	Arg	Ala	Glu	Ile	Ala	Lys	Ile	His	Arg	Arg	Ile	Gly	Ala	Thr
			85						90				95		
Thr	Ile	Tyr	Val	Thr	His	Asp	Gln	Thr	Glu	Ala	Met	Thr	Leu	Ala	Asp
			100						105				110		
Arg	Ile	Val	Ile	Met	Ser	Ala	Thr	Lys	Asn	Pro	Ala	Gly	Thr	Gly	Thr
		115					120					125			
Ile	Gly	Ser	Val	Glu	Gln	Ile	Gly	Thr	Pro	Gln	Glu	Val	Tyr	Lys	Asn
	130					135					140				
Pro	Val	Asn	Lys	Phe	Val	Ala	Gly	Phe	Ile	Gly	Ser	Pro	Ala	Met	Asn
145					150					155					160
Phe	Ile	Asn	Val	Lys	Leu	Val	Gly	Ser	Glu	Ile	Val	Ser	Asp	Gly	Phe
				165					170					175	

Arg	Leu	Lys	Val	Pro	Glu	Gly	Ala	Leu	Lys	Val	Leu	Arg	Glu	Lys	Gly
			180					185					190		
Tyr	Glu	Gly	Lys	Glu	Leu	Ile	Phe	Gly	Ile	Arg	Pro	Glu	Asn	Val	Asn
		195					200					205			
Ala	Glu	Pro	Ala	Phe	Leu	Glu	Thr	Phe	Pro	Asp	Cys	Val	Val	Lys	Ala
		210				215					220				
Thr	Ile	Ser	Val	Ser	Glu	Leu	Leu	Gly	Ser	Glu	Ser	His	Leu	Tyr	Cys
225					230					235					240
Gln	Val	Gly	Lys	Asp	Glu	Phe	Val	Ala	Lys	Val	Asp	Ala	Arg	Asp	Tyr
			245					250						255	
Leu	Gln	Thr	Gly	Ala	Thr	Val	Glu	Leu	Gly	Phe	Asp	Leu	Asn	Lys	Ala
			260				265						270		
His	Phe	Phe	Asp	Val	Glu	Thr	Glu	Lys	Thr	Ile	Tyr				
			275				280								

(2) INFORMATION FOR SEQ ID NO:3872:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...306

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3872:

Pro	Ser	Ile	Glu	Arg	Ile	Phe	Met	Thr	Ser	Lys	Val	Arg	Lys	Ala	Val
1				5					10					15	
Ile	Pro	Ala	Ala	Gly	Leu	Gly	Thr	Arg	Phe	Leu	Pro	Ala	Thr	Lys	Ala
		20					25					30			
Leu	Ala	Lys	Glu	Met	Leu	Pro	Ile	Val	Asp	Lys	Pro	Thr	Ile	Gln	Phe
		35				40					45				
Ile	Val	Glu	Glu	Ala	Leu	Lys	Ser	Gly	Ile	Glu	Asp	Ile	Leu	Val	Val
		50			55					60					
Thr	Gly	Lys	Ser	Lys	Arg	Ser	Ile	Glu	Asp	His	Phe	Asp	Ser	Asn	Phe
65				70					75					80	
Glu	Leu	Glu	Tyr	Asn	Leu	Lys	Glu	Lys	Gly	Lys	Thr	Asp	Leu	Leu	Lys
			85				90						95		
Leu	Val	Asp	Glu	Thr	Thr	Gly	Met	Arg	Leu	His	Phe	Ile	Arg	Gln	Thr
		100				105						110			
His	Pro	Arg	Gly	Leu	Gly	Asp	Ala	Val	Leu	Gln	Ala	Lys	Ala	Phe	Val
		115				120					125				
Gly	Asn	Glu	Pro	Phe	Val	Val	Met	Leu	Gly	Asp	Asp	Leu	Met	Asp	Ile
		130				135				140					
Thr	Asp	Glu	Lys	Ala	Val	Pro	Leu	Thr	Lys	Gln	Leu	Met	Asp	Asp	Tyr
145				150					155					160	
Glu	Arg	Thr	His	Ala	Ser	Thr	Ile	Ala	Val	Met	Pro	Val	Pro	His	Asp
			165					170					175		

Glu	Val	Ser	Ala	Tyr	Gly	Val	Ile	Ala	Pro	Gln	Gly	Glu	Gly	Lys	Asp
			180					185					190		
Gly	Leu	Tyr	Ser	Val	Glu	Thr	Phe	Val	Glu	Lys	Pro	Ala	Pro	Glu	Asp
		195					200					205			
Ala	Pro	Ser	Asp	Leu	Ala	Ile	Ile	Gly	Arg	Tyr	Leu	Leu	Thr	Pro	Glu
	210					215					220				
Ile	Phe	Glu	Ile	Leu	Glu	Lys	Gln	Ala	Pro	Gly	Ala	Gly	Asn	Glu	Ile
225					230					235				240	
Gln	Leu	Thr	Asp	Ala	Ile	Asp	Thr	Leu	Asn	Lys	Thr	Gln	Arg	Val	Phe
			245						250					255	
Ala	Arg	Glu	Phe	Thr	Gly	Ala	Arg	Tyr	Asp	Val	Gly	Asp	Lys	Phe	Gly
			260					265					270		
Phe	Met	Lys	Thr	Ser	Ile	Asp	Tyr	Ala	Leu	Lys	His	Pro	Gln	Val	Lys
	275					280						285			
Asp	Asp	Leu	Lys	Asn	Tyr	Leu	Ile	Gln	Leu	Gly	Lys	Glu	Leu	Thr	Glu
	290					295					300				
Lys	Glu														
305															

(2) INFORMATION FOR SEQ ID NO:3873:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 237 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...237

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3873:

Ser	Arg	Ile	Asp	Ile	Lys	Asp	Leu	Ser	Phe	Ser	Tyr	Ser	Lys	Asp	Ser
1				5					10					15	
Ala	Pro	Val	Ile	Glu	Asn	Leu	Asn	Leu	Thr	Ile	Glu	Pro	Gly	Gln	Arg
			20					25					30		
Ile	Ala	Leu	Val	Gly	Gln	Ser	Gly	Ser	Gly	Lys	Ser	Thr	Leu	Ser	Lys
	35						40					45			
Ile	Pro	Ser	Gly	Leu	Tyr	Lys	Ile	Asp	Thr	Gly	Lys	Val	Leu	Phe	Asp
	50					55				60					
Gly	Val	Asn	Ile	Asn	Gln	Ile	Asp	Lys	Lys	Ile	Leu	Ser	Gln	Asn	Leu
65				70					75					80	
Gly	Val	Val	Pro	Gln	Asp	Ser	Phe	Leu	Leu	Asn	Arg	Ser	Ile	Leu	Asp
			85					90					95		
Asn	Ile	Thr	Leu	Lys	His	Glu	Val	Thr	Ser	Gln	Lys	Ile	Glu	Glu	Val
		100					105					110			
Cys	Lys	Ala	Val	Gln	Ile	Tyr	Asp	Glu	Ile	Met	Ala	Met	Pro	Met	Lys
	115					120					125				
Phe	Asn	Thr	Ile	Ile	Ser	Glu	Met	Gly	Ser	Asn	Ile	Ser	Gly	Gly	Gln
	130					135					140				

Arg	Gln	Arg	Ile	Ala	Leu	Ala	Arg	Ala	Leu	Ile	Asn	Asn	Pro	Ser	Ile
145					150					155					160
Val	Ile	Leu	Asp	Glu	Ala	Thr	Ser	Ala	Leu	Asp	Thr	Ile	Asn	Glu	Lys
				165					170					175	
Arg	Ile	Thr	Lys	Tyr	Ile	Gln	Ser	Gln	Gly	Cys	Thr	Gln	Ile	Ile	Ile
			180					185					190		
Ala	His	Arg	Leu	Ser	Thr	Ile	Lys	Asp	Ala	Asp	Ile	Ile	Phe	Val	Met
		195					200					205			
Lys	Gly	Gly	Lys	Ile	Val	Glu	Ser	Gly	Asn	His	Lys	Tyr	Leu	Met	Thr
	210					215					220				
Leu	Gly	Gly	Glu	Tyr	Tyr	Ser	Leu	Tyr	Thr	Lys	Arg	Lys			
225					230					235					

(2) INFORMATION FOR SEQ ID NO:3874:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...105

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3874:

Leu	Ala	Val	Asp	Phe	Lys	Met	Ile	Lys	Thr	Tyr	Asn	Ser	Arg	Cys	Ser
1				5					10					15	
Val	Leu	Pro	Pro	Lys	Lys	Leu	Asp	Arg	Lys	Asn	Leu	Thr	Phe	Trp	Gly
			20					25					30		
Val	Phe	Ile	Met	Lys	Leu	Ser	Tyr	Asp	Asp	Lys	Val	Gln	Ile	Tyr	Glu
		35					40					45			
Leu	Arg	Lys	Gln	Gly	Tyr	Ser	Leu	Glu	Lys	Leu	Ser	Asn	Lys	Phe	Gly
	50					55					60				
Ile	Asn	Asn	Ser	Asn	Leu	Arg	Tyr	Met	Ile	Lys	Leu	Ile	Asp	Arg	Tyr
65					70					75				80	
Gly	Ile	Glu	Phe	Gly	Lys	Lys	Gly	Lys	Asn	Arg	Tyr	Tyr	Ser	Pro	Asp
				85				90						95	
Leu	Lys	Gln	Glu	Met	Ile	His	Lys	Val							
			100					105							

(2) INFORMATION FOR SEQ ID NO:3875:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 359 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...359

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3875:

```
Ile Gly Val Glu Met Thr Lys Glu Lys Asn Val Ile Leu Thr Ala Arg
1          5          10          15
Asp Ile Val Val Glu Phe Asp Val Arg Asp Lys Val Leu Thr Ala Ile
          20          25          30
Arg Gly Val Ser Leu Glu Leu Val Glu Gly Glu Val Leu Ala Leu Val
          35          40          45
Gly Glu Ser Gly Ser Gly Lys Ser Val Leu Thr Lys Thr Phe Thr Gly
          50          55          60
Met Leu Glu Glu Asn Gly Arg Ile Ala Gln Gly Ser Ile Asp Tyr Arg
65          70          75          80
Gly Gln Asp Leu Thr Ala Leu Ser Ser His Lys Glu Trp Glu Gln Ile
          85          90          95
Arg Gly Ala Lys Ile Ala Thr Ile Phe Gln Asp Pro Met Thr Ser Leu
          100          105          110
Asp Pro Ile Lys Thr Ile Gly Ser Gln Ile Thr Glu Val Ile Val Lys
          115          120          125
His Gln Gly Lys Thr Ala Lys Glu Ala Lys Glu Leu Ala Ile Asp Tyr
          130          135          140
Met Asn Lys Val Gly Ile Pro Asp Ala Asp Arg Arg Phe Asn Glu Tyr
145          150          155          160
Pro Phe Gln Tyr Ser Gly Gly Met Arg Gln Arg Ile Val Ile Ala Ile
          165          170          175
Ala Leu Ala Cys Arg Pro Asp Val Leu Ile Cys Asp Glu Pro Thr Thr
          180          185          190
Ala Leu Asp Val Thr Ile Gln Ala Gln Ile Ile Asp Leu Leu Lys Ser
          195          200          205
Leu Gln Asn Glu Tyr His Phe Thr Thr Ile Phe Ile Thr His Asp Leu
          210          215          220
Gly Val Val Ala Ser Ile Ala Asp Lys Val Ala Val Met Tyr Ala Gly
225          230          235          240
Glu Ile Val Glu Tyr Gly Thr Val Glu Glu Val Phe Tyr Asp Pro Arg
          245          250          255
His Pro Tyr Thr Trp Ser Leu Leu Ser Ser Leu Pro Gln Leu Ala Asp
          260          265          270
Asp Lys Gly Asp Leu Tyr Ser Ile Pro Gly Thr Pro Pro Ser Leu Tyr
          275          280          285
Thr Asp Leu Lys Gly Asp Ala Phe Ala Leu Arg Ser Asp Tyr Ala Met
          290          295          300
Gln Ile Asp Phe Glu Gln Lys Ala Pro Gln Phe Ser Val Ser Glu Thr
305          310          315          320
His Trp Ala Lys Thr Trp Leu Leu His Glu Asp Ala Pro Lys Val Glu
          325          330          335
Lys Pro Ala Val Ile Ala Asn Leu His Asp Lys Ile Arg Glu Lys Met
          340          345          350
Gly Phe Ala His Leu Ala Asp
```

(2) INFORMATION FOR SEQ ID NO:3876:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 259 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...259

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3876:

```

Thr Gly Val Glu Met Ser Ile Arg Val Ile Ile Ala Gly Phe Lys Gly
1      5      10      15
Lys Met Gly Gln Ala Ala Cys Gln Met Val Leu Thr Asp Pro Asp Leu
20      25      30
Asp Leu Val Ala Val Leu Asp Pro Phe Glu Ser Glu Ser Glu Trp Gln
35      40      45
Gly Ile Pro Val Phe Lys Asp Lys Ala Asp Leu Ala Gly Phe Glu Ala
50      55      60
Asp Val Trp Val Asp Phe Thr Thr Pro Ala Val Ala Tyr Glu Asn Thr
65      70      75      80
Arg Phe Ala Leu Glu Asn Gly Phe Ala Pro Val Val Gly Thr Thr Gly
85      90      95
Phe Thr Ser Glu Glu Ile Ala Glu Leu Lys Glu Phe Ser Arg Ala Gln
100     105     110
Asp Leu Gly Gly Leu Ile Ala Pro Asn Phe Ala Leu Gly Ala Val Leu
115     120     125
Leu Met Gln Phe Ala Thr Gln Ala Ala Lys Tyr Phe Pro Asn Val Glu
130     135     140
Ile Ile Glu Leu His His Asp Lys Lys Lys Asp Ala Pro Ser Gly Thr
145     150     155     160
Ala Ile Lys Thr Ala Glu Leu Met Ala Glu Val Arg Glu Ser Ile Gln
165     170     175
Gln Gly Ala Ala Asp Glu Glu Glu Leu Ile Ala Gly Ala Arg Gly Ala
180     185     190
Asp Phe Asp Gly Met Arg Ile His Ser Val Arg Leu Pro Gly Leu Val
195     200     205
Ala His Gln Glu Val Ile Phe Gly Asn Gln Gly Glu Gly Leu Thr Leu
210     215     220
Arg His Asp Ser Tyr Asp Arg Ile Ser Phe Met Thr Gly Val Asn Leu
225     230     235     240
Gly Ile Lys Glu Val Val Lys Arg His Glu Leu Val Tyr Gly Leu Glu
245     250     255
His Leu Leu

```

(2) INFORMATION FOR SEQ ID NO:3877:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 574 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...574

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3877:

Phe	Gly	Val	Asp	Val	Phe	Phe	Thr	Phe	Ser	Gly	Phe	Leu	Ile	Thr	Ala
1				5					10					15	
Leu	Leu	Ile	Glu	Glu	Phe	Ser	Lys	Asn	His	Glu	Ile	Asp	Leu	Ile	Gly
			20					25					30		
Phe	Phe	Arg	Arg	Arg	Phe	Tyr	Arg	Ile	Val	Pro	Pro	Val	Val	Leu	Met
		35					40					45			
Val	Leu	Val	Thr	Met	Pro	Phe	Thr	Phe	Leu	Val	Arg	Gln	Asp	Tyr	Val
	50					55				60					
Ala	Gly	Ile	Gly	Gly	Gln	Ile	Ala	Ser	Val	Leu	Gly	Phe	Met	Thr	Asn
65					70				75					80	
Phe	Tyr	Glu	Leu	Leu	Thr	Gly	Gly	Ser	Tyr	Glu	Ser	Gln	Phe	His	Pro
			85					90					95		
His	Leu	Phe	Val	His	Asn	Trp	Ser	Leu	Ala	Val	Glu	Val	His	Tyr	Tyr
			100					105					110		
Ile	Leu	Trp	Gly	Leu	Ala	Val	Trp	Phe	Leu	Ser	Thr	His	Ala	Lys	Ser
	115						120					125			
Asn	Gly	Gln	Leu	Lys	Gly	Met	Val	Phe	Leu	Leu	Ser	Ala	Val	Ala	Phe
	130					135					140				
Leu	Ile	Ser	Phe	Phe	Ser	Met	Phe	Ile	Gly	Ser	Phe	Leu	Val	Thr	Ser
145					150					155				160	
Tyr	Ser	Ser	Val	Tyr	Phe	Ser	Ser	Leu	Thr	His	Val	Tyr	Pro	Phe	Phe
			165						170					175	
Leu	Gly	Ser	Met	Leu	Ala	Thr	Ile	Val	Gly	Val	Arg	Gln	Thr	Thr	Ser
			180					185					190		
Leu	Val	Lys	Gln	Leu	Asp	Lys	Ile	Trp	Asp	Leu	Arg	Lys	Thr	Leu	Val
	195						200					205			
Val	Phe	Gly	Gly	Gly	Phe	Gly	Phe	Leu	Val	Leu	Leu	Thr	Phe	Phe	Val
	210					215					220				
Lys	Phe	Thr	Tyr	Leu	Phe	Ala	Tyr	Leu	Ile	Gly	Phe	Leu	Leu	Ala	Ser
225					230					235				240	
Leu	Ala	Ala	Leu	Ala	Met	Ile	Leu	Ala	Ala	Arg	Val	Leu	His	Glu	Lys
			245						250					255	
Thr	His	His	Ile	Gln	Glu	Pro	Lys	Ile	Ile	Ser	Phe	Leu	Ala	Asp	Thr
			260					265					270		
Ser	Tyr	Ala	Val	Tyr	Leu	Phe	His	Trp	Pro	Phe	Tyr	Ile	Ile	Phe	Ser
	275						280						285		

Gln	Leu	Thr	Ser	Asn	Leu	Leu	Ala	Val	Leu	Leu	Thr	Leu	Ile	Cys	Ser
290						295					300				
Tyr	Gly	Phe	Ala	Ser	Leu	Ser	Phe	Tyr	Val	Leu	Glu	Pro	Trp	Ile	Ala
305					310					315					320
Gly	Lys	Asn	Thr	Pro	Ile	Val	Gln	Thr	Leu	Arg	Pro	Leu	Pro	Tyr	Ile
				325					330					335	
His	Ala	Ile	Leu	Ala	Ala	Gly	Thr	Gly	Ile	Leu	Thr	Ile	Ile	Val	Cys
			340					345					350		
Thr	Val	Asn	Leu	Leu	Ala	Thr	Gln	Val	Gly	Ala	Phe	Glu	Thr	Asp	Leu
		355					360					365			
Thr	Val	Asn	Gly	Leu	Lys	Gln	Ala	Ala	Thr	Asn	Ile	Gly	Gln	Thr	Lys
	370					375					380				
Val	Met	Ala	Glu	Arg	Ala	Asp	Ala	Asn	Ser	Leu	Gly	Ile	Ala	Asp	Gly
385					390					395					400
Thr	Met	Leu	Ile	Gly	Asp	Ser	Val	Ala	Leu	Arg	Ala	Asn	Thr	Ala	Leu
				405					410					415	
Gln	Thr	Ala	Leu	Pro	Gly	Ala	Gln	Ile	Asn	Ala	Gln	Val	Ser	Val	Thr
			420					425					430		
Thr	Lys	Thr	Ala	Asn	Glu	Ile	Met	Leu	Asn	Asn	Ser	Gln	Asn	Lys	Phe
		435					440					445			
Leu	Pro	Lys	Thr	Val	Val	Ile	Ala	Thr	Gly	Val	Asn	Asn	Pro	Glu	Asn
	450					455					460				
Tyr	Lys	Asp	Asp	Trp	Asp	Ser	Ile	Val	Lys	Asn	Leu	Pro	Lys	Gly	His
465					470					475					480
His	Met	Ile	Leu	Val	Thr	Pro	Tyr	Glu	Gly	Asp	Lys	Thr	Lys	Glu	Thr
				485					490					495	
Tyr	Ala	Ile	Val	Glu	Lys	Ala	Ala	Ala	Tyr	Met	Arg	Glu	Leu	Ala	Glu
			500					505					510		
Lys	Thr	Pro	Tyr	Ile	Thr	Ile	Ala	Asp	Trp	Asn	Gln	Val	Ala	Lys	Glu
		515					520					525			
His	Pro	Glu	Ile	Trp	Ala	Gly	Thr	Asp	Gln	Val	His	Phe	Gly	Ser	Glu
	530					535					540				
Ser	Ser	Thr	Ile	Glu	Ala	Gly	Ala	Lys	Leu	Tyr	Ala	Asp	Thr	Ile	Ala
545					550					555					560
Thr	Ala	Leu	Gln	Thr	Ala	Gln	Asp	Lys	Pro	Val	Lys	Ser	Lys		

565

570

(2) INFORMATION FOR SEQ ID NO:3878:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 168 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...168

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3878:

```

Pro Asn Ser Glu Gly Leu Ile Gly Ala Thr Ile Pro Ala Phe Glu Glu
1      5      10      15
Lys Tyr Gly Ile Lys Ile Glu Leu Ile Gln Ala Gly Thr Gly Glu Leu
20     25     30
Phe Lys Lys Leu Glu Ser Glu Lys Glu Val Pro Val Ala Asp Val Ile
35     40     45
Phe Gly Gly Ser Tyr Thr Gln Tyr Ala Thr His Gly Glu Leu Phe Glu
50     55     60
Asn Tyr Ile Ser Lys Glu Asn Asp Asn Val Ile Lys Glu Tyr Gln Asn
65     70     75     80
Thr Thr Gly Phe Ser Thr Pro Tyr Thr Leu Asp Gly Ser Val Leu Ile
85     90     95
Val His Pro Asp Leu Thr Lys Gly Met Asn Ile Glu Gly Tyr Ser Asp
100    105    110
Leu Leu Lys Pro Glu Leu Lys Gly Lys Ile Ala Thr Ala Asp Pro Ala
115    120    125
Asn Ser Ser Ser Ala Phe Ala Gln Leu Thr Asn Met Leu Gln Ala Gln
130    135    140
Gly Gly Tyr Lys Asp Asp Lys Ala Trp Ser Tyr Val Lys Asp Leu Phe
145    150    155    160
Thr Leu Ile Asp Gly Ile Val Lys
165

```

(2) INFORMATION FOR SEQ ID NO:3879:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...400

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3879:

```

Gly Lys Ser Glu Gly Ala Phe Ser Ser Gly Gln Ala Glu Val Ile Ala
1      5      10      15
Tyr Tyr Pro Leu Gln Gly Glu Lys Val Ile Ser Ser Val Arg Glu Leu
20     25     30
Ile Asn Gln Asp Val Lys Asp Lys Leu Glu Ser Lys Asp Asn Leu Val
35     40     45
Phe Tyr Tyr Thr Glu Gln Glu Glu Ser Gly Leu Lys Gly Val Val Asn
50     55     60
Arg Asn Val Thr Lys Gln Ile Tyr Asp Leu Val Ala Phe Lys Val Glu
65     70     75     80
Glu Thr Glu Lys Thr Ser Leu Gly Lys Val His Leu Thr Glu Asp Gly
85     90     95
Gln Pro Phe Thr Leu Asp Gln Leu Phe Ser Asp Ala Ser Lys Ala Lys

```

			100					105				110			
Glu	Gln	Leu	Ile	Lys	Glu	Leu	Thr	Ser	Phe	Ile	Glu	Asp	Lys	Lys	Ile
		115					120					125			
Glu	Gln	Asp	Gln	Ser	Glu	Gln	Ile	Val	Lys	Asn	Phe	Ser	Asp	Gln	Asp
	130					135					140				
Leu	Ser	Ala	Trp	Asn	Phe	Asp	Tyr	Lys	Asp	Ser	Gln	Ile	Ile	Leu	Tyr
145				150					155					160	
Pro	Ser	Pro	Val	Val	Glu	Asn	Leu	Glu	Glu	Ile	Ala	Leu	Pro	Val	Ser
			165					170					175		
Ala	Phe	Phe	Asp	Val	Ile	Gln	Ser	Ser	Tyr	Leu	Leu	Glu	Lys	Asp	Ala
		180					185					190			
Ala	Leu	Tyr	Gln	Ser	Tyr	Phe	Asp	Lys	Lys	Tyr	Gln	Lys	Val	Val	Ala
	195					200					205				
Leu	Thr	Phe	Asp	Asp	Gly	Pro	Asn	Pro	Ala	Thr	Thr	Pro	Gln	Val	Leu
210					215					220					
Glu	Thr	Leu	Ala	Lys	Tyr	Asp	Ile	Lys	Ala	Thr	Phe	Phe	Val	Leu	Gly
225				230					235					240	
Lys	Asn	Val	Ser	Gly	Asn	Glu	Asp	Leu	Val	Lys	Arg	Ile	Lys	Ser	Glu
		245					250						255		
Gly	His	Val	Val	Gly	Asn	His	Ser	Trp	Ser	His	Pro	Ile	Leu	Ser	Gln
	260						265					270			
Leu	Ser	Leu	Asp	Glu	Ala	Lys	Lys	Gln	Ile	Thr	Asp	Thr	Glu	Asp	Val
	275					280					285				
Leu	Thr	Lys	Val	Leu	Gly	Ser	Ser	Ser	Lys	Leu	Met	Arg	Pro	Pro	Tyr
290					295					300					
Gly	Ala	Ile	Thr	Asp	Asp	Ile	Arg	Asn	Ser	Leu	Asp	Leu	Ser	Phe	Ile
305				310					315					320	
Met	Trp	Asp	Val	Asp	Ser	Leu	Asp	Trp	Lys	Ser	Lys	Asn	Glu	Ala	Ser
			325				330						335		
Ile	Leu	Thr	Glu	Ile	Gln	His	Gln	Val	Ala	Asn	Gly	Ser	Ile	Val	Leu
	340						345					350			
Met	His	Asp	Ile	His	Ser	Pro	Thr	Val	Asn	Ala	Leu	Pro	Arg	Val	Ile
	355					360					365				
Glu	Tyr	Leu	Lys	Asn	Gln	Gly	Tyr	Thr	Phe	Val	Thr	Ile	Pro	Glu	Met
370					375					380					
Leu	Asn	Thr	Arg	Leu	Lys	Ala	His	Glu	Leu	Tyr	Tyr	Ser	Arg	Asp	Glu
385				390					395					400	

(2) INFORMATION FOR SEQ ID NO:3880:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 349 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...349
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3880:

Lys	Met	Ser	Asp	Ser	Pro	Ile	Lys	Tyr	Arg	Leu	Ile	Lys	Lys	Glu	Lys	1	5	10	15
His	Thr	Gly	Ala	Arg	Leu	Gly	Glu	Ile	Ile	Thr	Pro	His	Gly	Thr	Phe	20	25	30	
Pro	Thr	Pro	Met	Phe	Met	Pro	Val	Gly	Thr	Gln	Ala	Thr	Val	Lys	Thr	35	40	45	
Gln	Ser	Pro	Glu	Glu	Leu	Lys	Glu	Met	Gly	Ser	Gly	Ile	Ile	Leu	Ser	50	55	60	
Asn	Thr	Tyr	His	Leu	Trp	Leu	Arg	Pro	Gly	Asp	Glu	Leu	Ile	Ala	Arg	65	70	75	80
Ala	Gly	Gly	Leu	His	Lys	Phe	Met	Asn	Trp	Asp	Gln	Pro	Ile	Leu	Thr	85	90	95	
Asp	Ser	Gly	Gly	Phe	Gln	Val	Tyr	Ser	Leu	Ala	Asp	Ser	Arg	Asn	Ile	100	105	110	
Thr	Glu	Glu	Gly	Val	Thr	Phe	Lys	Asn	His	Leu	Asn	Gly	Ser	Lys	Met	115	120	125	
Phe	Leu	Ser	Pro	Glu	Lys	Ala	Ile	Ser	Ile	Gln	Asn	Asn	Leu	Gly	Ser	130	135	140	
Asp	Ile	Met	Met	Ser	Phe	Asp	Glu	Cys	Pro	Gln	Phe	Tyr	Gln	Pro	Tyr	145	150	155	160
Asp	Tyr	Val	Lys	Lys	Ser	Ile	Glu	Arg	Thr	Ser	Arg	Trp	Ala	Glu	Arg	165	170	175	
Gly	Leu	Lys	Ala	His	Arg	Arg	Pro	His	Asp	Gln	Gly	Leu	Phe	Gly	Ile	180	185	190	
Val	Gln	Gly	Ala	Gly	Phe	Glu	Asp	Leu	Arg	Arg	Gln	Ser	Ala	His	Asp	195	200	205	
Leu	Val	Ser	Met	Asp	Phe	Ser	Gly	Tyr	Ser	Ile	Gly	Gly	Leu	Ala	Val	210	215	220	
Gly	Glu	Thr	His	Glu	Glu	Met	Asn	Ala	Val	Leu	Asp	Phe	Thr	Thr	Gln	225	230	235	240
Leu	Leu	Pro	Glu	Asn	Lys	Pro	Arg	Tyr	Leu	Met	Gly	Val	Gly	Ala	Pro	245	250	255	
Asp	Ser	Leu	Ile	Asp	Gly	Val	Ile	Arg	Gly	Val	Asp	Met	Phe	Asp	Cys	260	265	270	
Val	Leu	Pro	Thr	Arg	Ile	Ala	Arg	Asn	Gly	Thr	Cys	Met	Thr	Ser	Gln	275	280	285	
Gly	Arg	Leu	Val	Val	Lys	Asn	Ala	Gln	Phe	Ala	Glu	Asp	Phe	Thr	Pro	290	295	300	
Leu	Asp	Pro	Glu	Cys	Asp	Cys	Tyr	Thr	Cys	Asn	Asn	Tyr	Thr	Arg	Ala	305	310	315	320
Tyr	Leu	Arg	His	Leu	Lys	Gly	Asp	Glu	Thr	Phe	Gly	Ile	Arg	Leu		325	330	335	
Thr	Ser	Tyr	His	Asn	Leu	Tyr	Phe	Leu	Leu	Asn	Leu	Met				340	345		

(2) INFORMATION FOR SEQ ID NO:3881:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...148

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3881:

```
Arg Trp Ser Asp Trp Glu Arg Ser Ser Gln Glu Ile Gly Glu Leu Ile
1          5          10          15
Val Glu Thr Ile Leu Gly Ile Leu Ser Ser Arg Gly Ile His Leu Ala
20          25          30
Val Gln Gly Cys Glu His Val Asn Arg Ala Leu Val Val Glu Arg Gln
35          40          45
Val Ala Glu Gln Phe Gly Leu Glu Ile Val Ser Val His Pro Thr Leu
50          55          60
His Ala Gly Gly Ser Gly Gln Leu Ala Ala Phe Lys Phe Met Gln Asp
65          70          75          80
Pro Val Glu Val Glu Phe Ile Lys Ala His Ala Gly Leu Asp Ile Gly
85          90          95
Asp Thr Ala Ile Gly Met His Val Lys His Val Gln Val Pro Ile Arg
100         105         110
Pro Ile Leu Arg Glu Ile Gly His Ala His Val Thr Ala Leu Ala Ser
115         120         125
Arg Pro Lys Leu Ile Gly Gly Ala Arg Ala His Tyr Pro Gln Asp Ala
130         135         140
Ile Arg Lys Ser
145
```

(2) INFORMATION FOR SEQ ID NO:3882:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 214 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...214

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3882:

```
Asp Asp Thr Glu Ser Leu Asn Trp Ser Gly Asp Val Leu Ile Tyr Ile
1          5          10          15
Ser Leu Ile Met Lys Met Glu Arg Leu Ser Met Val Ile Leu Glu Leu
20          25          30
Tyr Gln Asn Asp Tyr Ser Lys Asp Leu Val Ala Phe Asp Ser Ile Glu
35          40          45
```


Asp	Gly	Lys	Ala	Phe	Val	Ala	Gln	Ile	Pro	Gly	Tyr	Thr	Leu	Glu	Thr
50						55					60				
Glu	Asp	Gly	Phe	Glu	Val	Glu	Tyr	Phe	Asn	Pro	Lys	Asn	Ile	Pro	Asp
65					70					75					80
Tyr	Met	Glu	Ile	Ile	Phe	Asn	Gly	Asn	Ile	Val	Pro	Leu	Ser	Lys	Phe
				85					90					95	
Met	Phe	Asp	Pro	Glu	Glu	Asn	Val	Asn	Ile	Ile	Trp	Lys	Glu	Ile	Ser
			100					105					110		
Asn	Leu	Ser	Leu	Lys	Asn	Asp	Arg	Val	Ile	Glu	Gly	Tyr	Ser	Lys	Ile
			115				120					125			
Asp	Ala	Tyr	Val	Val	Asn	Asn	His	Glu	Val	Lys	Ala	Tyr	Val	Glu	Thr
	130						135				140				
Arg	Glu	Thr	Asn	Tyr	Arg	Lys	Ala	Lys	Asp	Phe	Leu	Glu	Ser	Arg	Gly
145					150					155					160
Tyr	Glu	Ile	Asp	Arg	Ser	Phe	Phe	Gly	Ser	Glu	Asp	Gly	Glu	Ala	Ile
				165					170					175	
Leu	Tyr	Arg	Lys	Lys	Gly	Ile	Glu	Val	Trp	His	Phe	Leu	Cys	His	Leu
			180					185					190		
Asp	Pro	Met	Phe	Val	Glu	Ile	Glu	Asp	Val	Glu	Gly	Tyr	Val	Lys	Glu
		195					200					205			
Glu	Val	Gly	Glu	Ile	Gln										
	210														

(2) INFORMATION FOR SEQ ID NO:3883:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 88 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...88

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3883:

Arg	Asp	Thr	Asp	Met	Asp	Lys	Gln	Tyr	Leu	His	Glu	Lys	Leu	Asp	Ala
1				5					10					15	
Met	Arg	Gln	Asn	Phe	Val	Glu	Ser	Thr	His	His	Glu	Arg	Ala	Val	Gly
			20					25					30		
Val	Leu	Asp	Gln	Ala	His	Met	Ser	Lys	Lys	Met	Leu	Lys	Ile	Lys	Lys
		35				40					45				
Lys	Leu	Val	Ala	Leu	Glu	Met	Glu	Arg	Cys	Gln	Arg	Lys	Ile	Glu	His
	50					55				60					
Lys	Asp	Cys	Ser	Lys	Ile	Asp	Gln	Lys	Ile	Lys	Glu	Gln	Lys	Glu	Ile
65				70					75						80
Phe	Glu	Ser	Cys	Cys	Lys	Lys	Asp								
				85											

(2) INFORMATION FOR SEQ ID NO:3884:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 153 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3884:

Glu	Ile	Thr	Asp	Ala	Asp	Thr	Arg	Ala	Leu	Val	Ala	Gly	Thr	Met	Val
1				5					10					15	
Glu	Asn	Pro	Glu	Gly	Phe	His	Phe	Asp	Asp	Leu	Gln	Leu	Gln	Thr	His
			20					25					30		
Ala	Asp	Asn	Asp	Ile	Glu	Ala	Leu	Val	Ser	Leu	Ala	Asn	Met	Asp	Gly
		35					40					45			
Glu	Lys	Val	Glu	Phe	Asn	Ala	Thr	Gly	Gln	Gly	Ser	Val	Gln	Ala	Ile
	50					55				60					
Phe	Asn	Ala	Ile	Asp	Lys	Phe	Phe	Asn	Gln	Ser	Val	Arg	Leu	Val	Ser
65					70				75					80	
Tyr	Thr	Ile	Asn	Ala	Val	Thr	Asp	Gly	Ile	Asp	Ala	Gln	Asp	Arg	Val
			85					90					95		
Leu	Val	Thr	Val	Glu	Asn	Arg	Asp	Thr	Glu	Thr	Ile	Phe	Asn	Ala	Ala
			100					105					110		
Gly	Leu	Asp	Phe	Asp	Val	Leu	Lys	Ala	Ser	Ala	Ile	Ala	Tyr	Ile	Asn
		115					120				125				
Ala	Asn	Thr	Phe	Val	Gln	Lys	Glu	Asn	Ala	Gly	Glu	Met	Gly	Arg	Ser
	130					135					140				
Val	Ser	Tyr	His	Asp	Met	Pro	Ser	Val							
145					150										

(2) INFORMATION FOR SEQ ID NO:3885:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 97 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...97

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3885:

```
Ser Ala Thr Asp Ser Lys Glu Glu Val Glu Ser Leu Leu Ser Lys Ala
1      5      10      15
Asn Gln Leu Leu Glu Gln Ile His Glu Gly Ile Arg Gln Ser Leu

      20      25      30
Ala Glu Glu Val Glu Asn Leu Lys Ala Ala Thr Asn Lys Val Asp Ala
      35      40      45
Asp Leu Asp Glu Val Asn Ser Gln Val Lys Asp Val Leu Thr Arg Ile
      50      55      60
Ala Ser Ala Leu Gln Gln Glu Lys Glu Asn Ala Glu Gln Asp Ser Gln
65      70      75      80
Thr Leu Val Leu Tyr Gln Lys Leu Tyr Asp Ile Leu Met Ser Leu Arg
      85      90      95
Lys
```

(2) INFORMATION FOR SEQ ID NO:3886:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 82 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...82

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3886:

```
Leu Phe Ala Asp Asn Lys His Leu Tyr Lys Val Ile Lys Glu Asp Phe
1      5      10      15
Pro Met Thr Leu Asn Glu Tyr Ile Leu Gln Tyr Arg Leu Lys Gln Ala
      20      25      30
Ile Asp Lys Met Ala Glu Ser Pro Asn Ser Pro Leu Ser Ala Ile Ser
      35      40      45
Asp Gln Val Gly Phe Ser Asp Tyr Lys Tyr Phe Ala Lys Val Phe Lys
      50      55      60
Lys His Leu His Ile Ser Pro Lys Glu Leu Lys Leu Leu Gly Arg Ile
65      70      75      80
Val Lys
```

(2) INFORMATION FOR SEQ ID NO:3887:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 453 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...453

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3887:

```

Leu Ile Ala Glu Ala Lys Lys Arg Asp Ile Arg Ile Ile Met Asp Leu
1      5      10      15
Val Val Asn His Thr Ser Asp Glu His Ala Trp Phe Val Glu Ala Cys
      20      25      30
Glu Asn Thr Asp Ser Pro Glu Arg Asp Tyr Tyr Ile Trp Arg Asp Glu
      35      40      45
Pro Asn Asp Leu Asp Ser Ile Phe Ser Gly Ser Ala Trp Glu Tyr Asp
      50      55      60
Glu Lys Ser Gly Gln Tyr Tyr Leu His Phe Phe Ser Lys Lys Gln Pro
65      70      75      80
Asp Leu Asn Trp Glu Asn Glu Lys Leu Arg Gln Lys Ile Tyr Glu Met
      85      90      95
Met Asn Phe Trp Ile Asp Lys Gly Ile Gly Gly Phe Arg Met Asp Val
      100     105     110
Ile Asp Met Ile Gly Lys Ile Pro Asp Glu Lys Val Val Asn Asn Gly
      115     120     125
Pro Met Leu His Pro Tyr Leu Lys Glu Met Asn Gln Ala Thr Phe Gly
      130     135     140
Asp Lys Asp Leu Leu Thr Val Gly Glu Thr Trp Gly Ala Thr Pro Glu
145     150     155     160
Ile Ala Lys Leu Tyr Ser Asp Pro Lys Gly Gln Glu Leu Ser Met Val
      165     170     175
Phe Gln Phe Glu His Ile Gly Leu Gln Tyr Gln Glu Gly Gln Pro Lys
      180     185     190
Trp His Tyr Gln Lys Glu Leu Asn Ile Ala Lys Leu Lys Glu Ile Phe
      195     200     205
Asn Lys Trp Gln Thr Glu Leu Gly Val Glu Asp Gly Trp Asn Ser Leu
      210     215     220
Phe Trp Asn Asn His Asp Leu Pro Arg Ile Val Ser Ile Trp Gly Asn
225     230     235     240
Asp Gln Glu Tyr Arg Glu Lys Ser Ala Lys Ala Phe Ala Ile Leu Leu
      245     250     255
His Leu Met Arg Gly Thr Pro Tyr Ile Tyr Gln Gly Glu Glu Ile Gly
      260     265     270
Met Thr Asn Tyr Pro Phe Glu Thr Leu Asp Gln Val Glu Asp Ile Glu
      275     280     285
Ser Leu Asn Tyr Ala Arg Glu Ala Leu Glu Lys Gly Val Pro Ile Glu
      290     295     300
Glu Ile Met Asp Ser Ile Arg Val Ile Gly Arg Asp Asn Ala Arg Thr
305     310     315     320
Pro Met Gln Trp Asp Glu Ser Lys Asn Ala Gly Phe Ser Thr Gly Gln
      325     330     335

```

Pro	Trp	Leu	Ala	Val	Asn	Pro	Asn	Tyr	Glu	Met	Ile	Asn	Val	Gln	Glu
			340					345					350		
Ala	Leu	Ala	Asn	Pro	Asp	Ser	Ile	Phe	Tyr	Thr	Tyr	Gln	Lys	Leu	Val
		355					360					365			
Gln	Ile	Arg	Lys	Glu	Asn	Ser	Trp	Leu	Val	Arg	Ala	Asp	Phe	Glu	Leu
	370					375					380				
Leu	Asp	Thr	Ala	Asp	Lys	Val	Phe	Ala	Tyr	Ile	Arg	Lys	Asp	Gly	Asp
385					390					395					400
Arg	Arg	Phe	Leu	Val	Val	Ala	Asn	Leu	Ser	Asn	Asp	Lys	Gln	Asn	Phe
				405					410					415	
Ser	Val	Asp	Gly	Lys	Val	Arg	Ser	Val	Leu	Ile	Glu	Asn	Thr	Ala	Ala
			420					425					430		
Lys	Glu	Val	Leu	Glu	Lys	Gln	Val	Leu	Ala	Pro	Trp	Asp	Ala	Phe	Cys
		435					440					445			
Val	Glu	Met	Thr	Asp											
		450													

(2) INFORMATION FOR SEQ ID NO:3888:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 775 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...775

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3888:

Glu	Tyr	Gln	Asp	Arg	Leu	Asp	Gln	Glu	Leu	Ser	Val	Ile	His	Asp	Met
1				5				10						15	
Gly	Phe	Asp	Asp	Tyr	Phe	Leu	Val	Val	Trp	Asp	Leu	Leu	Arg	Phe	Gly
		20						25					30		
Arg	Ser	Asn	Gly	Tyr	Tyr	Met	Gly	Met	Gly	Arg	Gly	Ser	Ala	Val	Gly
		35					40					45			
Ser	Leu	Val	Ser	Tyr	Ala	Leu	Asp	Ile	Thr	Gly	Thr	Asp	Pro	Val	Glu
	50					55					60				
Lys	Asn	Leu	Ile	Phe	Glu	Arg	Phe	Leu	Asn	Arg	Glu	Arg	Tyr	Thr	Met
65				70					75					80	
Pro	Asp	Ile	Asp	Ile	Asp	Ile	Pro	Asp	Ile	Tyr	Arg	Pro	Asp	Phe	Ile
			85					90					95		
Arg	Tyr	Val	Gly	Asn	Lys	Tyr	Gly	Ser	Lys	His	Ala	Ala	Gln	Ile	Val
		100					105						110		
Thr	Phe	Ser	Thr	Phe	Gly	Ala	Lys	Gln	Ala	Leu	Arg	Asp	Val	Leu	Lys
	115					120						125			
Arg	Phe	Gly	Val	Pro	Glu	Tyr	Glu	Leu	Ser	Ala	Ile	Thr	Lys	Lys	Ile
	130					135					140				
Ser	Phe	Arg	Asp	Asn	Leu	Lys	Ser	Ala	Tyr	Glu	Gly	Asn	Leu	Gln	Phe
145					150					155					160

Arg	Gln	Gln	Ile	Asn	Ser	Lys	Leu	Glu	Tyr	Gln	Lys	Ala	Phe	Glu	Ile
				165					170					175	
Ala	Cys	Lys	Ile	Glu	Gly	Tyr	Pro	Arg	Gln	Thr	Ser	Val	His	Ala	Ala
			180					185					190		
Gly	Val	Val	Ile	Ser	Asp	Gln	Asp	Leu	Thr	Asn	Tyr	Ile	Pro	Leu	Lys
		195					200					205			
Tyr	Gly	Asp	Glu	Ile	Pro	Leu	Thr	Gln	Tyr	Asp	Ala	His	Gly	Val	Glu
	210					215					220				
Ala	Ser	Gly	Leu	Leu	Lys	Met	Asp	Phe	Leu	Gly	Leu	Arg	Asn	Leu	Thr
225					230					235					240
Phe	Val	Gln	Lys	Met	Gln	Glu	Leu	Leu	Ala	Glu	Ile	Glu	Gly	Ile	His
			245						250					255	
Leu	Lys	Ile	Glu	Glu	Ile	Asp	Leu	Glu	Asp	Lys	Glu	Thr	Leu	Asp	Leu
			260					265					270		
Phe	Ala	Ser	Gly	Asn	Thr	Lys	Gly	Ile	Phe	Gln	Phe	Glu	Gln	Pro	Gly
		275					280					285			
Ala	Ile	Arg	Leu	Leu	Lys	Arg	Val	Gln	Pro	Val	Cys	Phe	Glu	Asp	Val
	290					295					300				
Val	Ala	Thr	Thr	Ser	Leu	Asn	Arg	Pro	Gly	Ala	Ser	Asp	Tyr	Ile	Asn
305					310					315					320
Asn	Phe	Val	Ala	Arg	Lys	His	Gly	Gln	Glu	Glu	Val	Thr	Val	Leu	Asp
			325						330					335	
Pro	Val	Leu	Glu	Asp	Met	Leu	Ala	Pro	Thr	Tyr	Gly	Ile	Met	Leu	Tyr
		340						345					350		
Gln	Glu	Gln	Val	Met	Gln	Val	Ala	Gln	Arg	Phe	Ala	Gly	Phe	Ser	Leu
		355					360					365			
Gly	Lys	Ala	Asp	Ile	Leu	Arg	Arg	Ala	Met	Gly	Lys	Lys	Asp	Ala	Ser
	370					375					380				
Ala	Met	His	Glu	Met	Arg	Ala	Ser	Phe	Ile	Gln	Gly	Ser	Leu	Glu	Ala
385					390					395					400
Gly	His	Thr	Val	Glu	Lys	Ala	Glu	Gln	Val	Phe	Asp	Val	Met	Glu	Arg
			405						410					415	
Phe	Ala	Gly	Tyr	Gly	Phe	Asn	Arg	Ser	His	Ala	Tyr	Ala	Tyr	Ser	Ala
		420						425					430		
Leu	Ala	Phe	Gln	Leu	Ala	Tyr	Phe	Lys	Thr	His	Tyr	Pro	Ala	Ile	Phe
	435						440					445			
Tyr	Gln	Ile	Met	Leu	Asn	Ser	Ala	Asn	Ser	Asp	Tyr	Leu	Ile	Asp	Ala
	450					455					460				
Leu	Glu	Ala	Gly	Phe	Glu	Val	Ala	Pro	Leu	Ser	Ile	Asn	Thr	Ile	Pro
465					470					475					480
Tyr	His	Asp	Lys	Ile	Ala	Asn	Lys	Ala	Ile	Tyr	Leu	Gly	Leu	Lys	Ser
			485						490					495	
Ile	Lys	Gly	Val	Ser	Asn	Asp	Leu	Ala	Leu	Trp	Ile	Ile	Glu	His	Arg
		500						505					510		
Pro	Tyr	Ser	Asn	Ile	Glu	Asp	Phe	Ile	Ala	Lys	Leu	Pro	Glu	Asn	Tyr
	515						520					525			
Leu	Lys	Leu	Pro	Leu	Leu	Glu	Pro	Leu	Val	Lys	Val	Gly	Leu	Phe	Asp
	530					535					540				
Ser	Phe	Glu	Lys	Asn	Arg	Gln	Lys	Val	Phe	Asn	Asn	Leu	Ala	Asn	Leu
545					550					555					560
Phe	Glu	Phe	Val	Lys	Glu	Leu	Gly	Ser	Leu	Phe	Gly	Asp	Ala	Ile	Tyr
			565						570					575	
Ser	Trp	Gln	Glu	Ser	Glu	Asp	Trp	Thr	Glu	Gln	Glu	Lys	Phe	Tyr	Met
		580						585					590		
Glu	Gln	Glu	Leu	Leu	Gly	Ile	Gly	Val	Ser	Lys	His	Pro	Leu	Gln	Ala
	595						600					605			
Ile	Ala	Ser	Lys	Ala	Ile	Tyr	Pro	Ile	Thr	Pro	Ile	Gly	Asn	Leu	Ser

610		615		620
Glu Asn Ser Tyr Ala Ile	Ile Leu Val Glu Val	Gln Lys Ile Lys Val		
625	630	635	640	
Ile Arg Thr Lys Lys Gly	Glu Asn Met Ala Phe	Leu Gln Ala Asp Asp		
	645	650	655	
Ser Lys Lys Lys Leu Asp	Val Thr Leu Phe Ser	Asp Leu Tyr Arg Gln		
660	665	670		
Val Gly Gln Glu Ile Lys	Glu Gly Ala Phe Tyr	Tyr Val Lys Gly Lys		
675	680	685		
Ile Gln Ser Arg Asp Gly	Arg Leu Gln Met Ile	Ala Gln Glu Ile Arg		
690	695	700		
Glu Ala Val Ala Glu Arg	Phe Trp Ile Gln Val	Lys Asn His Glu Ser		
705	710	715	720	
Asp Gln Glu Ile Ser Arg	Ile Leu Glu Gln Phe	Lys Gly Pro Ile Pro		
	725	730	735	
Val Ile Ile Arg Tyr Glu	Glu Glu Gln Lys Thr	Ile Val Ser Pro His		
740	745	750		
His Phe Val Ala Lys Ser	Asn Glu Leu Glu Glu	Lys Leu Asn Glu Ile		
755	760	765		
Val Met Lys Thr Ile Tyr	Arg			
770	775			

(2) INFORMATION FOR SEQ ID NO:3889:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...74

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3889:

Pro Gly Gln Glu Val Thr Phe Asn Glu Val Val Leu Val Gly Gly Glu	
1	5 10 15
Asn Thr Val Val Gly Thr Pro Leu Val Ala Gly Ala Thr Val Val Gly	
	20 25 30
Thr Val Glu Lys Gln Gly Lys Gln Lys Lys Val Val Thr Tyr Lys Tyr	
	35 40 45
Lys Pro Lys Lys Gly Ser His Arg Lys Gln Gly His Arg Gln Pro Tyr	
	50 55 60
Thr Lys Val Val Ile Asn Ala Ile Asn Ala	
65	70

(2) INFORMATION FOR SEQ ID NO:3890:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...88

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3890:

Asn	Leu	Gln	Asp	Phe	Thr	Asn	Lys	Leu	Met	Lys	Leu	Lys	Lys	Glu	Lys
1				5				10						15	
Lys	Met	Ala	Glu	Phe	Thr	Phe	Glu	Ile	Glu	Glu	His	Leu	Leu	Ile	Leu
		20					25					30			
Ser	Glu	Asn	Glu	Lys	Gly	Trp	Thr	Lys	Glu	Ile	Asn	Arg	Val	Ser	Phe
		35				40					45				
Asn	Gly	Ala	Pro	Ala	Lys	Phe	Asp	Ile	Arg	Ala	Trp	Ser	Pro	Asp	His
50					55				60						
Thr	Lys	Met	Gly	Lys	Gly	Ile	Thr	Leu	Ser	Asn	Glu	Glu	Phe	Gln	Thr
65				70				75						80	
Met	Val	Asp	Ala	Phe	Lys	Gly	Asn								
				85											

(2) INFORMATION FOR SEQ ID NO:3891:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 291 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...291

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3891:

Lys	Gly	Gln	Asp	Val	Thr	Lys	Gln	Ala	Phe	Lys	Glu	Ala	Val	Phe	Arg
1				5				10						15	
Ala	Ile	Phe	Phe	Met	Ser	Ala	Thr	Val	Ala	Val	Val	Ala	Ile	Leu	Leu
		20					25					30			
Ile	Cys	Phe	Phe	Ile	Phe	Ser	Asn	Gly	Leu	Pro	Phe	Met	Ala	Asn	Tyr
		35				40					45				
Gly	Phe	Ala	Arg	Phe	Leu	Leu	Gly	Ser	Asp	Trp	Ser	Pro	Thr	Asn	Ile
50					55					60					


```

Pro Ala Ser Tyr Gly Ile Leu Pro Met Ile Val Gly Ser Leu Leu Ile
65          70          75          80
Thr Leu Gly Ala Ile Val Ile Gly Val Pro Thr Gly Ile Leu Thr Ser
85          90          95
Val Phe Met Val Tyr Tyr Cys Pro Lys Pro Val Tyr Gly Phe Leu Lys
100        105        110
Ser Ala Ile Asn Leu Met Ala Ala Ile Pro Ser Ile Val Tyr Gly Phe
115        120        125
Phe Gly Leu Gln Leu Leu Val Pro Trp Ile Arg Thr Phe Leu Gly Asn
130        135        140
Gly Met Ser Val Leu Thr Ala Ser Leu Leu Leu Gly Ile Met Ile Leu
145        150        155        160
Pro Thr Ile Ile Ser Leu Ser Glu Ser Ala Ile Arg Thr Val Pro Lys
165        170        175
Thr Tyr Tyr Ser Gly Ser Leu Ala Leu Gly Ala Ser His Glu Arg Ser
180        185        190
Ile Phe Ser Val Ile Leu Pro Ala Ala Arg Ser Gly Ile Leu Ser Ala
195        200        205
Val Ile Leu Gly Ile Gly Arg Ala Val Gly Glu Thr Met Ala Val Ile
210        215        220
Leu Val Ala Gly Asn Gln Pro Ile Ile Pro Ser Gly Leu Phe Ser Gly
225        230        235        240
Thr Arg Thr Leu Thr Thr Asn Ile Val Leu Glu Met Ala Tyr Ala Ser
245        250        255
Gly Gln His Arg Glu Ala Leu Ile Ala Thr Ser Ala Val Leu Phe Phe
260        265        270
Leu Ile Leu Leu Ile Asn Ala Tyr Phe Ala Tyr Leu Lys Gly Lys Ser
275        280        285
Ser Tyr Glu
290

```

(2) INFORMATION FOR SEQ ID NO:3892:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 394 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...394
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3892:

```

Thr Val Lys Asp Val Asp Leu Lys Gly Lys Lys Val Leu Val Arg Val
1          5          10          15
Asp Phe Asn Val Pro Leu Lys Asp Gly Val Ile Thr Asn Asp Asn Arg
20        25        30
Ile Thr Ala Ala Leu Pro Thr Ile Lys Tyr Ile Ile Glu Gln Gly Gly
35        40        45

```

Arg	Ala	Ile	Leu	Phe	Ser	His	Leu	Gly	Arg	Val	Lys	Glu	Glu	Ala	Asp
50						55					60				
Lys	Ala	Gly	Lys	Ser	Leu	Ala	Pro	Val	Ala	Ala	Asp	Leu	Ala	Ala	Lys
65					70				75						80
Leu	Gly	Gln	Asp	Val	Val	Phe	Pro	Gly	Val	Thr	Arg	Gly	Ala	Glu	Leu
				85					90					95	
Glu	Ala	Ala	Ile	Asn	Ala	Leu	Glu	Asp	Gly	Gln	Val	Leu	Leu	Val	Glu
			100					105						110	
Asn	Thr	Arg	Tyr	Glu	Asp	Val	Asp	Gly	Lys	Lys	Glu	Ser	Lys	Asn	Asp
		115					120					125			
Pro	Glu	Leu	Gly	Lys	Tyr	Trp	Ala	Ser	Leu	Gly	Asp	Gly	Ile	Phe	Val
	130					135					140				
Asn	Asp	Ala	Phe	Gly	Thr	Ala	His	Arg	Ala	His	Ala	Ser	Asn	Val	Gly
145					150					155					160
Ile	Ser	Ala	Asn	Val	Glu	Lys	Ala	Val	Ala	Gly	Phe	Leu	Leu	Glu	Asn
			165						170					175	
Glu	Ile	Ala	Tyr	Ile	Gln	Glu	Ala	Val	Glu	Thr	Pro	Glu	Arg	Pro	Phe
		180						185					190		
Val	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Ser	Asp	Lys	Ile	Gly	Val	Ile
	195						200					205			
Glu	Asn	Leu	Leu	Glu	Lys	Ala	Asp	Lys	Val	Leu	Ile	Gly	Gly	Gly	Met
	210					215					220				
Thr	Tyr	Thr	Phe	Tyr	Lys	Ala	Gln	Gly	Ile	Glu	Ile	Gly	Asn	Ser	Leu
225					230					235					240
Val	Glu	Glu	Asp	Lys	Leu	Asp	Val	Ala	Lys	Ala	Leu	Leu	Glu	Lys	Ala
			245						250					255	
Asn	Gly	Lys	Leu	Ile	Leu	Pro	Val	Asp	Ser	Lys	Glu	Ala	Asn	Ala	Phe
			260					265					270		
Ala	Gly	Tyr	Thr	Glu	Val	Arg	Asp	Thr	Glu	Gly	Glu	Ala	Val	Ser	Glu
		275					280					285			
Gly	Phe	Leu	Gly	Leu	Asp	Ile	Gly	Pro	Lys	Ser	Ile	Ala	Lys	Phe	Asp
	290					295					300				
Glu	Ala	Leu	Thr	Gly	Ala	Lys	Thr	Val	Val	Trp	Asn	Gly	Pro	Met	Gly
305					310					315					320
Val	Phe	Glu	Asn	Pro	Asp	Phe	Gln	Ala	Gly	Thr	Ile	Gly	Val	Met	Asp
			325						330					335	
Ala	Ile	Val	Lys	Gln	Pro	Gly	Val	Lys	Ser	Ile	Ile	Gly	Gly	Gly	Asp
		340						345					350		
Ser	Ala	Ala	Ala	Ala	Ile	Asn	Leu	Gly	Arg	Ala	Asp	Lys	Phe	Ser	Trp
	355					360						365			
Ile	Ser	Thr	Gly	Gly	Gly	Ala	Ser	Met	Glu	Leu	Leu	Glu	Gly	Lys	Val
	370					375					380				
Leu	Pro	Gln	Leu	Ala	Ala	Leu	Thr	Glu	Lys						
385					390										

(2) INFORMATION FOR SEQ ID NO:3893:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 786 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...786

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3893:

```
Thr Phe Lys Asp Lys Glu Ile Lys Met Asn Lys Lys Ile Leu Glu Thr
1      5      10      15
Leu Glu Phe Asp Lys Val Lys Ala Leu Phe Glu Pro His Leu Leu Thr

      20      25      30
Glu Gln Gly Leu Glu Gln Leu Arg Gln Leu Ala Pro Thr Ala Lys Ala
      35      40      45
Asp Lys Ile Lys Gln Ala Phe Ala Glu Met Lys Glu Met Gln Ala Leu
      50      55      60
Phe Val Glu Gln Pro His Phe Thr Ile Leu Ser Thr Lys Glu Ile Ala
      65      70      75      80
Gly Val Cys Lys Arg Leu Glu Met Gly Ala Asp Leu Asn Ile Glu Glu
      85      90      95
Phe Leu Leu Leu Lys Arg Val Leu Leu Thr Ser Arg Glu Leu Gln Ser
      100      105      110
Phe Tyr Ala Asn Leu Glu Asn Val Ser Leu Glu Glu Leu Ala Leu Trp
      115      120      125
Phe Glu Lys Leu His Asp Phe Pro Gln Leu Gln Gly Asn Leu Gln Ala
      130      135      140
Phe Asn Asp Ala Gly Phe Ile Glu Asn Phe Ala Ser Glu Glu Leu Ala
      145      150      155      160
Arg Ile Arg Arg Lys Ile His Asp Ser Glu Ser Gln Val Arg Asp Val
      165      170      175
Leu Gln Asp Leu Leu Lys Gln Lys Ala Gln Met Leu Thr Glu Gly Ile
      180      185      190
Val Ala Ser Arg Asn Gly Arg Gln Val Leu Pro Val Lys Asn Thr Tyr
      195      200      205
Arg Asn Lys Ile Ala Gly Val Val His Asp Ile Ser Ala Ser Gly Asn
      210      215      220
Thr Val Tyr Ile Glu Pro Arg Glu Val Val Lys Leu Ser Glu Glu Ile
      225      230      235      240
Ala Ser Leu Arg Ala Asp Glu Arg Tyr Glu Met Leu Arg Ile Leu Gln
      245      250      255
Glu Ile Ser Glu Arg Val Arg Pro His Ala Ala Glu Ile Ala Asn Asp
      260      265      270
Ala Trp Ile Ile Gly His Leu Asp Leu Ile Arg Ala Lys Val Arg Phe
      275      280      285
Ile Gln Glu Arg Gln Ala Val Val Pro Gln Leu Ser Glu Asn Gln Glu
      290      295      300
Ile Gln Leu Leu His Val Cys His Pro Leu Val Lys Asn Ala Val Ala
      305      310      315      320
Asn Asp Val Tyr Phe Gly Gln Asp Leu Thr Ala Ile Val Ile Thr Gly
      325      330      335
Pro Asn Thr Gly Gly Lys Thr Ile Met Leu Lys Thr Leu Gly Leu Thr
      340      345      350
Gln Val Met Ala Gln Ser Gly Leu Pro Ile Leu Ala Asp Lys Gly Ser
      355      360      365
Arg Val Gly Ile Phe Glu Glu Ile Phe Ala Asp Ile Gly Asp Glu Gln
      370      375      380
```

Ser	Ile	Glu	Gln	Ser	Leu	Ser	Thr	Phe	Ser	Ser	His	Met	Thr	Asn	Ile
385					390				395						400
Val	Asp	Ile	Leu	Gly	Lys	Val	Asn	Gln	His	Ser	Leu	Leu	Leu	Leu	Asp
				405					410						415
Glu	Leu	Gly	Ala	Gly	Thr	Asp	Pro	Gln	Glu	Gly	Ala	Ala	Leu	Ala	Met
			420					425					430		
Ala	Ile	Leu	Glu	Asp	Leu	Arg	Leu	Arg	Gln	Ile	Lys	Thr	Met	Ala	Thr
		435					440					445			
Thr	His	Tyr	Pro	Glu	Leu	Lys	Ala	Tyr	Gly	Ile	Glu	Thr	Ala	Phe	Val
	450					455					460				
Gln	Asn	Ala	Ser	Met	Glu	Phe	Asp	Thr	Ala	Thr	Leu	Arg	Pro	Thr	Tyr
465					470					475					480
Arg	Phe	Met	Gln	Gly	Val	Pro	Gly	Arg	Ser	Asn	Ala	Phe	Glu	Ile	Ala
			485						490						495
Lys	Arg	Leu	Gly	Leu	Ser	Glu	Val	Ile	Val	Gly	Asp	Ala	Ser	Gln	Gln
			500					505					510		
Ile	Asp	Gln	Asp	Asn	Asp	Val	Asn	Arg	Ile	Ile	Glu	Gln	Leu	Glu	Glu
	515						520					525			
Gln	Thr	Leu	Glu	Ser	Arg	Lys	Arg	Leu	Asp	Asn	Ile	Arg	Glu	Val	Glu
	530					535					540				
Gln	Glu	Asn	Leu	Lys	Met	Asn	Arg	Val	Leu	Lys	Lys	Leu	Tyr	Asn	Glu
545					550					555					560
Leu	Asn	Arg	Glu	Lys	Glu	Thr	Glu	Leu	Asn	Lys	Ala	Arg	Glu	Gln	Ala
			565						570						575
Ala	Glu	Ile	Val	Asp	Met	Ala	Leu	Ser	Glu	Ser	Asp	Gln	Ile	Leu	Lys
			580					585					590		
Asn	Leu	His	Ser	Lys	Ser	Gln	Leu	Lys	Pro	His	Glu	Ile	Ile	Glu	Ala
	595						600					605			
Lys	Ala	Lys	Leu	Lys	Lys	Leu	Ala	Pro	Glu	Lys	Val	Asp	Leu	Ser	Lys
	610					615					620				
Asn	Lys	Val	Leu	Gln	Lys	Ala	Lys	Lys	Lys	Arg	Ala	Pro	Lys	Val	Gly
625					630					635					640
Asp	Asp	Ile	Val	Val	Leu	Ser	Tyr	Gly	Gln	Arg	Gly	Thr	Leu	Thr	Ser
			645						650						655
Gln	Leu	Lys	Asp	Gly	Arg	Trp	Glu	Ala	Gln	Val	Gly	Leu	Ile	Lys	Met
			660					665					670		
Thr	Leu	Glu	Glu	Lys	Glu	Phe	Asp	Leu	Val	Gln	Ala	Gln	Gln	Glu	Lys
	675						680					685			
Pro	Val	Lys	Lys	Lys	Gln	Val	Asn	Val	Val	Lys	Arg	Thr	Ser	Gly	Arg
	690					695					700				
Gly	Pro	Gln	Ala	Arg	Leu	Asp	Leu	Arg	Gly	Lys	Arg	Tyr	Glu	Glu	Ala
705					710					715					720
Met	Asn	Glu	Leu	Asp	Ala	Phe	Ile	Asp	Gln	Ala	Leu	Leu	Asn	Asn	Met
			725						730						735
Ala	Gln	Val	Asp	Ile	Ile	His	Gly	Ile	Gly	Thr	Gly	Val	Ile	Arg	Glu
			740					745					750		
Gly	Val	Thr	Lys	Tyr	Leu	Gln	Arg	Asn	Lys	His	Val	Lys	Ser	Phe	Gly
	755							760				765			
Tyr	Ala	Pro	Gln	Asn	Ala	Gly	Gly	Ser	Gly	Ala	Thr	Ile	Val	Thr	Phe
	770					775						780			
Lys	Gly														
785															

(2) INFORMATION FOR SEQ ID NO:3894:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 62 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...62

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3894:

Ser	Ile	Lys	Glu	Met	His	Thr	Ile	Asp	Val	Ile	Gly	Lys	Ala	Pro	Asp
1				5					10					15	
Val	Thr	Pro	Ser	Gln	Val	Ser	Lys	Glu	Leu	Met	Val	Thr	Leu	Gly	Thr
			20					25					30		
Val	Thr	Thr	Ser	Leu	Asn	Asn	Leu	Glu	Arg	Lys	Gly	Tyr	Ile	Glu	Arg
		35					40					45			
Val	Arg	Ser	Glu	Gln	Asp	Arg	Arg	Val	Val	His	Leu	His	Leu		
	50					55					60				

(2) INFORMATION FOR SEQ ID NO:3895:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 521 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...521

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3895:

Arg	Ile	Lys	Glu	Arg	Glu	Leu	Met	Asn	Ile	Gln	Glu	Glu	Ile	Lys	Lys
1				5					10					15	
Arg	Arg	Thr	Phe	Ala	Ile	Ile	Ser	His	Pro	Asp	Ala	Gly	Lys	Thr	Thr
			20					25					30		
Ile	Thr	Glu	Gln	Leu	Leu	Tyr	Phe	Gly	Gly	Glu	Ile	Arg	Glu	Ala	Gly
		35					40					45			
Thr	Val	Lys	Gly	Lys	Lys	Thr	Gly	Thr	Phe	Ala	Lys	Ser	Asp	Trp	Met
	50					55					60				
Asp	Ile	Glu	Lys	Gln	Arg	Gly	Ile	Ser	Val	Thr	Ser	Ser	Val	Met	Gln
65				70					75					80	
Phe	Asp	Tyr	Asp	Gly	Lys	Arg	Val	Asn	Ile	Leu	Asp	Thr	Pro	Gly	His
			85					90						95	

(2) INFORMATION FOR SEQ ID NO:3896:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 247 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...247
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3896:

```

Leu Ser Lys Glu Asp Leu Ser Ala His Asn Asn Cys Ile Ile Ser Arg
1          5          10          15
Trp Glu Val Leu Phe Leu Asp Trp Ser Ile Val Glu Gln Tyr Leu Pro
          20          25          30
Leu Tyr Gln Lys Ala Phe Phe Leu Thr Leu His Ile Ala Val Trp Gly
          35          40          45
Ile Leu Gly Ser Phe Leu Leu Gly Leu Ile Val Ser Ile Ile Arg His
          50          55          60
Tyr Arg Ile Pro Val Leu Ala Gln Val Ala Thr Ala Tyr Ile Glu Leu
65          70          75          80
Ser Arg Asn Thr Pro Leu Leu Ile Gln Leu Phe Phe Leu Tyr Phe Gly
          85          90          95
Leu Pro Arg Ile Gly Ile Val Leu Ser Ser Glu Val Cys Ala Thr Leu
          100          105          110
Gly Leu Val Phe Leu Gly Gly Ser Tyr Met Ala Glu Ser Phe Arg Ser
          115          120          125
Gly Leu Glu Ala Ile Ser Gln Thr Gln Gln Glu Ile Gly Leu Ala Ile
          130          135          140
Gly Leu Thr Pro Leu Gln Val Phe Arg Tyr Val Val Leu Pro Gln Ala
145          150          155          160
Thr Ala Val Ala Leu Pro Ser Phe Ser Ala Asn Val Ile Phe Leu Ile
          165          170          175
Lys Glu Thr Ser Val Phe Ser Ala Val Ala Leu Ala Asp Leu Met Tyr
          180          185          190

Val Ala Lys Asp Leu Ile Gly Leu Tyr Tyr Glu Thr Asp Ile Ala Leu
          195          200          205
Ala Met Leu Val Val Ala Tyr Leu Ile Met Leu Leu Pro Ile Ser Leu
          210          215          220
Val Phe Ser Trp Ile Glu Arg Arg Thr Arg His Ala Gly Phe Gly Asn
225          230          235          240
Pro Ser Thr Leu Ser Arg Lys
          245

```

(2) INFORMATION FOR SEQ ID NO:3897:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 76 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...76

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3897:

```
Asn Ile Lys Glu Lys Lys Lys Asn Pro Leu Phe Val Gly Ile Leu Ser
1           5           10           15
Ile Ile Leu Gly Leu Leu Phe Pro Ile Val Gly Leu Ile Leu Gly Ile
          20          25          30
Ile Gly Leu Val Leu Ala Ile Ser Tyr Gln Lys Glu Ser Gln Leu Asp
          35          40          45
Tyr Lys Ile Glu Lys Ile Leu Asn Ile Ile Gly Ile Val Ile Ser Val
          50          55          60
Val Asn Trp Ile Val Ala Ile Ala Leu Ile Phe Arg
65          70          75
```

(2) INFORMATION FOR SEQ ID NO:3898:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 399 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...399

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3898:

```
Met Ser Lys Asp Lys Lys Asn Glu Asp Lys Glu Ile Leu Glu Glu Leu
1           5           10           15
Lys Glu Leu Ser Glu Trp Gln Lys Arg Asn Gln Glu Tyr Leu Lys Lys
          20          25          30
Lys Ala Glu Glu Glu Ala Ala Leu Ala Glu Glu Lys Glu Lys Glu Arg
          35          40          45
Gln Ala Arg Met Gly Glu Glu Ser Glu Lys Ser Glu Asp Lys Gln Asp
          50          55          60
Gln Glu Ser Glu Thr Asp Gln Glu Asp Ser Glu Ser Ala Lys Glu Glu
```


65					70					75				80
Ser	Glu	Glu	Lys	Val	Ala	Ser	Ser	Glu	Ala	Asp	Lys	Glu	Lys	Glu
				85					90					95
Lys	Glu	Glu	Ser	Glu	Ser	Lys	Glu	Lys	Glu	Gln	Asp	Lys	Lys	Leu
			100					105				110		
Ala	Lys	Lys	Ala	Thr	Lys	Glu	Lys	Pro	Ala	Lys	Ala	Lys	Ile	Pro
			115				120					125		Gly
Ile	His	Ile	Leu	Arg	Ala	Phe	Thr	Ile	Leu	Phe	Pro	Ser	Leu	Leu
	130					135					140			
Leu	Ile	Val	Ser	Ala	Tyr	Leu	Leu	Ser	Pro	Tyr	Ala	Thr	Met	Lys
145					150					155				160
Ile	Arg	Val	Glu	Gly	Thr	Val	Gln	Thr	Thr	Ala	Asp	Asp	Ile	Arg
			165					170						175
Ala	Ser	Gly	Ile	Gln	Asp	Ser	Asp	Tyr	Thr	Ile	Asn	Leu	Leu	Leu
			180					185						190
Lys	Ala	Lys	Tyr	Glu	Lys	Gln	Ile	Lys	Ser	Asn	Tyr	Trp	Val	Glu
			195				200					205		Ser
Ala	Gln	Leu	Val	Tyr	Gln	Phe	Pro	Thr	Lys	Ile	Thr	Ile	Lys	Val
	210					215					220			Lys
Glu	Tyr	Asp	Ile	Val	Ala	Tyr	Tyr	Ile	Ser	Gly	Glu	Asn	His	Tyr
225					230					235				240
Ile	Leu	Ser	Ser	Gly	Gln	Leu	Glu	Thr	Ser	Ser	Val	Ser	Leu	Asn
				245					250					255
Leu	Pro	Glu	Thr	Tyr	Leu	Ser	Val	Leu	Phe	Asn	Asp	Ser	Glu	Gln
			260					265					270	Ile
Lys	Val	Phe	Val	Ser	Glu	Leu	Ala	Gln	Ile	Ser	Pro	Glu	Leu	Lys
		275					280					285		Ala
Thr	Ile	Gln	Lys	Val	Glu	Leu	Ala	Pro	Ser	Lys	Val	Thr	Ser	Asp
	290					295					300			Leu
Ile	Arg	Leu	Thr	Met	Asn	Asp	Ser	Asp	Glu	Val	Leu	Val	Pro	Leu
305					310					315				320
Glu	Met	Ser	Lys	Lys	Leu	Pro	Tyr	Tyr	Ser	Lys	Ile	Lys	Pro	Gln
			325						330					335
Ser	Glu	Pro	Ser	Val	Val	Asp	Met	Glu	Ala	Gly	Ile	Tyr	Ser	Tyr
			340					345					350	Thr
Val	Ala	Asp	Lys	Leu	Ile	Met	Glu	Ala	Glu	Glu	Lys	Ala	Lys	Gln
		355					360					365		Glu
Ala	Lys	Glu	Ala	Glu	Lys	Lys	Gln	Glu	Glu	Glu	Gln	Lys	Lys	Gln
	370					375					380			Glu
Glu	Glu	Ser	Asn	Arg	Asn	Gln	Thr	Thr	Gln	Arg	Ser	Ser	Arg	Arg
385				390					395					

(2) INFORMATION FOR SEQ ID NO:3899:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...202

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3899:

Leu	Ala	Lys	Glu	Thr	Asn	Phe	Ala	Lys	Phe	Asp	Ala	Thr	Val	Glu	Val
1				5					10					15	
Ala	Tyr	Asn	Leu	Asn	Ile	Asp	Val	Lys	Lys	Ala	Asp	Gln	Gln	Ile	Leu
			20					25					30		
Cys	Gly	Ala	Met	Val	Leu	Pro	Asn	Gly	Thr	Gly	Lys	Thr	Ser	Arg	Val
		35					40					45			
Leu	Val	Phe	Ala	Arg	Gly	Ala	Lys	Ala	Glu	Glu	Ala	Lys	Ala	Ala	Gly
	50					55					60				
Ala	Asp	Phe	Val	Gly	Glu	Asp	Asp	Leu	Val	Ala	Lys	Ile	Asn	Asp	Gly
65					70					75				80	
Trp	Leu	Asp	Phe	Asp	Val	Val	Ile	Ala	Thr	Pro	Asp	Met	Met	Ala	Leu
			85						90					95	
Val	Gly	Arg	Leu	Gly	Arg	Val	Leu	Gly	Pro	Arg	Asn	Leu	Met	Pro	Asn
		100						105					110		
Pro	Lys	Thr	Gly	Thr	Val	Thr	Met	Asp	Val	Ala	Lys	Ala	Val	Glu	Glu
		115					120					125			
Ser	Lys	Gly	Gly	Lys	Ile	Thr	Tyr	Arg	Ala	Asp	Arg	Ala	Gly	Asn	Val
	130					135					140				
Gln	Ala	Ile	Ile	Gly	Lys	Val	Ser	Phe	Glu	Ala	Glu	Lys	Leu	Val	Glu
145					150					155					160
Asn	Phe	Lys	Ala	Phe	Asn	Glu	Thr	Ile	Gln	Lys	Ala	Lys	Pro	Ala	Thr
			165						170					175	
Ala	Lys	Gly	Thr	Tyr	Val	Thr	Asn	Leu	Thr	Ile	Thr	Thr	Thr	Gln	Gly
			180					185						190	
Val	Gly	Ile	Lys	Val	Asp	Val	Asn	Ser	Leu						
		195					200								

(2) INFORMATION FOR SEQ ID NO:3900:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 290 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...290

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3900:

Val	Glu	Lys	Glu	Met	Glu	Leu	Phe	Met	Lys	Ile	Thr	Asn	Tyr	Glu	Ile
1				5					10					15	
Tyr	Lys	Leu	Lys	Lys	Ser	Gly	Leu	Thr	Asn	Gln	Gln	Ile	Leu	Lys	Val
		20						25					30		
Leu	Glu	Tyr	Gly	Glu	Asn	Val	Asp	Gln	Glu	Leu	Leu	Leu	Gly	Asp	Ile

35	40	45
Ala Asp Ile Ser Gly Cys Arg Asn Pro Ala Val Phe Met Glu Arg Tyr		
50	55	60
Phe Gln Ile Asp Asp Ala His Leu Ser Lys Glu Phe Gln Lys Phe Pro		
65	70	75
Ser Phe Ser Ile Leu Asp Asp Cys Tyr Pro Trp Asp Leu Ser Glu Ile		
85	90	95
Tyr Asp Ala Pro Val Leu Leu Phe Tyr Lys Gly Asn Leu Asp Leu Leu		
100	105	110
Lys Phe Pro Lys Val Ala Val Val Gly Ser Arg Ala Cys Ser Lys Gln		
115	120	125
Gly Ala Lys Ser Val Glu Lys Val Ile Gln Gly Leu Glu Asn Glu Leu		
130	135	140
Val Ile Val Ser Gly Leu Ala Lys Gly Ile Asp Thr Ala Ala His Met		
145	150	155
Ala Ala Leu Gln Asn Gly Gly Lys Thr Ile Ala Val Ile Gly Thr Gly		
165	170	175
Leu Asp Val Phe Tyr Pro Lys Ala Asn Lys Arg Leu Gln Asp Tyr Ile		
180	185	190
Gly Asn Asp His Leu Val Leu Ser Glu Tyr Gly Pro Gly Glu Gln Pro		
195	200	205
Leu Lys Phe His Phe Pro Ala Arg Asn Arg Ile Ile Ala Gly Leu Cys		
210	215	220
Arg Gly Val Ile Val Ala Glu Ala Lys Met Arg Ser Gly Ser Leu Ile		
225	230	235
Thr Cys Glu Arg Ala Met Glu Glu Gly Arg Asp Val Phe Ala Ile Pro		
245	250	255
Gly Ser Ile Leu Asp Gly Leu Ser Asp Gly Cys His His Leu Ile Gln		
260	265	270
Glu Gly Ala Lys Leu Val Thr Ser Gly Gln Asp Val Leu Ala Glu Phe		
275	280	285
Glu Phe		
290		

(2) INFORMATION FOR SEQ ID NO:3901:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 208 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...208
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3901:

Lys Glu Lys Glu Val Leu Gln Met Ala Ile Ile Leu Pro Glu Leu Pro
1 5 10 15
Tyr Ala Tyr Asp Ala Leu Glu Pro Tyr Ile Asp Ala Glu Thr Met His

		20					25				30				
Leu	His	His	Asp	Lys	His	His	Gln	Thr	Tyr	Val	Asn	Asn	Ala	Asn	Ala
		35					40					45			
Ala	Leu	Glu	Lys	His	Pro	Glu	Ile	Gly	Glu	Asp	Leu	Glu	Ala	Leu	Leu
		50					55					60			
Ala	Asp	Val	Glu	Ser	Ile	Pro	Ala	Asp	Ile	Arg	Gln	Ala	Leu	Ile	Asn
65					70					75					80
Asn	Gly	Gly	Gly	His	Leu	Asn	His	Ala	Leu	Phe	Trp	Glu	Leu	Met	Thr
				85					90					95	
Pro	Glu	Lys	Thr	Ala	Pro	Ser	Ala	Glu	Leu	Ala	Ala	Ala	Ile	Asp	Ala
			100					105					110		
Thr	Phe	Gly	Ser	Phe	Glu	Glu	Phe	Gln	Ala	Ala	Phe	Thr	Ala	Ala	Ala
		115					120					125			
Thr	Thr	Arg	Phe	Gly	Ser	Gly	Trp	Ala	Trp	Leu	Val	Val	Asn	Lys	Glu
		130				135					140				
Gly	Lys	Leu	Glu	Val	Thr	Ser	Thr	Ala	Asn	Gln	Asp	Thr	Pro	Ile	Ser
145					150					155					160
Glu	Gly	Lys	Lys	Pro	Ile	Leu	Gly	Leu	Asp	Val	Trp	Glu	His	Ala	Tyr
				165					170					175	
Tyr	Val	Lys	Tyr	Arg	Asn	Val	Arg	Pro	Asp	Tyr	Ile	Lys	Ala	Phe	Phe
			180					185					190		
Ser	Val	Ile	Asn	Trp	Asn	Lys	Val	Asp	Glu	Leu	Tyr	Ala	Ala	Ala	Lys
		195					200					205			

(2) INFORMATION FOR SEQ ID NO:3902:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...302

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3902:

Asn	Arg	Lys	Asp	Lys	Asn	Thr	Gln	Ile	Leu	Val	His	Ile	Cys	Lys	Val
1				5					10					15	
Asn	Ile	Thr	Arg	Ile	Tyr	Lys	Val	Tyr	Arg	Gly	Arg	Ser	Ile	Met	Ser
			20					25					30		
Asp	Arg	Lys	Asn	Met	Lys	Leu	Phe	Ala	Leu	Asn	Ser	Asn	Gln	Glu	Ile
		35					40					45			
Ala	Gln	Lys	Ile	Ala	Gln	Ala	Val	Gly	Val	Pro	Leu	Gly	Lys	Leu	Ser
		50				55					60				
Ser	Arg	Gln	Phe	Ser	Asp	Gly	Glu	Ile	Gln	Val	Asn	Ile	Glu	Glu	Ser
65				70						75					80
Val	Arg	Gly	Tyr	Asp	Val	Tyr	Ile	Ile	Gln	Ser	Thr	Ser	Phe	Pro	Val
			85					90					95		
Asn	Asn	His	Leu	Met	Glu	Leu	Leu	Ile	Met	Val	Asp	Ala	Cys	Val	Arg

Arg	Leu	Asn	Trp	Ile	Ile	Leu	Leu	Leu	Phe	Ala	Ser	Val	Leu	Gly	Val
		20						25					30		
Thr	Phe	Tyr	Leu	Asn	Ser	Gln	Thr	Ala	Asn	Ser	His	Ser	Leu	Glu	Ser
		35				40						45			
Arg	Leu	Glu	Ser	Arg	Ile	Ala	Ala	Asn	Glu	Arg	Ala	Ile	Asn	Glu	Asn
		50			55						60				
Glu	Ala	Lys	Leu	Ser	Gln	Met	Ser	Asp	Thr	Ser	Ser	Glu	Glu	Tyr	Gln
65					70					75					80
Phe	Ala	Lys	Ser	Asn	Leu	Glu	Leu	Gln	Lys	Asn	Leu	Leu	Lys	Arg	Lys
			85						90					95	
Thr	Glu	Ile	Leu	Thr	Leu	Leu	Lys	Glu	Gly	Arg	Trp	Lys	Glu	Ala	Tyr
			100					105					110		
Tyr	Leu	Gln	Trp	Gln	Asp	Glu	Glu	Lys	Asn	Tyr	Glu	Phe	Val	Ser	Asn
		115				120						125			
Asp	Pro	Thr	Ala	Ser	Ser	Gly	Leu	Lys	Met	Gly	Val	Asp	Arg	Glu	Arg
		130				135					140				
Lys	Ile	Tyr	Gln	Ala	Leu	Tyr	Pro	Leu	Asn	Ile	Lys	Ala	His	Thr	Leu
145					150					155					160
Glu	Phe	Pro	Thr	His	Gly	Ile	Asp	Gln	Ile	Ile	Trp	Ile	Leu	Glu	Ala
				165					170					175	
Ile	Ile	Pro	Ser	Leu	Phe	Val	Val	Ala	Ile	Ile	Phe	Met	Leu	Thr	Gln
			180					185					190		
Leu	Phe	Ala	Glu	Arg	Tyr	Gln	Asn	His	Leu	Asp	Thr	Ala	His	Leu	Tyr
		195				200						205			
Pro	Val	Ser	Lys	Val	Thr	Phe	Ala	Met	Ser	Ser	Leu	Gly	Val	Gly	Val
		210				215						220			
Gly	Tyr	Val	Thr	Val	Leu	Phe	Ile	Gly	Ile	Cys	Gly	Phe	Ser	Phe	Leu
225					230					235					240
Val	Gly	Ser	Leu	Ile	Ser	Gly	Phe	Gly	Gln	Leu	Asp	Tyr	Pro	Tyr	Pro
			245						250				255		
Ile	Tyr	Ser	Leu	Val	Lys	Gln	Glu	Val	Thr	Ile	Gly	Lys	Met	Gln	Asp
			260					265					270		
Val	Leu	Phe	Pro	Ser	Leu	Leu	Leu	Ala	Phe	Leu	Ala	Phe	Ile	Val	Ile
		275						280				285			
Val	Glu	Val	Val	Tyr	Leu	Ile	Ala	Tyr	Phe	Phe	Lys	Gln	Lys	Met	Pro
		290				295					300				
Val	Leu	Phe	Leu	Ser	Leu	Ile	Gly	Ile	Val	Gly	Leu	Leu	Phe	Gly	Ile
305					310					315					320
Gln	Thr	Ile	Gln	Pro	Leu	Gln	Lys	Ile	Ala	His	Leu	Ile	Pro	Phe	Thr
			325						330				335		
Tyr	Leu	Arg	Ser	Val	Glu	Ile	Leu	Ser	Gly	Arg	Leu	Pro	Lys	Gln	Ile
			340					345					350		
Asp	Asn	Val	Asp	Leu	Asn	Trp	Ser	Met	Gly	Met	Val	Leu	Leu	Pro	Cys
		355				360						365			
Leu	Ile	Ile	Phe	Leu	Leu	Leu	Gly	Ile	Leu	Phe	Ile	Glu	Arg	Trp	Gly
		370				375					380				
Ser	Ser	Gln	Lys	Lys	Arg	Ile	Phe								
385					390										

(2) INFORMATION FOR SEQ ID NO:3905:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 634 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...634

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3905:

Ile	Met	Lys	Glu	Glu	Arg	Arg	Gln	Phe	Phe	Glu	Arg	Ile	Asp	Gly	Asn
1				5					10					15	
Gln	Cys	Arg	Asp	Tyr	Ile	Leu	Ser	His	Cys	Ser	Lys	Asp	Tyr	Glu	Lys
			20					25					30		
Val	Lys	Ser	Ser	Leu	Glu	Arg	Leu	Met	Asp	Asn	Arg	Phe	Met	Phe	Asp
		35					40					45			
Ser	Pro	Trp	Asp	Met	Glu	Pro	Cys	Ser	Lys	Ile	His	Gln	Asn	Gln	Pro
	50					55					60				
Met	Val	Trp	Asp	Gln	Val	Phe	Glu	Asp	Asp	Pro	Glu	Trp	Ala	Tyr	Met
65					70					75					80
Leu	Asn	Arg	Gln	Glu	Tyr	Leu	Leu	Gln	Phe	Met	Ile	Gly	Tyr	Val	Val
				85					90					95	
Glu	Gly	Asp	Lys	Asp	Tyr	Ile	Gln	Lys	Cys	Lys	Phe	Phe	Leu	Phe	Asp
			100					105					110		
Trp	Ile	Glu	Gln	Val	Arg	Glu	Phe	Ser	Pro	Gln	Ser	Leu	Met	Thr	Arg
		115					120					125			
Thr	Leu	Asp	Thr	Gly	Ile	Arg	Ser	Phe	Thr	Trp	Leu	Lys	Leu	Leu	Leu
	130					135					140				
Leu	Leu	Leu	Lys	Phe	Asp	Leu	Leu	Glu	Glu	Lys	Glu	Leu	Glu	Lys	Ile
145					150					155					160
Leu	Val	Ser	Leu	Glu	Lys	Gln	Ile	Asp	Phe	Met	Lys	Ser	Tyr	Tyr	Arg
				165					170					175	
Ala	Lys	Tyr	Thr	Leu	Ser	Asn	Trp	Gly	Ile	Leu	Gln	Thr	Ile	Pro	Met
			180					185					190		
Leu	Ala	Ile	Tyr	His	Phe	Phe	Ser	Asp	Lys	Met	Asp	Leu	Glu	Glu	Ala
	195						200					205			
Tyr	His	Phe	Ala	Ser	Glu	Glu	Leu	Lys	Gln	Gln	Ile	Glu	Thr	Gln	Ile
	210					215					220				
Leu	Gly	Asp	Gly	Ser	Gln	Phe	Glu	Gln	Ser	Ile	Leu	Tyr	His	Val	Glu
225					230					235					240
Val	Tyr	Lys	Ala	Leu	Leu	Asp	Leu	Cys	Leu	Leu	Leu	Pro	Asp	Leu	Gln
				245					250					255	
Asp	Ser	Tyr	Gln	Glu	Leu	Leu	Glu	Lys	Met	Ala	Thr	Tyr	Ile	Gln	Met
			260					265					270		
Met	Thr	Gly	Leu	Asp	Gly	Arg	Thr	Leu	Ala	Phe	Gly	Asp	Ser	Asp	Ser
		275					280					285			
Thr	Glu	Thr	Thr	Glu	Met	Leu	Ser	Leu	Ser	Ala	Val	Val	Leu	Asn	Lys
	290					295					300				
Glu	Asp	Leu	Leu	Asn	Gly	Leu	Asp	Val	Lys	Val	Asp	Leu	Leu	Ser	Leu
305					310					315					320
Leu	Phe	Leu	Gly	Arg	Glu	Lys	Val	Lys	Arg	Leu	Gln	Glu	Phe	Glu	Arg
				325					330					335	
Arg	Ala	Trp	Gln	Pro	Lys	Ser	Met	Ile	Phe	Glu	Asp	Ser	Gly	His	Val
			340					345					350		

Cys	Ile	Lys	Asp	Glu	His	Arg	Tyr	Leu	Phe	Phe	Lys	Asn	Gly	Pro	Leu	355	360	365
Gly	Ser	Ala	His	Ser	His	Ser	Asp	Glu	Asn	Ser	Phe	Cys	Leu	Gln	Tyr	370	375	380
Gln	Gly	Gln	Pro	Ile	Phe	Ile	Asp	Ala	Gly	Arg	Tyr	Ser	Tyr	Arg	Glu	385	390	395
Ile	Tyr	Glu	Arg	Tyr	Leu	Leu	Lys	Ser	Ala	Trp	Ser	His	Ser	Thr	Cys	405	410	415
Ile	Val	Asp	Gly	Lys	Ala	Pro	Glu	Arg	Ile	Thr	Gly	Ser	Trp	Glu	Tyr	420	425	430
Glu	Tyr	Tyr	Pro	His	Ser	Leu	Phe	Cys	His	His	Lys	Glu	Arg	Glu	Gly	435	440	445
Val	His	Tyr	Ile	Glu	Gly	Ala	Tyr	Trp	Ser	Ala	Glu	Pro	Asp	Leu	Pro	450	455	460
Tyr	Leu	His	Lys	Arg	Lys	Ile	Leu	Met	Leu	Val	Glu	Asp	Val	Trp	Leu	465	470	475
Leu	Val	Asp	Asp	Ile	Arg	Cys	Gln	Gly	Gln	His	Glu	Ala	Leu	Thr	Gln	485	490	495
Phe	Ile	Leu	Asp	Lys	Asp	Val	Thr	Tyr	Gln	Asp	Gly	Lys	Ile	Asn	Gln	500	505	510
Leu	Arg	Leu	Trp	Ser	Glu	Val	Asp	Phe	Asp	Leu	Glu	Asp	Thr	Ile	Ile	515	520	525
Ser	Pro	Lys	Tyr	Asn	Glu	Leu	Glu	Arg	Ser	Ser	Lys	Leu	Thr	Lys	Arg	530	535	540
Gln	Phe	Phe	Glu	Asn	Gln	Met	Leu	Asp	Tyr	Thr	Ile	Ile	Ala	His	Glu	545	550	555
Ser	Phe	Glu	Ile	Ile	Arg	His	Ser	Val	Tyr	Gln	Thr	Asp	Asp	Arg	Glu	565	570	575
Val	Glu	Asn	Ala	Leu	Ala	Phe	Glu	Val	Lys	Asn	Asp	Glu	Thr	Asp	Lys	580	585	590
Leu	Ile	Leu	Leu	Leu	Ser	Glu	Asp	Ile	Cys	Val	Gly	Glu	Lys	Leu	Cys	595	600	605
Leu	Val	Asp	Gly	Thr	Lys	Met	Arg	Gly	Lys	Cys	Leu	Val	Tyr	Asp	Lys	610	615	620
Ile	Asn	Glu	Arg	Met	Ile	Arg	Leu	Gln	Cys							625	630	

(2) INFORMATION FOR SEQ ID NO:3906:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...726

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3906:

Met	Met	Lys	Asp	Thr	Phe	Lys	Asn	Val	Leu	Ser	Phe	Glu	Phe	Trp	Gln
1				5					10					15	
Lys	Phe	Gly	Lys	Ala	Leu	Met	Val	Val	Ile	Ala	Val	Met	Pro	Ala	Ala
			20					25					30		
Gly	Leu	Met	Ile	Ser	Ile	Gly	Lys	Ser	Ile	Val	Met	Ile	Asn	Pro	Thr
		35					40					45			
Phe	Thr	Pro	Leu	Val	Ile	Thr	Gly	Gly	Ile	Leu	Glu	Gln	Ile	Gly	Trp
	50					55					60				
Gly	Val	Ile	Gly	Asn	Leu	His	Ile	Leu	Phe	Ala	Leu	Ala	Ile	Gly	Gly
65				70					75						80
Ser	Trp	Ala	Lys	Glu	Arg	Ala	Gly	Gly	Ala	Phe	Ala	Ala	Gly	Leu	Ala
			85						90					95	
Phe	Ile	Leu	Ile	Asn	Arg	Ile	Thr	Gly	Thr	Ile	Phe	Gly	Val	Ser	Gly
			100					105					110		
Asp	Met	Leu	Lys	Asn	Pro	Asp	Ala	Met	Val	Thr	Thr	Phe	Phe	Gly	Gly
		115					120					125			
Ser	Ile	Lys	Val	Ala	Asp	Tyr	Phe	Ile	Ser	Val	Leu	Glu	Ala	Pro	Ala
	130					135					140				
Leu	Asn	Met	Gly	Val	Phe	Val	Gly	Ile	Ile	Ser	Gly	Phe	Val	Gly	Ala
145					150					155					160
Thr	Ala	Tyr	Asn	Lys	Tyr	Tyr	Asn	Phe	Arg	Lys	Leu	Pro	Asp	Ala	Leu
			165						170					175	
Ser	Phe	Phe	Asn	Gly	Lys	Arg	Phe	Val	Pro	Phe	Val	Val	Ile	Leu	Arg
			180					185					190		
Ser	Ala	Ile	Ala	Ala	Ile	Leu	Leu	Ala	Ala	Phe	Trp	Pro	Val	Val	Gln
		195					200					205			
Thr	Gly	Ile	Asn	Asn	Phe	Gly	Ile	Trp	Ile	Ala	Asn	Ser	Gln	Glu	Thr
	210					215					220				
Ala	Pro	Ile	Leu	Ala	Pro	Phe	Leu	Tyr	Gly	Thr	Leu	Glu	Arg	Leu	Leu
225					230					235					240
Leu	Pro	Phe	Gly	Leu	His	His	Met	Leu	Thr	Ile	Pro	Met	Asn	Tyr	Thr
			245						250					255	
Ala	Leu	Gly	Gly	Thr	Tyr	Asp	Ile	Leu	Thr	Gly	Ala	Ala	Lys	Gly	Thr
			260					265					270		
Gln	Val	Phe	Gly	Gln	Asp	Pro	Leu	Trp	Leu	Ala	Trp	Val	Thr	Asp	Leu
	275						280					285			
Val	Asn	Leu	Lys	Gly	Thr	Asp	Ala	Ser	Gln	Tyr	Gln	His	Leu	Leu	Asp
	290					295					300				
Thr	Val	His	Pro	Ala	Arg	Phe	Lys	Val	Gly	Gln	Met	Ile	Gly	Ser	Phe
305					310					315					320
Gly	Ile	Leu	Met	Gly	Val	Ile	Val	Ala	Ile	Tyr	Arg	Asn	Val	Asp	Ala
			325						330					335	
Asp	Lys	Lys	His	Lys	Tyr	Lys	Gly	Met	Met	Ile	Ala	Thr	Ala	Leu	Ala
			340					345					350		
Thr	Phe	Leu	Thr	Gly	Val	Thr	Glu	Pro	Ile	Glu	Tyr	Met	Phe	Met	Phe
		355					360					365			
Ile	Ala	Thr	Pro	Met	Tyr	Leu	Val	Tyr	Ser	Leu	Val	Gln	Gly	Ala	Ala
	370					375					380				
Phe	Ala	Met	Ala	Asp	Val	Val	Asn	Leu	Arg	Met	His	Ser	Phe	Gly	Ser
385					390					395					400
Ile	Glu	Phe	Leu	Thr	Arg	Thr	Pro	Ile	Ala	Ile	Ser	Ala	Gly	Ile	Gly
			405						410					415	
Met	Asp	Ile	Val	Asn	Phe	Val	Trp	Val	Thr	Val	Leu	Phe	Ala	Val	Ile
		420						425					430		
Met	Tyr	Phe	Ile	Ala	Asn	Phe	Met	Ile	Gln	Lys	Phe	Asn	Tyr	Ala	Thr
	435						440					445			
Pro	Gly	Arg	Asn	Gly	Asn	Tyr	Glu	Thr	Ala	Glu	Gly	Ser	Glu	Glu	Thr